

MOLECULAR HEPATOTOXICOLOGY MODELING**RELATED APPLICATIONS**

[0001] This application claims priority to U.S. Provisional Applications 60/364,045 filed on March 15, 2002, 60/364,055 filed on March 15, 2002, and 60/436,643 filed on December 30, 2002, and is a continuation-in-part of pending U.S. Application 10/060,087 filed January 31, 2002. In addition, this application is related to U.S. Provisional Applications 60/222,040, 60/244,880, 60/290,029, 60/290,645, 60/292,336, 60/295,798, 60/297,457, 60/298,884, 60/303,459, and 60/331,273, as well as to pending U.S. Application 09/917,800, filed July 31, 2001, all of which are herein incorporated by reference in their entirety.

SEQUENCE LISTING SUBMISSION ON COMPACT DISC

[0002] The Sequence Listing submitted concurrently herewith on compact disc is herein incorporated by reference in its entirety. Four copies of the Sequence Listing, one on each of four compact discs are provided. Copies 1, 2, and 3 are identical. Copies 1, 2, and 3 are also identical to the CRF. Each electronic copy of the Sequence Listing was created on January 30, 2003 with a file size of 5795 KB. The file names are as follows: Copy 1- gl5038us01.txt; Copy 2- gl5038us01.txt; Copy 3- gl5038us01.txt; and CRF- gl5038us01.txt.

BACKGROUND OF THE INVENTION

[0003] The need for methods of assessing the toxic impact of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism has led to the development of procedures which utilize living organisms as biological monitors. The simplest and most convenient of these systems utilize unicellular microorganisms such as yeast and bacteria, since they are most easily maintained and manipulated. Unicellular screening systems also often use easily detectable changes in phenotype to monitor the effect of test compounds on the cell. Unicellular organisms, however, are inadequate models for estimating the potential effects of many compounds on complex multicellular animals, as they do not have the ability to carry out biotransformations to the extent or at levels found in higher organisms.

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[0004] The biotransformation of chemical compounds by multicellular organisms is a significant factor in determining the overall toxicity of agents to which they are exposed. Accordingly, multicellular screening systems may be preferred or required to detect the toxic effects of compounds. The use of multicellular organisms as toxicology screening tools has been significantly hampered, however, by the lack of convenient screening mechanisms or endpoints, such as those available in yeast or bacterial systems. In addition, previous attempts to produce toxicology prediction systems have failed to provide the necessary modeling data and statistical information to accurately predict toxic responses (*e.g.*, WO 00/12760, WO 00/47761, WO 00/63435, WO 01/32928 and WO 01/38579).

SUMMARY OF THE INVENTION

[0005] The present invention is based on the elucidation of the global changes in gene expression in tissues or cells exposed to known toxins, in particular hepatotoxins, as compared to unexposed tissues or cells as well as the identification of individual genes that are differentially expressed upon toxin exposure.

[0006] In various aspects, the invention includes methods of predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, and predicting the hepatotoxicity of a compound. The invention also includes methods of identifying agents that modulate the onset or progression of a toxic response. Also provided are methods of predicting the cellular pathways that a compound modulates in a cell. The invention includes methods of identifying agents that modulate protein activities.

[0007] In a further aspect, the invention provides probes comprising sequences that specifically hybridize to genes in Tables 1-5WWW. Also provided are solid supports comprising at least two of the previously mentioned probes. The invention also includes a computer system that has a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes in Tables 1-5WWW.

[0008] The invention further provides a core set of genes in Tables 5A-5WWW from which probes can be made and attached to solid supports. These core genes serve as a preferred set of markers of liver toxicity and can be used with the methods of the

invention to predict or monitor a toxic effect of a compound or to modulate the onset or progression of a toxic response.

DETAILED DESCRIPTION

[0009] Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.* through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death are often characterized by the variations in the expression levels of groups of genes.

[0010] Changes in gene expression are also associated with the effects of various chemicals, drugs, toxins, pharmaceutical agents and pollutants on an organism or cells. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes after exposure to an agent could lead to tumorigenesis or hyperplastic growth of cells (Marshall (1991) *Cell* 64: 313-326; Weinberg (1991) *Science* 254:1138-1146). Thus, changes in the expression levels of particular genes (*e.g.* oncogenes or tumor suppressors) may serve as signposts for the presence and progression of toxicity or other cellular responses to exposure to a particular compound.

[0011] Monitoring changes in gene expression may also provide certain advantages during drug screening and development. Often drugs are screened for the ability to interact with a major target without regard to other effects the drugs have on cells. These cellular effects may cause toxicity in the whole animal, which prevents the development and clinical use of the potential drug.

[0012] The present inventors have examined tissue from animals exposed to the known hepatotoxins which induce detrimental liver effects, to identify global changes in gene expression induced by these compounds. These global changes in gene expression, which can be detected by the production of gene expression profiles, provide useful toxicity markers that can be used to monitor toxicity and/or toxicity progression by a test compound. Some of these markers may also be used to monitor or detect various disease or physiological states, disease progression, drug efficacy and drug metabolism.

Identification of Toxicity Markers

[0013] To evaluate and identify gene expression changes that are predictive of toxicity, studies using selected compounds with well characterized toxicity have been conducted by the present inventors to catalogue altered gene expression during exposure *in vivo*. In the present study, acetaminophen, 2-acetylaminofluorene (2-AAF), acyclovir, ANIT, AY-25329, BI liver toxin, chloroform, bicalutamide, carbon tetrachloride, chloroform, CI-1000, clofibrate, colchicine, CPA, diclofenac, diflunisal, dimethylnitrosamine (DMN), dioxin, 17 α -ethinylestradiol, gemfibrozil, hydrazine, indomethacin, LPS, menadione, phenobarbital, tacrine, thioacetamide, valproate, Wy-14643, and zileuton were selected as known hepatotoxins.

[0014] Aromatic and aliphatic isothiocyanates are commonly used soil fumigants and pesticides (Shaaya *et al.* (1995) *Pesticide Science* 44(3):249-253; Cairns *et al.* (1988) *J Assoc Official Analytical Chemists* 71(3):547-550). These compounds are also environmental hazards, because they remain as toxic residues in plants (Cerny *et al.* (1996) *J Agricultural and Food Chemistry* 44(12):3835-3839) and because they are released from the soil into the surrounding air (Gan *et al.* (1998) *J Agricultural and Food Chemistry* 46(3):986-990).

[0015] Exposure to α -naphthylisothiocyanate (ANIT) has been shown to increase serum levels of total bilirubin, alkaline phosphatase, serum glutamic oxaloacetic transaminase and serum glutamic pyruvic transaminase, while total bile flow was reduced, all of which are indications of severe biliary dysfunction. ANIT also induces jaundice and cholestasis (the condition caused by failure to secrete bile, resulting in plasma accumulation of bile substances, liver cell necrosis and bile duct obstruction) (Tanaka *et al.* (1993) *Clinical and Experimental Pharmacology and Physiology* 20:543-547). ANIT fails to produce extensive necrosis, but was found to produce inflammation and edema in the portal tract of the liver (Maziasa *et al.* (1991) *Toxicol Appl Pharmacol* 110:365-373). ANIT-induced hepatotoxicity may also be characterized by cholangiolitic hepatitis and bile duct damage. Acute hepatotoxicity caused by ANIT in rats is manifested as neutrophil-dependent necrosis of bile duct epithelial cells (BDECs) and hepatic parenchymal cells. These changes mirror the cholangiolitic hepatitis found in humans (Hill (1999) *Toxicol Sci* 47:118-125).

[0016] Histological changes include an infiltration of polymorphonuclear neutrophils and elevated number of apoptotic hepatocytes (Calvo *et al.* (2001) *J Cell Biochem*

80(4):461-470). Other known hepatotoxic effects of exposure to ANIT include a damaged antioxidant defense system, decreased activities of superoxide dismutase and catalase (Ohta *et al.* (1999) *Toxicology* 139(3):265-275), and the release of proteases from the infiltrated neutrophils, alanine aminotransferase, cathepsin G, elastase, which mediate hepatocyte killing (Hill *et al.* (1998) *Toxicol Appl Pharmacol* 148(1):169-175).

[0017] The effects of the model compound 2-acetylaminofluorene (2-AAF), a strong carcinogen and liver tumor inducer, have been studied in rat livers. 2-AAF has been shown to cause changes in the mitochondria which trigger apoptosis and regenerative cell proliferation. These in turn, cause cirrhosis-like changes in the liver. Exposure to 2-AAF also produces elevated levels of ALT and AST, hemoglobin adducts and foci containing the placental form of glutathione S-transferase. Chromosome aberrations, micronuclei and sister-chromatid exchanges have also been observed (Bitsch *et al.* (2000) *Toxicol Sci* 55(1):44-51; Lorenzini *et al.* (1996) *Carcinogenesis* 17:1323-1329; Sawada *et al.* (1991) *Mutat Res* 251(1):59-69).

[0018] Acyclovir (9-[(2-hydroxyethyl) methyl] guanine, Zovirax®), an anti-viral guanosine analogue, is used to treat herpes simplex virus (HSV), varicella zoster virus (VZV) and Epstein-Barr virus (EBV) infections. The most common adverse effect of acyclovir treatment is damage to various parts of the kidney, particularly the renal tubules, although the drug can also cause damage to the liver and nervous system. Crystalluria, or the precipitation of crystals of acyclovir in the lumina of the renal tubules can occur (Fogazzi (1996) *Nephrol Dial Transplant* 11(2):379-387). If the drug crystallizes in the renal collecting tubules, obstructive nephropathy and tubular necrosis can result (Richardson (2000) *Vet Hum Toxicol* 42(6):370-371). Examination of biopsy tissues from affected patients showed dilation of the proximal and distal renal tubules, with loss of the brush border, flattening of the lining cells and focal nuclear loss (Becker *et al.* (1993) *Am J Kidney Dis* 22(4):611-615).

[0019] Liver damage in patients taking acyclovir is indicated clinically by abnormal liver function tests (http://www.hopkins-aids.edu/publications/book/ch6_acyclovir.html).

Adverse effects in the liver include hepatitis, hyperbilirubinemia and jaundice

(Physicians' Desk Reference, 56th ed., p. 1707, Medical Economics Co. Inc., Montvale, NJ, 2002), although findings of hepatotoxicity in animals have not yet been published. Studies by the present inventors on rats treated with acyclovir have found elevated serum levels of BUN and creatinine. Decreased levels of ALT, AST and triglycerides

(indicators of liver function) have also been found, but these may be attributed to kidney damage as well as to liver damage. While classic signs of hepatotoxicity in rats due to acyclovir administration have not been published, gene expression changes can be used to predict that the drug will be a liver toxin in humans.

[0020] Acetaminophen (APAP) is a widely used analgesic and antipyretic agent that is an effective substitute for aspirin. Although acetaminophen does not have anti-inflammatory properties, it is preferably given to patients with ulcers or patients in whom prolonged clotting times would not be desirable. It also preferably taken by people who do not tolerate aspirin well.

[0021] Acetaminophen is metabolized to *N*-acetyl-*p*-benzoquinoneimine (NAPQI) by *N*-hydroxylation in a cytochrome P450-mediated process. This highly reactive intermediate, which reacts with sulfhydryl groups in glutathione, and in other liver proteins following the depletion of glutathione, can cause centrilobular hepatic necrosis (particularly in zone 3), renal tubular necrosis, and hepatic and renal failure (Goodman and Gilman's The Pharmacological Basis of Therapeutics, Ninth Ed., Hardman *et al.*, eds., pp. 631-633, McGraw-Hill, New York, 1996; Chanda *et al.* (1995) *Hepatology* 21(2):477-486). Less serious side effects include skin rashes (erythemas and urticarias) and allergic reactions.

[0022] Upon treatment of rats with acetaminophen, hepatotoxicity can be observed 24 hours after dosing, as determined by statistically significant elevations of ALT and AST in the serum and by hepatocellular necrosis visualized at the light microscopic level (Hessel *et al.* (1996) *Braz J Med Biol Res* 29(6):793-796; Bruck *et al.* (1999) *Dig Dis Sci* 44(6):1228-1235). High, but non-lethal, doses of acetaminophen given to rats also produced elevated levels of genes involved in hepatic acute phase response and liver cell maintenance and repair: arginase, beta-fibrinogen, alpha 1-acid glycoprotein, alpha-tubulin, histone 3, TGF beta and cyclin d. Expression levels of genes regulated by the cell cycle were decreased (Tygstrup *et al.* (1996) *J Hepatol* 25(2):183-190; Tygstrup *et al.* (1997) *J Hepatol* 27(1):156-162). In mice, expression levels of genes that encode growth arrest and cell cycle regulatory proteins were increased, along with expression levels of stress-induced genes, transcription factor LRG-21, SOCS-2 (cytokine signaling repressor) and PAI-1 (plasminogen activator inhibitor-1) (Reilly *et al.* (2001) *Biochem Biophys Res Comm* 282(1):321-328).

[0023] **AY-25329**, a proprietary compound, is a phenothiazine that has been shown to be toxic in liver and in kidney tissue, where it can cause nephrosis. Phenothiazines are a class of psychoactive drugs that are used to treat schizophrenia, paranoia, mania, hyperactivity in children, some forms of senility, and anxiety (<http://www.encyclopedia.com/articlesnew/36591.html>). Side effects associated with prolonged use of these drugs are reduced blood pressure, Parkinsonism, reduction of motor activity, and visual impairment.

[0024] The present inventors have noted indications of liver and renal effects of **AY-25329** by changes in serum chemistry. As early as 6 hours after the first dose, statistically significant increases in serum levels of creatinine, BUN, ALT, triglycerides and cholesterol were observed. Most of these markers of renal and liver dysfunction remained altered throughout the 14 day study period. Light microscopic analysis revealed effects in the liver as early as 6 and 24 hours, as evidenced by an increased number of hepatocytic mitotic figures and decreased glycogen content. Following 14 days of repeated dosing, nephrosis and alterations in the peripheral lobes of the liver and in the cytoplasm of hepatocytes were evident in rats dosed with 250 mg/kg/day of **AY-25329**.

[0025] **BI liver toxin**, a model compound, produces cardiac changes (QT_C prolongation) in dogs and liver and cardiac changes in rats. Liver samples collected from rats over a four-week period showed that this compound induces sedation, lowers body weight, increases liver weight, and slightly increases serum levels of AST, ALP and BUN. Over a three-month period, cardiovascular effects are observed as well.

[0026] The toxicological profile of **bicalutamide**, a drug for treating prostate-cancer, is closely associated with the drug's non-steroidal anti-androgenic activity. Bicalutamide produces typical effects of an anti-androgen, including atrophy of the prostate, testis and seminal vesicles and Leydig cell hyperplasia resulting from inhibition of pituitary feedback by testosterone. Benign Leydig cell tumors and elevated levels of CYP3A1 were seen in rats, but not in humans, although liver toxicity in humans has been observed. Bicalutamide causes liver enlargement and is a mixed function oxidase inducer in rodents and dogs. These effects lead to thyroid hypertrophy and adenoma in the rat and hepatocellular carcinoma in the male mouse (Iswaran *et al.* (1997) *J Toxicol Sci* 22(2):75-88; Oh *et al.* (2002) *Urology* 60(3 Suppl 1):87-93; McKillop *et al.* (1998) *Xenobiotica* 28(5):465-478). In prostate cancer patients treated with bicalutamide,

elevated levels of the liver enzymes glutamic-oxalacetic transaminase (GOT), glutamic-pyruvic transaminase (GPT), alkaliphosphatase (AL-P) and gamma guanosine 5'-triphosphate (gamma-GTP) have been noted, along with breast pain, gynecomastia and hot flashes (Kotake *et al.* (1996) *Hinyokika Kyo* 42(2):143-153) .

[0027] The pathogenesis of acute **carbon tetrachloride (CCl₄)**-induced hepatotoxicity follows a well-characterized course in humans and experimental animals resulting in centrilobular necrosis and steatosis, followed by hepatic regeneration and tissue repair. Severity of the hepatocellular injury is also dose-dependent and may be affected by species, age, gender and diet.

[0028] Differences in susceptibility to CCl₄ hepatotoxicity are primarily related to the ability of the animal model to metabolize CCl₄ to reactive intermediates. CCl₄-induced hepatotoxicity is dependent on CCl₄ bioactivation to trichloromethyl free radicals by cytochrome P450 enzymes (CYP2E1), localized primarily in centrilobular hepatocytes. Formation of the free radicals leads to membrane lipid peroxidation and protein denaturation resulting in hepatocellular damage or death.

[0029] The onset of hepatic injury is rapid following acute administration of CCl₄ to male rats. Morphologic studies have shown cytoplasmic accumulation of lipids in hepatocytes within 1 to 3 hours of dosing, and by 5 to 6 hours, focal necrosis and hydropic swelling of hepatocytes are evident. Centrilobular necrosis and inflammatory infiltration peak by 24 to 48 hours post dose. The onset of recovery is also evident within this time frame by increased DNA synthesis and the appearance of mitotic figures. Removal of necrotic debris begins by 48 hours and is usually completed by one week, with full restoration of the liver by 14 days.

[0030] Increases in serum transaminase levels also parallel CCl₄-induced hepatic histopathology. In male Sprague Dawley (SD) rats, alanine aminotransferase (ALT) and aspartate aminotransferase (AST) levels increase within 3 hours of CCl₄ administration (0.1, 1, 2, 3, 4 mL/kg, ip; 2.5 mL/kg, po) and reach peak levels (approximately 5-10 fold increases) within 48 hours post dose. Significant increases in serum α -glutathione s-transferase (α -GST) levels have also been detected as early as 2 hours after CCl₄ administration (25 μ L/kg, po) to male SD rats.

[0031] At the molecular level, induction of the growth-related proto-oncogenes, c-fos and c-jun, is reportedly the earliest event detected in an acute model of CCl₄-induced

hepatotoxicity (Schiaffonato *et al.* (1997) *Liver* 17:183-191). Expression of these early-immediate response genes has been detected within 30 minutes of a single dose of CCl₄ to mice (0.05 -1.5 mL/kg, ip) and by 1 to 2 hours post dose in rats (2 mL/kg, po; 5 mL/kg,po) (Schiaffonato *et al.*, *supra*, and Hong *et al.*(1997) *Yonsei Medical J* 38:167-177). Similarly, hepatic c-myc gene expression is increased by 1 hour following an acute dose of CCl₄ to male SD rats (5 mL/kg, po) (Hong *et al.*, *supra*). Expression of these genes following exposure to CCl₄ is rapid and transient. Peak hepatic mRNA levels for c-fos, c-jun, and c-myc, after acute administration of CCl₄ have been reported at 1 to 2 hours, 3 hours, and 1 hour post dose, respectively.

[0032] The expression of tumor necrosis factor- α (TNF- α) is also increased in the livers of rodents exposed to CCl₄, and TNF- α has been implicated in initiation of the hepatic repair process. Pre-treatment with anti-TNF- α antibodies has been shown to prevent CCl₄-mediated increases in c-jun and c-fos gene expression, whereas administration of TNF- α induced rapid expression of these genes (Bruccoli *et al.* (1997) *Hepatology* 25:133-141). Up-regulation of transforming growth factor- β (TGF- β) and transforming growth factor receptors (TGF- β RII) later in the repair process (24 and 48 hours after CCl₄ administration) suggests that TGF- β may play a role in limiting the regenerative response by induction of apoptosis (Grasl-Kraupp *et al.* (1998) *Hepatology* 28:717-7126).

[0033] Chloroform (CHCl₃) is an obsolete anesthetic that was abandoned due to its hepatotoxicity. The pathogenesis of acute CHCl₃ - induced hepatotoxicity follows a well-characterized course in humans and experimental animals resulting in centrilobular necrosis and steatosis, followed by hepatic regeneration and tissue repair. Severity of the hepatocellular injury is dose-dependent and may be affected by the animal species, strain, age, gender, diet, vehicle and/or route of administration (Lilly *et al.* (1997) *Fund Appl Toxicol* 40:101-110 and Raymond *et al.* (1997) *J Toxicol Environ Health* 52:463-476).

[0034] Differences in susceptibility to CHCl₃ toxicity are considered related to differential metabolism. CHCl₃ - induced hepatotoxicity is primarily mediated by formation of reactive species, such as phosgene and trichloromethyl free radicals, by cytochrome P450 enzymes (CYP2E1). CHCl₃ hepatotoxicity is also increased by exposure to agents that induce cytochrome P450 (*i.e.*, ethanol, phenobarbital), and

deplete hepatic glutathione (GSH). Formation of the free radicals leads to membrane lipid peroxidation and protein denaturation resulting in hepatocellular damage or death.

[0035] Chronic administration of CHCl_3 to rodents induces an increased incidence of hepatic and renal carcinomas by a nongenotoxic-cytotoxic mode of action.

Carcinogenicity of CHCl_3 is considered secondary to chemically-induced cytotoxicity with subsequent compensatory cell proliferation, rather than to direct interaction of CHCl_3 or its metabolites with DNA.

[0036] The onset of hepatic toxicity is rapid following acute administration of CHCl_3 to male rats. Morphologic studies have shown cytoplasmic accumulation of lipids in hepatocytes within 1 to 3 hours of dosing, and by 5 to 6 hours, focal necrosis and hydropic swelling of hepatocytes are evident. Centrilobular necrosis and inflammatory infiltration peak by 24 to 48 hours post dose. The onset of recovery is also evident within this time frame by increased DNA synthesis and the appearance of mitotic figures. Removal of necrotic debris begins by 48 hours and is usually completed by one week, with full restoration of the liver by 14 days.

[0037] In studies on rats and mice, significant changes in clinical parameters included increased levels of BUN and serum creatinine and decreased levels of phosphatidylethanolamine and tissue glutathione (GSH). There is a strong correlation between the formation of the phospholipid adducts, GSH depletion and liver toxicity (Di Consiglio *et al.* (2001) *Toxicology* 159(1-2):43-53). Experiments on mice have shown that exposure to chloroform also increases the liver weight:body weight ratio and the proliferating cell nuclear antigen-labeling index. Decreased levels of 5-methylcytosine and of the methylated c-myc gene (associated with increased carcinogenic activity) were also found (Coffin *et al.* (2000) *Toxicol Sci* 58(2):243-252). Other studies on mice have noted that elevated levels of the P450 cytochromes, such as P450 2E1 and CYP2A5, are involved in cytotoxic metabolic conversions (Constan *et al.* (1999) *Toxicol Appl Pharmacol* 160(2):120-126; Camus-Randon *et al.* (1996) *Toxicol Appl Pharmacol* 138(1):140-148).

[0038] Studies of chloroform poisoning in humans have noted hepatocellular necrosis characterized by decreased levels of serum biomarkers (AST, ALT, alkaline phosphatase and lactate dehydrogenase) and increased levels of markers of hepatocellular regeneration (alpha-fetoprotein, retinol-binding protein, gamma-glutamyl transferase and des-gamma-carboxyprothrombin) (Horn *et al.* (1999) *Am J Clin Pathol* 112(3):351-357).

[0039] At the molecular level, CHCl_3 -induced changes in mRNA levels of 2 known genes, MUSTI21 (a mouse primary response gene induced by growth factors and tumor promoters) and MUSMRNAH (a gene highly homologous to a gene isolated from a prostate carcinoma cell line), and 2 novel genes (MUSFRA and MUSFRB) have been identified by differential display in regenerating mouse liver (Kegelmeyer *et al.* (1997) *Molecul Carcin* 20:288-297). These genes have been postulated to play a role in hepatic regeneration or possibly CHCl_3 -induced hepatocarcinogenesis.

[0040] CI-1000 (4H-pyrrolo:3,2-d:pyrimidin-4-one, 2-amino-3,5-dihydro-7-(3-thienylmethyl)-monohydrochloride monohydrate) is a compound with anti-inflammatory properties. After treatment with CI-1000, increased serum ALT levels, a standard marker of liver toxicity, were observed in dogs.

[0041] Clofibrate, a halogenated phenoxypropanoic acid derivative (ethyl ester of clofibric acid), is an antilipemic agent. The exact mechanism by which clofibrate lowers serum concentrations of triglycerides and low-density lipoprotein (LDL) cholesterol, as well as raising high-density lipoprotein (HDL) cholesterol is uncertain. The drug has several antilipidemic actions, including activating lipoprotein lipase, which enhances the clearance of triglycerides and very-low-density lipoprotein (VLDL) cholesterol, inhibition of cholesterol and triglyceride biosynthesis, mobilization of cholesterol from tissues, increasing fecal excretion of neutral steroids, decreasing hepatic lipoprotein synthesis and secretion, and decreasing free fatty acid release.

[0042] Clofibrate has a number of effects on the rat liver, including hepatocellular hypertrophy, cellular proliferation, hepatomegaly, induction of CYP450 isozymes, and induction of palmitoyl CoA oxidation. Long term administration of clofibrate causes increased incidence of hepatocellular carcinoma, benign testicular Leydig cell tumors, and pancreatic acinar adenomas in rats. Clofibrate induces proliferation of peroxisomes in rodents and this effect, rather than genotoxic damage, is believed to be the causative event in rodent carcinogenesis (AHFS Drug Information Handbook 2001, McEvoy, ed., pp.1735-1738; Electronic Physicians' Desk Reference- Atromid-S (clofibrate) at www.pdr.net; Brown and Goldstein, "Drugs used in the treatment of hyperliproteinemias," in Goodman and Gilman's The Pharmacological Basis of Therapeutics, Eighth ed., Goodman *et al.*, eds., pp. 874-896, Pergamon Press, New York, 1990).

[0043] Clofibrate also increases hepatic lipid content and alters its normal composition by significantly increasing levels of phosphatidylcholine and phosphatidyl-ethanolamine (Adinehzadeh *et al.* (1998) *Chem Res Toxicol* 11(5):428-440). A rat study of liver hyperplasia and liver tumors induced by peroxisome proliferators revealed that administration of clofibrate increased levels of copper and altered copper-related gene expression in the neoplastic liver tissues. Down-regulation of the ceruloplasmin gene and of the Wilson's Disease gene (which encodes P-type ATPase), along with up-regulation of the metallothionein gene, were noted in these tissues (Eagon *et al.* (1999) *Carcinogenesis* 20(6):1091-1096). Clofibrate-induced peroxisome proliferation and carcinogenicity are believed to be rodent-specific, and have not been demonstrated in humans.

[0044] Colchicine, an alkaloid of *Colchicum autumnale*, is an antiinflammatory agent used in the treatment of gouty arthritis (Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9th ed., p. 647, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). An antimitotic agent, colchicine binds to tubulin which leads to depolymerization and disappearance of the fibrillar microtubules in granulocytes and other motile cells. As a result, the migration of granulocytes into the inflamed area is inhibited, thereby suppressing the inflammatory response.

[0045] Some common, mild side effects associated with colchicine treatment are gastrointestinal disturbances, loss of appetite and hair loss. More serious side effects include hepatotoxicity, nausea, vomiting, and severe diarrhea and/or abdominal pain. Colchicine overdose can induce convulsions, coma, and multiorgan failure with a high incidence of mortality. Renal failure is multifactorial and related to prolonged hypotension, hypoxemia, sepsis, and rhabdomyolysis. In rats, less dramatic doses have been shown to inhibit the secretion of many endogenous proteins such as insulin and parathyroid hormone. Signs of liver damage are leakage of marker compounds, such as lactate dehydrogenase and albumin, into plasma and bile (Dvorak *et al.* (2002) *Toxicol In Vitro* 16(3):219-227; Crocenzi *et al.* (1997) *Toxicology* 121(2):127-142).

[0046] Cyproterone acetate (CPA) is a potent androgen antagonist and has been used to treat acne, male pattern baldness, precocious puberty, and prostatic hyperplasia and carcinoma (Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9th ed., p. 1453, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). Additionally, CPA has been used clinically in hormone replacement therapy to protect the endometrium and

decrease menopausal symptoms and the risk of osteoporotic fracture (Schneider, "The role of antiandrogens in hormone replacement therapy," *Climacteric* 3 (Suppl. 2): 21-27 (2000)).

[0047] In experiments with rats, CPA was shown to induce unscheduled DNA synthesis *in vitro*. After a single oral dose, continuous DNA repair activity was observed after 16 hours. CPA also increased the occurrence of S phase cells, which corroborated the mitogenic potential of CPA in rat liver (Kasper *et al.* (1996) *Carcinogenesis* 17(10): 2271-2274). CPA has also been shown to produce cirrhosis in humans (Garty *et al.* (1999) *Eur J Pediatr* 158(5): 367-370).

[0048] Diclofenac, a non-steroidal anti-inflammatory drug, has been frequently administered to patients suffering from rheumatoid arthritis, osteoarthritis, and ankylosing spondylitis. Following oral administration, diclofenac is rapidly absorbed and then metabolized in the liver by cytochrome P450 isozyme of the CYC2C subfamily (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 637, J.G. Hardman *et al.*, eds., McGraw Hill, New York, 1996). In addition, diclofenac has been applied topically to treat pain due to corneal damage (Jayamanne *et al.*, (1997) *Eye* 11(Pt. 1): 79-83; Dornic *et al.* (1998) *Am J Ophthalmol* 125(5): 719-721).

[0049] Although diclofenac has numerous clinical applications, adverse side-effects have been associated with the drug, such as corneal complications, including corneal melts, ulceration, and severe keratopathy (Guidera *et al.* (2001) *Ophthalmology* 108(5): 936-944). Another study investigated 180 cases of patients who had reported adverse reactions to diclofenac to the Food and Drug Administration (Banks *et al.* (1995) *Hepatology* 22(3): 820-827). Of the 180 reported cases, the most common symptom was jaundice (75% of the symptomatic patients). Liver sections were taken and analyzed, and hepatic injury was apparent one month after drug treatment. An additional report showed that a patient developed severe hepatitis five weeks after beginning diclofenac treatment for osteoarthritis (Bhogaraju *et al.* (1999) *South Med J* 92(7): 711-713).

[0050] In one study on diclofenac-treated Wistar rats (Ebong *et al.* (1998) *Afr J Med Sci* 27(3-4): 243-246), diclofenac treatment induced an increase in serum chemistry levels of alanine aminotransferase, aspartate aminotransferase, methaemoglobin, and total and conjugated bilirubin. Additionally, diclofenac enhanced the activity of alkaline phosphatase and 5'nucleotidase. A study on humans revealed elevated levels of hepatic

transaminases and serum creatine when compared to the control group (McKenna *et al.* (2001) *Scand J Rheumatol* 30(1): 11-18).

[0051] Diflunisal, a non-steroidal anti-inflammatory drug (NSAID), is a difluorophenyl derivative of salicylic acid (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th ed., p. 631, J.G. Hardman *et al.*, Eds., McGraw Hill, New York, 1996). It is most frequently used in the treatment of osteoarthritis and musculoskeletal strains. NSAIDs have analgesic, antipyretic and anti-inflammatory actions, however, hepatotoxicity is known to be an adverse side effect of NSAID treatment (Masubuchi *et al.* (1998) *J Pharmacol Exp Ther* 287:208-213). Diflunisal has been shown to be less toxic than other NSAIDs, but it can eventually have deleterious effects on platelet or kidney function (Bergamo *et al.* (1989) *Am J Nephrol* 9:460-463). Other side effects that have been associated with diflunisal treatment are diarrhea, dizziness, drowsiness, gas or heartburn, headache, nausea, vomiting, and insomnia (<http://arthritisinsight.com/medical/meds/dolobid.html>).

[0052] In a comparative hepatotoxicity study of 18 acidic NSAIDs, diflunisal was shown to increase LDH leakage in rat hepatocytes, a marker for cell injury, when compared to control samples. Additionally, treatment with diflunisal led to decreased intracellular ATP concentrations. In a study comparing the effects of diflunisal and ibuprofen, (Muncie and Nasrallah (1989) *Clin Ther* 11:539-544) both drugs appeared to cause abdominal cramping, even during short-term usage. Because the toxic dosages were selected to be below the level at which gastric ulceration occurs, more severe gastrointestinal effects were not detected. But, increased serum levels of creatinine, a sign of renal injury, were also observed (Muncie *et al.* (1989) *Clin Ther* 11:539-544).

[0053] Dioxin, an environmental and workplace toxin, is the name given to a class of compounds that are bi-products in the manufacture of chlorinated herbicides, pesticides and plastics. The most toxic and carcinogenic of these is 2,3,7,8-tetrachlorodibenzo-p-dioxin (2,3,7,8-TCDD). Exposure to dioxin increases expression of the aromatic hydrocarbon (Ah) receptor and also increases the production of reactive oxygen species in the mitochondria. Dioxin also increases mitochondrial levels of CYP1A1, CYP1A2 and glutathione, as well as hepatocyte levels of SOD and enzymes associated with oxidative stress (Senft *et al.* (2002) *Free Radic Biol Med* 33: 1268-1278; Kern *et al.* (2002) *Toxicology* 171: 117-1125).

[0054] Another model compound, **dimethylnitrosamine (DMN)**, is a known carcinogen and inducer of liver fibrosis and lipid peroxidation. DMN causes oxidative stress in liver cells, which may be the link between chronic liver damage and liver fibrosis. Rats treated with DMN showed diffuse fibronectin deposition, elevated hydroxyproline levels (an indicator of fibrosis), increased levels of collagens, fibrous septa, and impaired oxidative balance. Serum levels of ALT and malondialdehyde (MDA) were increased, while serum levels of SOD were decreased (Vendemiale *et al.* (2001) *Toxicol Appl Pharmacol* 175: 130-139; Liu *et al.* (2001) *Zhonghua Gan Zang Bing Za Zhi* 9 Suppl:18-20). Other studies in rats have noted severe centrilobular congestion and haemorrhagic necrosis several days after a three-day period of DMN administration. Following additional periods of DMN treatment, the rats developed centrilobular necrosis and intense neutrophilic infiltration, which progressed to severe centrilobular necrosis, fiber deposition, focal fatty deposits, bile duct proliferation, bridging necrosis and fibrosis around the central veins (cirrhosis-like symptoms). A decrease in total protein and increase in DNA were also observed (George *et al.* (2001) *Toxicology* 156: 129-138).

[0055] **17 α -ethinylestradiol**, a synthetic estrogen, is a component of oral contraceptives, often combined with the progestational compound norethindrone. It is also used in post-menopausal estrogen replacement therapy (PDR 47th Ed., pp. 2415-2420, Medical Economics Co., Inc., Montvale, NJ, 1993; Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th Ed., pp. 1419-1422, J.G. Hardman *et al.* Eds., McGraw Hill, New York, 1996).

[0056] The most frequent adverse effects of 17 α -ethinylestradiol usage are increased risks of cardiovascular disease: myocardial infarction, thromboembolism, vascular disease and high blood pressure, and of changes in carbohydrate metabolism, in particular, glucose intolerance and impaired insulin secretion. There is also an increased risk of developing benign hepatic neoplasia. Because this drug decreases the rate of liver metabolism, it is cleared slowly from the liver, and carcinogenic effects, such as tumor growth, may result.

[0057] 17 α -ethinylestradiol has been shown to cause a reversible intrahepatic cholestasis in male rats, mainly by reducing the bile-salt-independent fraction of bile flow (BSIF) (Kooen *et al.* (1998) *Hepatology* 27: 537-545). Plasma levels of bilirubin, bile salts, aspartate aminotransferase (AST) and alanine aminotransferase (ALT) in this study were not changed. This study also showed that 17 α -ethinylestradiol produced a decrease in

plasma cholesterol and plasma triglyceride levels, but an increase in the weight of the liver after 3 days of drug administration, along with a decrease in bile flow. Further results from this study are as follows. The activities of the liver enzymes leucine aminopeptidase and alkaline phosphatase initially showed significant increases, but enzyme levels decreased after 3 days. Bilirubin output increased, although glutathione (GSH) output decreased. The increased secretion of bilirubin into the bile without affecting the plasma level suggests that the increased bilirubin production must be related to an increased degradation of heme from heme-containing proteins. Similar results were obtained in another experiment (Bouchard *et al.*, (1993) *Liver* 13: 193-202) in which the livers were also examined by light and electron microscopy. Daily doses of 17 α -ethinylestradiol have been shown to cause cholestasis as well, although, following drug treatment, bile flow rates gradually returned to normal (Hamada *et al.* (1995) *Hepatology* 21: 1455-1464). Liver hyperplasia, possibly in response to the effects of tumor promoters, has also been observed (Mayol (1992) *Carcinogenesis* 13: 2381-2388).

[0058] The lipid-lowering drug **gemfibrozil** is a known peroxisome proliferator in liver tissue, causing both hyperplasia and enlargement of liver cells. Upon exposure to gemfibrozil, hepatocarcinogenesis has been observed in rats and mice, and a decrease in alpha-tocopherol and an increase in DT-diaphorase activity have been observed in rats and hamsters (impaired antioxidant capability). Peroxisome proliferators increase the activities of enzymes involved in peroxisomal beta-oxidation and omega-hydroxylation of fatty acids, which results in oxidative stress (O'Brien *et al.* (2001) *Toxicol Sci* 60: 271-278; Carthew *et al.* (1997) *J Appl Toxicol* 17: 47-51).

[0059] **Hydrazine** (NH₂=NH₂), is a component of many industrial chemicals, such as aerospace and airplane fuels, corrosion inhibitors, dyes and photographic chemicals. Its derivatives are used in pharmaceuticals such as hydrazine sulphate, used to treat cachexia in cancer patients, isoniazid, an anti-tuberculosis drug, and hydralazine, an anti-hypertensive. These drugs are metabolized *in vivo* to produce hydrazine, among other by-products. Consequently, exposure to hydrazine is by direct contact, *e.g.*, among military and airline personnel, or the result of its production in the body, *e.g.*, in patients with cancer or high blood pressure.

[0060] Studies on rat hepatocytes have shown that hydrazine causes a dose-dependent loss of viability, leakage of LDH, depletion of GSH and ATP and a decreased rate of protein synthesis (Delaney *et al.* (1995) *Xenobiotica* 25: 1399-1410). When

administered to rats, hepatotoxic changes, characterized by GSH and ATP depletion and induction of fatty liver (increases in liver weight and triglycerides, with the appearance of fatty droplets, swelling of mitochondria and appearance of microbodies) were also found to be dose-dependent (Jenner *et al.* (1994) *Arch Toxicol* 68: 349-357; Scales *et al.* (1982) *J Toxicol Environ Health* 10: 941-953). The hepatotoxicity, as well as renal toxicity, associated with hydrazine exposure has been linked to free radical damage resulting from oxidative metabolism by cytochrome P4502E1 (CYP2E1), which catalyzes the conjugation of free radicals with reduced glutathione. Although exposure to hydrazine and several hydrazine derivatives increased enzyme levels in kidney tissue, increased enzyme levels were not detected in liver tissue (Runge-Morris *et al.* (1996) *Drug Metab Dispos* 24: 734-737).

[0061] The mutagenic and hepatocarcinogenic effects of hydrazine were examined in hamster livers. *In vivo*, hydrazine reacts with formaldehyde to form formaldehyde hydrazone ($\text{CH}_2=\text{N}-\text{NH}_2$), an alkylating intermediate that methylates guanine in DNA. Upon treatment with hydrazine, liver DNA showed the presence of methylated guanine, DNA adducts and the impairment of maintenance methylation (impaired methylation of deoxycytosine). Hepatic adenomas and carcinomas also developed in a dose-dependent manner and could be correlated with decreased maintenance methylation (FitzGerald *et al.* (1996) *Carcinogenesis* 17: 2703-2709).

[0062] **Indomethacin** is a non-steroidal antiinflammatory, antipyretic and analgesic drug commonly used to treat rheumatoid arthritis, osteoarthritis, ankylosing spondylitis, gout and a type of severe, chronic cluster headache characterized by many daily occurrences and jabbing pain. This drug acts as a potent inhibitor of prostaglandin synthesis; it inhibits the cyclooxygenase enzyme necessary for the conversion of arachidonic acid to prostaglandins (PDR 47th Ed., Medical Economics Co., Inc., Montvale, NJ, 1993; Goodman & Gilman's *The Pharmacological Basis of Therapeutics* 9th Ed., J.G. Hardman *et al.* eds., pp. 1074-1075, 1089-1095, McGraw Hill, New York, 1996; *Cecil Textbook of Medicine*, 20th Ed., part XII, pp. 772-773, 805-808, J. C. Bennett and F. Plum Eds., W. B. Saunders Co., Philadelphia, 1996).

[0063] The most frequent adverse effects of indomethacin treatment are gastrointestinal disturbances, usually mild dyspepsia, although more severe conditions, such as bleeding, ulcers and perforations can occur. Hepatic involvement is uncommon, although some fatal cases of hepatitis and jaundice have been reported. Renal toxicity can also result,

particularly after long-term administration. Renal papillary necrosis has been observed in rats, and interstitial nephritis with hematuria, proteinuria and nephrotic syndrome have been reported in humans. Patients suffering from renal dysfunction risk developing a reduction in renal blood flow, because renal prostaglandins play an important role in renal perfusion.

[0064] In rats, although indomethacin produces more adverse effects in the gastrointestinal tract than in the liver, it has been shown to induce changes in hepatocytic cytochrome P450. In one study, no widespread changes in the liver were observed, but a mild, focal, centrilobular response was noted. Serum levels of albumin and total protein were significantly reduced, while the serum level of urea was increased. No changes in creatinine or aspartate aminotransferase (AST) levels were observed (Falzon *et al.* (1985) *Br J exp Path* 66: 527-534). In another rat study, a single dose of indomethacin was shown to reduce liver and renal microsomal enzymes, including CYP450, and cause lesions in the GI tract (Fracasso *et al.* (1990) *Agents Actions* 31: 313-316).

[0065] Menadione (vitamin K₃) is a fat-soluble vitamin precursor that is converted into menaquinone in the liver. The primary known function of vitamin K is to assist in normal blood clotting, but it may also play a role in bone calcification. Menadione is a quinone compound that induces oxidative stress. It has been used as an anticancer agent and radiosensitizer and can produce toxicity in the kidney, lung, heart, and liver. In the kidney, signs of toxicity are dose-dependent, ranging from minor degranulation of tubular cells at lower doses to tubular dilatation, formation of protein casts in the renal tubules, calcium mineralization, vacuolization in the proximal and distal renal tubules, granular degeneration in the cortex and necrosis and apoptosis (Chiou *et al.* (1997) *Toxicology* 124: 193-202). Toxic effects in the liver include depletion of glutathione, increased levels of Ca²⁺, increased lipid peroxidation and protein thiol oxidation, DNA strand breaks, and plasma membrane protrusions (blebs), which lead to cell degeneration. Oxidative stress induced by menadione also causes cytoskeletal abnormalities, which are related to the surface blebs (Chiou *et al.* (1998) *Proc Natl Sci Counc Repub China B* 22: 13-21; Mirabelli *et al.* (1988) *Arch Biochem Biophys* 264: 261-269).

[0066] Phenobarbital is used as an anti-epileptic, sedative or hypnotic drug and can also be used to treat neuroses with related tension states, such as hypertension, coronary artery disease, gastrointestinal disturbances and preoperative apprehension.

Phenobarbital is also found in medications to treat insomnia and headaches (Remington: The Science and Practice of Pharmacy, 19th Ed., A. R. Gennaro ed., pp. 1164-1165, Mack Publishing Co., Easton, Pennsylvania, 1995). Although liver toxicity is not a common side effect, the drug produces elevated levels of CYP2B1, and incidences of cholestasis and hepatocellular injury have been found (Selim *et al.* (1999) *Hepatology* 29: 1347-1351; Gut *et al.* (1996) *Environ Health Perspect* 104: 1211-1218).

[0067] **Tacrine** (1,2,3,4-tetrahydro-9-aminoacridine-hydrochloride), a strong acetylcholinesterase (AChE) inhibitor, is used in the treatment of mild to moderate cases Alzheimer's dementias. Alzheimer's patients have synaptic loss, neuronal atrophy and degeneration of cholinergic nuclei in the forebrain, which are associated with reduced oxidative metabolism of glucose and decreased levels of ATP and acetyl CoA. Administration of AChE inhibitors, such as tacrine, is designed to increase cholinergic activity to combat this loss (Weinstock (1995) *Neurodegeneration* 4: 349-356). The effect seen in the patients is a reversal of the cognitive and functional decline, but the drug does not appear to change the neurodegenerative process (Goodman & Gilman's The Pharmacological Basis of Therapeutics 9th Ed., Hardman *et al.* eds., p. 174, McGraw Hill, New York, 1996).

[0068] Hepatotoxicity caused by tacrine is typically reversible, although cases of severe hepatotoxicity have been seen (Blackard *et al.* (1998) *J Clin Gastroenterol* 26: 57-59). The toxicity is characterized by decreased levels of protein synthesis and the release of lactate dehydrogenase, as well as by increased transaminase levels and decreased levels of ATP, glycogen and glutathione. The decrease in protein synthesis may represent a signal leading to cell death (Lagadic-Gossman *et al.* (1998) *Cell Biol Toxicol* 14: 361-373).

[0069] Preclinical studies have failed to detect adverse hepatic events, although tacrine displayed cytotoxicity to human hepatoma cell lines and primary rat hepatocytes (Viau *et al.* (1993) *Drug Chem Toxicol* 16: 227-239). While hepatotoxicity has been found in humans, *in vivo* rat studies have not shown a correlation between tacrine exposure and hepatotoxicity, and the mechanism of action is not completely understood. An *in vitro* study comparing the reaction of human and rat liver microsomal preparations to tacrine (Woolf *et al.* (1993) *Drug Metab Dispos* 21: 874-882) showed that the two species reacted differently to the drug, suggesting that the rat may not be the best model for

monitoring tacrine-induced elevations in liver marker enzymes (Woolf *et al.* (1993) *Drug Metab Dispos* 21: 874-882).

[0070] While tacrine does not reveal classic signs of hepatotoxicity in rats, gene expression changes due to tacrine administration can be used to predict that the drug will be a liver toxin in humans. This suggests that toxicogenomics might be able to detect drugs that prove to be toxic in the clinic even when classical but more crude measures in preclinical screening fail to detect toxicity.

[0071] Thioacetamide's only significant commercial use is as a replacement for hydrogen sulfide in qualitative analyses (IARC, Vol. 7, 1974). It has also been used as a fungicide, an organic solvent in the leather, textile and paper industries, as an accelerator in the vulcanization of buna rubber, and as a stabilizer of motor fuel. The primary routes of human exposure are inhalation and skin contact with products in which thioacetamide was used as a solvent (9th Report on Carcinogens, U.S. Dept. of Health and Human Services, Public Health Service, National Toxicology Program, <http://ehp.niehs.nih.gov/roc/toc9.html>). Thioacetamide is metabolized to a nonionic electrophile, leading to oxidative stress and other injurious events; both cytochrome P4502E1 and the flavin-containing monooxygenase system have been implicated in this bioactivation (R. Snyder & L. S. Andrews, Toxic Effects of Solvents and Vapors, in Casarett & Doull's Toxicology: The Basic Science of Poisons, Klaasen, ed., p. 737, McGraw-Hill, New York, 1996; Smith *et al.* (1983) *Toxicol Appl Pharmacol* 70: 467-479; Jurima-Romet *et al.* (1993) *Biochem Pharmacol* 14:46(12):2163-2170).

[0072] In exposed rats, thioacetamide was shown to accumulate in the liver and kidney, resulting in elevated levels of serum total bilirubin, aspartate aminotransferase, alanine aminotransferase, BUN, creatinine and TNF α . Impaired clearance of the toxin and increased secretion of TNF α are related to the progression of toxic effects in the liver and kidney (Nakatani *et al.* (2001) *Liver* 21(1):64-70). Additional histological changes in kidney tissue include glomerular tuft collapse and interstitial haemorrhage (Caballero *et al.* (2001) *Gut* 48: 34-40).

[0073] In the liver, low acute doses of thioacetamide induce apoptosis, while high acute doses induce necrosis (Casarett & Doull's Toxicology, *supra*). Long term exposure induces cirrhosis and tumors (Risteli *et al.* (1976) *Biochem J* 158: 361-367). The acute liver injury is characterized by severe perivenous necrosis, immediately followed by hepatocellular regeneration and this necrosis. Nitric oxide synthase activity and nitric

oxide release are thought to play a role in the pathophysiological mechanisms that trigger liver regeneration following thioacetamide exposure (Ala-Kokko *et al.* (1987) *Biochem J* 244: 75-79). Exposure to thioacetamide also decreases levels of antioxidants, such as SOD, glutathione peroxidase and uric acid. It also increases apoptosis, along with caspase-3 activity, and has been observed to affect hepatic nitrogen metabolism. Rates of urea production and excretion were decreased, as well as glutamate dehydrogenase activity and glutamine synthetase activity. Mitogenic activity and DNA synthesis, however, were observed to increase (Abul *et al.* (2002) *Anat Histo Embryol* 31: 66-71; Hayami *et al.* (1999) *Biochem Pharmacol* 58: 1941-1943; Masumi *et al.* (1999) *Toxicology* 135: 21-31; Maier *et al.* (1991) *Arch Toxicol* 65: 454-464).

[0074] Valproate (n-dipropylacetic acid, Depakene[®]) is routinely used to treat several types of epileptic seizures- absence seizures, myoclonic seizures and tonic-clonic seizures. Most other anti-epileptics are effective against only one type. Valproate acts on neurons to inhibit the sustained repetitive firing caused by depolarization of cortical or spinal cord neurons, and a prolonged recovery of inactivated voltage-activated Na⁺ channels follows. The drug also acts by reducing the low-threshold Ca²⁺ current and its multiple mechanisms contribute to its use in multiple types of seizures. Although valproate does not affect neuronal responses to GABA, it does increase the activity of the GABA synthetic enzyme, glutamic acid decarboxylase, and it inhibits enzymes that degrade GABA, GABA transaminase and succinic semialdehyde dehydrogenase (Goodman and Gilman's *The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman *et al.*, eds., pp. 462, 476 and 477, McGraw-Hill, New York, 1996).

[0075] The most common side effects are gastrointestinal symptoms, including anorexia, nausea and vomiting. Effects on the CNS include sedation, ataxia and tremor. Rash, hair loss, increased appetite and teratogenic effects have also been observed (Briggs *et al.*, *A Reference Guide to Fetal and Neonatal Risk. Drugs in Pregnancy and Lactation*, 4th ed., p. 869, Williams & Wilkins, Baltimore, 1994). With respect to liver toxicity, valproate produces elevated levels of hepatic enzymes in about 40% of patients, which may be an asymptomatic condition, and elevated levels of hepatic lipids. Fulminant hepatitis, microvesicular steatosis (fatty degeneration), hepatocyte necrosis and hepatic failure can also result. It is believed that hepatotoxicity is caused by an accumulation of unsaturated metabolites of valproate, in particular 4-en-valproate, which is structurally

similar to two known hepatotoxins, 4-en-pentanoate and methylenecyclopropylacetic acid (Eadie *et al.* (1988) *Med Toxicol Adverse Drug Exp* 3: 85-106).

[0076] In a study on rats, microvesicular steatosis caused by valproate was found to be accompanied by myeloid bodies, lipid vacuoles and mitochondrial abnormalities (Kesterson *et al.* (1984) *Hepatology* 4: 1143-1152). Experiments on cultured rat hepatocytes have shown that valproate produces a dose-dependent leakage of lactic acid dehydrogenase and increased amounts of acyl-CoA esters, compounds that interfere with the beta-oxidation of fatty acids (Vance *et al.* (1994) *Epilepsia* 35: 1016-1022).

Administration of valproate to rats has also been shown to cause enhanced excretion of dicarboxylic acids, a sign of impaired mitochondrial beta-oxidation. Other metabolic effects include hypoglycemia, hyperammonemia, decreased levels of beta-hydroxybutyrate and carnitine and decreased activities of acyl-CoA dehydrogenases, enzymes involved in fatty acid oxidation. mRNA levels of genes involved in fatty acid oxidation, however, such as the short-, medium- and long-chain acyl-CoA dehydrogenases, were found to have increased (Kibayashi *et al.* (1999) *Pediatr Int* 41: 52-60).

[0077] Wy-14643, a tumor-inducing compound that acts in the liver, has been used to study the genetic profile of cells during the various stages of carcinogenic development, with a view toward developing strategies for detecting, diagnosing and treating cancers (Rockett *et al.* (2000) *Toxicology* 144(1-3):13-29). In contrast to other carcinogens, Wy-14643 does not mutate DNA directly. Instead, it acts on the peroxisome proliferator activated receptor-alpha (PPARalpha), as well as on other signaling pathways that regulate growth (Johnson *et al.* (2001) *J Steroid Biochem Mol Biol* 77(1):59-71). The effect is elevated and sustained cell replication, accompanied by a decrease in apoptosis (Rusyn *et al.* (2000) *Carcinogenesis* 21(12):2141-2145). These authors (Rusyn *et al.*) noted an increase in the expression of enzymes that repair DNA by base excision, but no increased expression of enzymes that do not repair oxidative damage to DNA. In a study on rodents, Johnson *et al.* noted that Wy-14643 inhibited liver-X-receptor-mediated transcription in a dose-dependent manner, as well as *de novo* sterol synthesis.

[0078] In experiments with mouse liver cells (Peters *et al.* (1998) *Carcinogenesis* 19(11):1989-1994), exposure to Wy-14643 produced increased levels of acyl CoA oxidase and proteins involved in cell proliferation: CDK-1, 2 and 4, PCNA and c-myc. Elevated levels may be caused by accelerated transcription that is mediated directly or

indirectly by PPARalpha. It is likely that the carcinogenic properties of peroxisome proliferators are due to the PPARalpha-dependent changes in levels of cell cycle regulatory proteins.

[0079] Another study on rodents (Keller *et al.* (1992) *Biochim Biophys Acta* 1102(2):237-244) showed that Wy-14643 was capable of uncoupling oxidative phosphorylation in rat liver mitochondria. Rates of urea synthesis from ammonia and bile flow, two energy-dependent processes, were reduced, indicating that the energy supply for these processes was disrupted as a result of cellular exposure to the toxin. Wy-14643 has also been shown to activate nuclear factor kappaB, NADPH oxidase and superoxide production in Kupffer cells (Rusyn *et al.* (2000) *Cancer Res* 60(17):4798-4803). NADPH oxidase is known to induce mitogens, which cause proliferation of liver cells.

[0080] The anti-asthma drug **zileuton** is a 5-lipoxygenase inhibitor and leukotriene synthesis inhibitor and is given to asthma patients to counter the negative effects of leukotrienes- exacerbation of the harmful effects of the inflammatory process and bronchoconstriction. Zileuton has, however, been reported to cause hepatomegaly and elevated levels of liver peroxisomal palmitoyl CoA oxidase and microsomal cytochromes P450 2B and P450 4A. The monooxygenase activities of these cytochromes was also seen to increase (Rodrigues *et al.* (1996) *Toxicol Appl Pharmacol* 137(2):193-201; Sorkness (1997) *Pharmacotherapy* 17(1 Pt 2):50S-54S).

[0081] **LPS (lipopolysaccharide)** is an endotoxin released by gram-negative bacteria upon breakage or rupture of the cells that induces an acute inflammatory response in mammals and that can cause septic shock. LPS is also a research tool used to initiate liver injury in rats through an inflammatory mechanism. Typically, the membrane components of LPS are lipid-A, KDO (2-keto-3-deoxy-octulosonic acid), core polysaccharides and O-antigen polysaccharides, the polysaccharide units differing from one bacterium to another (Zinsser Microbiology 20th Ed., Joklik et al., eds., pp. 82-87, Appleton & Lange, Norwalk, CT, 1992).

[0082] Primary rat hepatocytes derived from liver parenchymal cells and sinusoidal cells of rats that have been exposed to LPS *in vivo* can directly respond to LPS in cell culture. Numerous effects of LPS-induced endotoxemia can be detected, including elevated levels of nitric oxide synthetase (NOS) with increased nitric oxide and nitrite production, cellular hypertrophy, vacuolization, chromosomal emargination, cytoplasmic DNA

fragmentation and necrosis (Pittner *et al.* (1992) *Biochem Biophys Res Commun* 185(1):430-435; Laskin *et al.*, (1995) *Hepatology* 22(1):223-234; Wang *et al.* (1995) *Am J Physiol* 269(2 Pt 1):G297-304). Other studies have indicated that the presence of Kupffer cells with primary rat hepatocytes is essential for the induction of hepatocyte apoptosis by LPS (Hamada *et al.* (1999) *J Hepatol* 30(5):807-818).

[0083] Exposure of rats or primary hepatocytes to LPS induces the expression of a number of acute-phase proteins in the liver. Recent evidence has indicated that rat hepatocytes express soluble CD14 protein, and LPS is capable of markedly increasing levels of CD14 at both the gene expression and protein expression levels (Liu *et al.* (1998) *Infect Immun* 66(11):5089-5098). Soluble CD14 is believed to be a critical LPS recognition protein required for the activation of a variety of cells to toxic levels of LPS, even in endothelial and epithelial cells (Pugin *et al.* (1993) *Proc Natl Acad Sci USA* 90(7):2744-2748). Another key component of the LPS recognition system is lipopolysaccharide-binding protein (LBP), which binds to LPS. The LPS-LBP complex interacts with the CD14 receptor, inducing LPS sensitive genes. LBP can be induced in hepatocytes isolated from rats that have not been primed with LPS, indicating that this key regulatory pathway is intact in primary rat hepatocytes (Wan *et al.* (1995) *Infect Immun* 63(7):2435-2442).

Toxicity Prediction and Modeling

[0084] The genes and gene expression information, as well as the portfolios and subsets of the genes provided in Tables 1-5 WWW, such as the core toxicity markers in Tables 5A-5 WWW, may be used to predict at least one toxic effect, including the hepatotoxicity of a test or unknown compound. As used, herein, at least one toxic effect includes, but is not limited to, a detrimental change in the physiological status of a cell or organism. The response may be, but is not required to be, associated with a particular pathology, such as tissue necrosis. Accordingly, the toxic effect includes effects at the molecular and cellular level. Hepatotoxicity is an effect as used herein and includes but is not limited to the pathologies of liver necrosis, hepatitis, steatosis (fatty degeneration of the liver), carcinogenesis, cholestasis, liver enlargement, inflammation and peroxisome proliferation.

[0085] In general, assays to predict the toxicity or hepatotoxicity of a test agent (or compound or multi-component composition) comprise the steps of exposing a cell

population to the test compound, assaying or measuring the level of relative or absolute gene expression of one or more of the genes in Tables 1-5WW and comparing the identified expression level(s) to the expression levels disclosed in the Tables and database(s) disclosed herein. Assays may include the measurement of the expression levels of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 50, 75, 100 or more genes from Tables 1-5WW to create multi-gene expression profiles. In some instances, expression levels are assayed and compared for and to all or substantially all the genes in the tables.

[0086] In the methods of the invention, the gene expression level for a gene or genes induced by the test agent, compound or compositions may be comparable to the levels found in the Tables or databases disclosed herein if the expression level varies within a factor of about 2, about 1.5 or about 1.0 fold. In some cases, the expression levels are comparable if the agent induces a change in the expression of a gene in the same direction (*e.g.*, up or down) as a reference toxin.

[0087] The cell population that is exposed to the test agent, compound or composition may be exposed *in vitro* or *in vivo*. For instance, cultured or freshly isolated hepatocytes, in particular rat hepatocytes, may be exposed to the agent under standard laboratory and cell culture conditions. In another assay format, *in vivo* exposure may be accomplished by administration of the agent to a living animal, for instance a laboratory rat.

[0088] Procedures for designing and conducting toxicity tests in *in vitro* and *in vivo* systems are well known, and are described in many texts on the subject, such as *Loomis et al.*, Loomis's Essentials of Toxicology, 4th Ed., Academic Press, New York, 1996; Echobichon, The Basics of Toxicity Testing, CRC Press, Boca Raton, 1992; Frazier, editor, In Vitro Toxicity Testing, Marcel Dekker, New York, 1992; and the like.

[0089] In *in vitro* toxicity testing, two groups of test organisms are usually employed. One group serves as a control and the other group receives the test compound in a single dose (for acute toxicity tests) or a regimen of doses (for prolonged or chronic toxicity tests). Because, in some cases, the extraction of tissue as called for in the methods of the invention requires sacrificing the test animal, both the control group and the group receiving compound must be large enough to permit removal of animals for sampling tissues, if it is desired to observe the dynamics of gene expression through the duration of an experiment.

[0090] In setting up a toxicity study, extensive guidance is provided in the literature for selecting the appropriate test organism for the compound being tested, route of

administration. dose ranges, and the like. Water or physiological saline (0.9% NaCl in water) is the solute of choice for the test compound since these solvents permit administration by a variety of routes. When this is not possible because of solubility limitations, vegetable oils such as corn oil or organic solvents such as propylene glycol may be used.

[0091] Regardless of the route of administration, the volume required to administer a given dose is limited by the size of the animal that is used. It is desirable to keep the volume of each dose uniform within and between groups of animals. When rats or mice are used, the volume administered by the oral route generally should not exceed about 0.005 ml per gram of animal. Even when aqueous or physiological saline solutions are used for parenteral injection the volumes that are tolerated are limited, although such solutions are ordinarily thought of as being innocuous. The intravenous LD₅₀ of distilled water in the mouse is approximately 0.044 ml per gram and that of isotonic saline is 0.068 ml per gram of mouse. In some instances, the route of administration to the test animal should be the same as, or as similar as possible to, the route of administration of the compound to man for therapeutic purposes.

[0092] When a compound is to be administered by inhalation, special techniques for generating test atmospheres are necessary. The methods usually involve aerosolization or nebulization of fluids containing the compound. If the agent to be tested is a fluid that has an appreciable vapor pressure, it may be administered by passing air through the solution under controlled temperature conditions. Under these conditions, dose is estimated from the volume of air inhaled per unit time, the temperature of the solution, and the vapor pressure of the agent involved. Gases are metered from reservoirs. When particles of a solution are to be administered, unless the particle size is less than about 2 μ m the particles will not reach the terminal alveolar sacs in the lungs. A variety of apparatuses and chambers are available to perform studies for detecting effects of irritant or other toxic endpoints when they are administered by inhalation. The preferred method of administering an agent to animals is via the oral route, either by intubation or by incorporating the agent in the feed.

[0093] When the agent is exposed to cells *in vitro* or in cell culture, the cell population to be exposed to the agent may be divided into two or more subpopulations, for instance, by dividing the population into two or more identical aliquots. In some preferred embodiments of the methods of the invention, the cells to be exposed to the agent are

derived from liver tissue. For instance, cultured or freshly isolated rat hepatocytes may be used.

[0094] The methods of the invention may be used to generally predict at least one toxic response, and as described in the Examples, may be used to predict the likelihood that a compound or test agent will induce various specific liver pathologies such as liver necrosis, fatty liver disease, protein adduct formation, hepatitis or other pathologies associated with at least one of the toxins herein described. The methods of the invention may also be used to determine the similarity of a toxic response to one or more individual compounds. In addition, the methods of the invention may be used to predict or elucidate the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin (see Tables 5A-5WWW).

Diagnostic Uses for the Toxicity Markers

[0095] As described above, the genes and gene expression information or portfolios of the genes with their expression information as provided in Tables 1-5WWW may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or to identify or predict the toxic effects of a compound or agent. For instance, a tissue sample such as a sample of peripheral blood cells or some other easily obtainable tissue sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-5WWW may be compared to the expression levels found in tissues or cells exposed to the toxins described herein. These methods may result in the diagnosis of a physiological state in the cell or may be used to identify the potential toxicity of a compound, for instance a new or unknown compound or agent. The comparison of expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described below.

[0096] In another format, the levels of a gene(s) of Tables 1-5WWW, its encoded protein(s), or any metabolite produced by the encoded protein may be monitored or detected in a sample, such as a bodily tissue or fluid sample to identify or diagnose a physiological state of an organism. Such samples may include any tissue or fluid

sample, including urine, blood and easily obtainable cells such as peripheral lymphocytes.

Use of the Markers for Monitoring Toxicity Progression

[0097] As described above, the genes and gene expression information provided in Tables 1-5WWW may also be used as markers for the monitoring of toxicity progression, such as that found after initial exposure to a drug, drug candidate, toxin, pollutant, etc. For instance, a tissue or cell sample may be assayed by any of the methods described above, and the expression levels from a gene or genes from Tables 1-5WWW may be compared to the expression levels found in tissue or cells exposed to the hepatotoxins described herein. The comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases.

Use of the Toxicity Markers for Drug Screening

[0098] According to the present invention, the genes identified in Tables 1-5WWW may be used as markers or drug targets to evaluate the effects of a candidate drug, chemical compound or other agent on a cell or tissue sample. The genes may also be used as drug targets to screen for agents that modulate their expression and/or activity. In various formats, a candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of a drug's effects by looking at the number of markers which the drug induces and comparing them. More specific drugs will have less transcriptional targets. Similar sets of markers identified for two drugs may indicate a similarity of effects.

[0099] Assays to monitor the expression of a marker or markers as defined in Tables 1-5WWW may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

[0100] In one assay format, gene chips containing probes to one, two or more genes from Tables 1-5WWW may be used to directly monitor or detect changes in gene expression in the treated or exposed cell. Cell lines, tissues or other samples are first

exposed to a test agent and in some instances, a known toxin, and the detected expression levels of one or more, or preferably 2 or more of the genes of Tables 1-5WWW are compared to the expression levels of those same genes exposed to a known toxin alone. Compounds that modulate the expression patterns of the known toxin(s) would be expected to modulate potential toxic physiological effects *in vivo*. The genes in Tables 1-5WWW are particularly appropriate marks in these assays as they are differentially expressed in cells upon exposure to a known hepatotoxin.

[0101] In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the transcriptional regulatory regions of a gene in Tables 1-5WWW and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.* (1990) *Anal Biochem* 188:245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

[0102] Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 1-5WWW. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.* (Molecular Cloning: A Laboratory Manual, Third Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001).

[0103] In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the gene products of Tables 1-5WWW fused to one or more antigenic fragments or other detectable

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markers, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct or other detectable tag. Such a process is well known in the art (see Sambrook *et al.*, *supra*).

[0104] Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells are disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample is then compared with the control samples (no exposure and exposure to a known toxin) where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control is used to distinguish the effectiveness and/or toxic effects of the agent.

[0105] Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein(s) encoded by the genes in Tables 1-5WWW. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

[0106] In one format, the relative amounts of a protein (Tables 1-5WWW) between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population and a cell population exposed to a known toxin may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control,

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unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

[0107] Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

[0108] As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

[0109] The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see G.A. Grant in: Molecular Biology and Biotechnology, Meyers, ed., pp. 659-664, VCH Publishers, New York, 1995). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Nucleic Acid Assay Formats

[0110] The genes identified as being differentially expressed upon exposure to a known hepatotoxin (Tables 1-5WWW) may be used in a variety of nucleic acid detection assays to detect or quantitate the expression level of a gene or multiple genes in a given sample. The genes described in Tables 1-5WWW may also be used in combination with one or more additional genes whose differential expression is associate with toxicity in a cell or tissue. In preferred embodiments, the genes in Tables 1-5WWW may be combined with one or more of the genes described in related U.S. applications

60/222,040, 60/244,880, 60/290,029, 60/290,645, 60/292,336, 60/295,798, 60/297,457, 60/298,884, 60/303,459, 60/331,273, 60/364,045, 60/364,055, 60/436,643, 09/917,800 and 10/060,087, all of which are herein incorporated by reference.

[0111] Any assay format to detect gene expression may be used. For example, traditional Northern blotting, dot or slot blot, nuclease protection, primer directed amplification, RT-PCR, semi- or quantitative PCR, branched-chain DNA and differential display methods may be used for detecting gene expression levels. Those methods are useful for some embodiments of the invention. In cases where smaller numbers of genes are detected, high throughput amplification-based assays may be most efficient. Methods and assays of the invention, however, may be most efficiently designed with hybridization-based methods for detecting the expression of a large number of genes.

[0112] Any hybridization assay format may be used, including solution-based and solid support-based assay formats. Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, particles, beads, microparticles or silicon or glass based chips, etc. Such chips, wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755).

[0113] Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or 400,000 or more of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of about a square centimeter. Probes corresponding to the genes of Tables 1-5WW or from the related applications described above may be attached to single or multiple solid support structures, *e.g.*, the probes may be attached to a single chip or to multiple chips to comprise a chip set.

[0114] Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.* (1996) *Nat Biotechnol* 14: 1675-1680; McGall *et al.* (1996) *Proc Nat Acad Sci USA* 93: 13555-

13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described in Tables 1-5WWW. For instance, such arrays may contain oligonucleotides that are complementary or hybridize to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70, 100 or more the genes described herein. Preferred arrays contain all, substantially all, or nearly all of the genes listed in Tables 1-5WWW, or individually, the gene sets of Tables 5A-5WWW. In another preferred embodiment, arrays are constructed that contain oligonucleotides to detect all or nearly all of the genes in any one of or all of Tables 1-5WWW on a single solid support substrate, such as a chip.

[0115] The sequences of the expression marker genes of Tables 1-5WWW are in the public databases. Table 1 provides the GenBank Accession Number for each of the sequences (see www.ncbi.nlm.nih.gov/). The sequences of the genes in GenBank are expressly herein incorporated by reference in their entirety as of the filing date of this application, as are related sequences, for instance, sequences from the same gene of different lengths, variant sequences, polymorphic sequences, genomic sequences of the genes and related sequences from different species, including the human counterparts, where appropriate (see Table 3). These sequences may be used in the methods of the invention or may be used to produce the probes and arrays of the invention. In some embodiments, the genes in Tables 1-5WWW that correspond to the genes or fragments previously associated with a toxic response may be excluded from the Tables.

[0116] As described above, in addition to the sequences of the GenBank Accessions Numbers disclosed in the Tables 1-5WWW, sequences such as naturally occurring variant or polymorphic sequences may be used in the methods and compositions of the invention. For instance, expression levels of various allelic or homologous forms of a gene disclosed in the Tables 1-5WWW may be assayed. Any and all nucleotide variations that do not alter the functional activity of a gene listed in the Tables 1-5WWW, including all naturally occurring allelic variants of the genes herein disclosed, may be used in the methods and to make the compositions (*e.g.*, arrays) of the invention.

[0117] Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for screening or assaying a tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes

will be at least about 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases, longer probes of at least 30, 40, or 50 nucleotides will be desirable.

[0118] As used herein, oligonucleotide sequences that are complementary to one or more of the genes described in Tables 1-5WWW refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequences of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

[0119] "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

[0120] The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (*e.g.* probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

[0121] The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or

sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

[0122] Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 100,000 or 1,000,000 or more different nucleic acid hybridizations.

[0123] As used herein a “probe” is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

[0124] The term “perfect match probe” refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a “test probe”, a “normalization control” probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a “mismatch control” or “mismatch probe.”

[0125] The terms “mismatch control” or “mismatch probe” refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

[0126] While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

[0127] The term “stringent conditions” refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other

sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

[0128] Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M Na⁺ ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

[0129] The “percentage of sequence identity” or “sequence identity” is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical submit (*e.g.* nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Probe design

[0130] One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of test probes that specifically hybridize to the sequences of interest. Probes may be produced from any region of the genes identified in the Tables and the attached representative sequence listing. In instances where the gene reference in the Tables is an EST, probes may be designed from that sequence or from other regions of the corresponding full-length transcript that may be available in any of the sequence databases, such as those herein described. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, any available software may be used to

produce specific probe sequences, including, for instance, software available from Molecular Biology Insights, Olympus Optical Co. and Biosoft International. In a preferred embodiment, the array will also include one or more control probes.

[0131] High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500, or about 7 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 35 nucleotides in length. In other particularly preferred embodiments, the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using native nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

[0132] In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes may fall into three categories referred to herein as 1) normalization controls; 2) expression level controls; and 3) mismatch controls.

[0133] Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample to be screened. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (*e.g.*, fluorescence intensity) read from all other probes in the array are divided by the signal (*e.g.*, fluorescence intensity) from the control probes thereby normalizing the measurements.

[0134] Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only

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one or a few probes are used and they are selected such that they hybridize well (*i.e.*, no secondary structure) and do not match any target-specific probes.

[0135] Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typically expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

[0136] Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (*e.g.*, stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a 20 mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

[0137] Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation, for instance, a mutation of a gene in the accompanying Tables 1-5WWW. The difference in intensity between the perfect match and the mismatch probe provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples

[0138] Cell or tissue samples may be exposed to the test agent *in vitro* or *in vivo*.

When cultured cells or tissues are used, appropriate mammalian liver extracts may also be added with the test agent to evaluate agents that may require biotransformation to exhibit toxicity. In a preferred format, primary isolates of animal or human hepatocytes which already express the appropriate complement of drug-metabolizing enzymes may be exposed to the test agent without the addition of mammalian liver extracts.

[0139] The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not. The genes may be amplified or not. The cloning and/or amplification do not appear to bias the representation of genes within a population. In some assays, it may be preferable, however, to use polyA⁺ RNA as a source, as it can be used with less processing steps.

[0140] As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 24, Hybridization With Nucleic Acid Probes: Theory and Nucleic Acid Probes, P. Tijssen, Ed., Elsevier Press, New York, 1993. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates are used.

[0141] Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a tissue or cell sample that has been exposed to a compound, agent, drug, pharmaceutical composition, potential environmental pollutant or other composition. In some formats, the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical samples include, but are not limited to, sputum, blood, blood cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

[0142] Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Forming High Density Arrays

[0143] Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a single or on multiple solid substrates by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung, U.S. Patent No. 5,143,854).

[0144] In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

[0145] In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in PCT Publication Nos. WO 93/09668 and WO 01/23614. High density nucleic acid arrays can also be fabricated by depositing pre-made or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

[0146] Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The

nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

[0147] In a preferred embodiment, hybridization is performed at low stringency, in this case in 6X SSPET at 37°C (0.005% Triton X-100), to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, 1 X SSPET at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25 X SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, etc.).

[0148] In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

[0149] The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art. See WO 99/32660.

Databases

[0150] The present invention includes relational databases containing sequence information, for instance, for the genes of Tables 1-5WWW, as well as gene expression information from tissue or cells exposed to various standard toxins, such as those herein described (see Tables 5A-5WWW). Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information (see Table 1), or descriptive information concerning the clinical status of the tissue sample, or the animal from which the sample was derived. The database may be designed to include different parts, for instance a sequence database and a gene expression database. Methods for the configuration and construction of such databases and computer-readable media to which such databases are saved are widely available, for instance, see U.S. Patent No. 5,953,727, which is herein incorporated by reference in its entirety.

[0151] The databases of the invention may be linked to an outside or external database such as GenBank (www.ncbi.nlm.nih.gov/entrez/index.html); KEGG (www.genome.ad.jp/kegg); SPAD (www.grt.kyushu-u.ac.jp/spad/index.html); HUGO (www.gene.ucl.ac.uk/hugo); Swiss-Prot (www.expasy.ch/sprot); Prosite (www.expasy.ch/tools/scnpsit1.html); OMIM (www.ncbi.nlm.nih.gov/omim); and GDB (www.gdb.org). In a preferred embodiment, as described in Tables 1-3, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI) (www.ncbi.nlm.nih.gov).

[0152] Any appropriate computer platform, user interface, etc. may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or information provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available from Silicon Graphics. Client/server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

[0153] The databases of the invention may be used to produce, among other things, electronic Northern blots that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

[0154] The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising one or more of the genes in Tables 1-5WWW, comprising the step of comparing the expression level of at least one gene in Tables 1-5WWW in a cell or tissue exposed to a test agent to the level of expression of the gene in the database. Such methods may be used to predict the toxic potential of a given compound by comparing the level of expression of a gene or genes in Tables 1-5WWW from a tissue or cell sample exposed to the test agent to the expression levels found in a control tissue or cell samples exposed to a standard toxin or hepatotoxin such as those herein described. Such methods may also be used in the drug or agent screening assays as described herein.

Kits

[0155] The invention further includes kits combining, in different combinations, high-density oligonucleotide arrays, reagents for use with the arrays, protein reagents encoded by the genes of the Tables, signal detection and array-processing instruments, gene expression databases and analysis and database management software described above. The kits may be used, for example, to predict or model the toxic response of a test compound, to monitor the progression of hepatic disease states, to identify genes that show promise as new drug targets and to screen known and newly designed drugs as discussed above.

[0156] The databases packaged with the kits are a compilation of expression patterns from human or laboratory animal genes and gene fragments (corresponding to the genes of Tables 1-5WWW). In particular, the database software and packaged information that may contain the databases saved to a computer-readable medium include the expression results of Tables 1-5WWW that can be used to predict toxicity of a test agent by comparing the expression levels of the genes of Tables 1-5WWW induced by the test agent to the expression levels presented in Tables 1-5WWW. In another format, database and software information may be provided in a remote electronic format, such as a website, the address of which may be packaged in the kit.

[0157] The kits may be used in the pharmaceutical industry, where the need for early drug testing is strong due to the high costs associated with drug development, but where bioinformatics, in particular gene expression informatics, is still lacking. These kits will reduce the costs, time and risks associated with traditional new drug screening using cell cultures and laboratory animals. The results of large-scale drug screening of pre-grouped patient populations, pharmacogenomics testing, can also be applied to select drugs with greater efficacy and fewer side-effects. The kits may also be used by smaller biotechnology companies and research institutes who do not have the facilities for performing such large-scale testing themselves.

[0158] Databases and software designed for use with microarrays are discussed in Balaban *et al.*, U.S. Patent Nos. 6,229,911, a computer-implemented method for managing information, stored as indexed tables and collected from small or large numbers of microarrays, and 6,185,561, a computer-based method with data mining capability for collecting gene expression level data, adding additional attributes and reformatting the data to produce answers to various queries. Chee *et al.*, U.S. Patent No. 5,974,164, discloses a software-based method for identifying mutations in a nucleic acid sequence based on differences in probe fluorescence intensities between wild type and mutant sequences that hybridize to reference sequences.

[0159] Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1: Identification of Toxicity Markers

[0160] The hepatotoxins 2-acetylaminofluorene (2-AAF), BI liver toxin, chloroform, CI-1000, dimethylnitrosamine (DMN), gemfibrozil, menadione, thioacetamide, acyclovir, AY-25329, bicalutamide, clofibrate, colchicine, diflunisal, dioxin, hydrazine, phenobarbital, valproate, zileuton and LPS were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols and dosing regimes as indicated in Table 6. The hepatotoxins ANIT, acetaminophen, carbon tetrachloride, chloroform, CPA, diclofenac, 17 α -ethinylestradiol, indomethacin, tacrine and Wy-14643 were administered to male Sprague-Dawley rats at various time points using administration diluents, protocols and dosing regimes as previously described in the art and previously described in the related applications discussed above.

[0161] After administration, the dosed animals were observed and tissues were collected as described below:

OBSERVATION OF ANIMALS

[0162] 1. Clinical Observations- Twice daily: mortality and moribundity check.

[0163] Cage Side Observations - skin and fur, eyes and mucous membrane, respiratory system, circulatory system, autonomic and central nervous system, somatomotor pattern, and behavior pattern.

[0164] Potential signs of toxicity, including tremors, convulsions, salivation, diarrhea, lethargy, coma or other atypical behavior or appearance, were recorded as they occurred and included a time of onset, degree, and duration.

[0165] 2. Physical Examinations- Prior to randomization, prior to initial treatment, and prior to sacrifice.

[0166] 3. Body Weights- Prior to randomization, prior to initial treatment, and prior to sacrifice.

CLINICAL PATHOLOGY

[0167] 1. Frequency Prior to necropsy.

[0168] 2. Number of animals All surviving animals.

[0169] 3. Bleeding Procedure Blood was obtained by puncture of the orbital sinus while under 70% CO₂/ 30% O₂ anesthesia.

[0170] 4. Collection of Blood Samples- Approximately 0.5 mL of blood was collected into EDTA tubes for evaluation of hematology parameters. Approximately 1 mL of blood was collected into serum separator tubes for clinical chemistry analysis. Approximately 200 uL of plasma was obtained and frozen at $\sim -80^{\circ}\text{C}$ for test compound/metabolite estimation. An additional ~ 2 mL of blood was collected into a 15 mL conical polypropylene vial to which ~ 3 mL of Trizol was immediately added. The contents were immediately mixed with a vortex and by repeated inversion. The tubes were frozen in liquid nitrogen and stored at approximately -80°C .

TERMINATION PROCEDURES

Terminal Sacrifice

[0171] At the sampling times indicated in Table 6 for each hepatotoxin, and as previously described in the related applications mentioned above, rats were weighed, physically examined, sacrificed by decapitation, and exsanguinated. The animals were necropsied within approximately five minutes of sacrifice. Separate sterile, disposable instruments were used for each animal, with the exception of bone cutters, which were used to open the skull cap. The bone cutters were dipped in disinfectant solution between animals.

[0172] Necropsies were conducted on each animal following procedures approved by board-certified pathologists.

[0173] Animals not surviving until terminal sacrifice were discarded without necropsy (following euthanasia by carbon dioxide asphyxiation, if moribund). The approximate time of death for moribund or found dead animals was recorded.

Postmortem Procedures

[0174] Fresh and sterile disposable instruments were used to collect tissues. Gloves were worn at all times when handling tissues or vials. All tissues were collected and frozen within approximately 7 minutes of the animal's death. The liver sections were frozen within approximately 2 minutes of the animal's death. The time of euthanasia, an interim time point at freezing of liver sections and kidneys, and time at completion of necropsy were recorded. Tissues were stored at approximately -80°C or preserved in 10% neutral buffered formalin.

Tissue Collection and Processing

Liver

- [0175] 1. Right medial lobe – snap frozen in liquid nitrogen and stored at ~-80°C.
- [0176] 2. Left medial lobe - Preserved in 10% neutral-buffered formalin (NBF) and evaluated for gross and microscopic pathology.
- [0177] 3. Left lateral lobe – snap frozen in liquid nitrogen and stored at ~-80°C.

Heart

- [0178] A sagittal cross-section containing portions of the two atria and of the two ventricles was preserved in 10% NBF. The remaining heart was frozen in liquid nitrogen and stored at ~-80°C.

Kidneys (both)

- [0179] 1. Left – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at ~-80°C.
- [0180] 2. Right – Hemi-dissected; half was preserved in 10% NBF and the remaining half was frozen in liquid nitrogen and stored at ~-80°C.

Testes (both)

- [0181] A sagittal cross-section of each testis was preserved in 10% NBF. The remaining testes were frozen together in liquid nitrogen and stored at ~-80°C.

Brain (whole)

- [0182] A cross-section of the cerebral hemispheres and of the diencephalon was preserved in 10% NBF, and the rest of the brain was frozen in liquid nitrogen and stored at ~-80°C.

Bone marrow

- [0183] Bone marrow was flushed from each femur using a syringe and fresh, cold RPMI (~1 mL of RPMI x 3 washes per femur) into two separate 15 mL conical vials, labeled to distinguish right from left femur samples. The vials were gently inverted several times after collection and maintained on wet ice.
- [0184] Microarray sample preparation was conducted with minor modifications, following the protocols set forth in the Affymetrix GeneChip Expression Analysis

Manual. Frozen tissue was ground to a powder using a Spex Certiprep 6800 Freezer Mill. Total RNA was extracted with Trizol (GibcoBRL) utilizing the manufacturer's protocol. The total RNA yield for each sample was 200-500 µg per 300 mg tissue weight. mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen) followed by ethanol precipitation. Double stranded cDNA was generated from mRNA using the SuperScript Choice system (GibcoBRL). First strand cDNA synthesis was primed with a T7-(dT24) oligonucleotide. The cDNA was phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 µg/ml. From 2 µg of cDNA, cRNA was synthesized using Ambion's T7 MegaScript in vitro Transcription Kit.

[0185] To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. Following a 37°C incubation for six hours, impurities were removed from the labeled cRNA following the RNeasy Mini kit protocol (Qiagen). cRNA was fragmented (fragmentation buffer consisting of 200 mM Tris-acetate, pH 8.1, 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C. Following the Affymetrix protocol, 55 µg of fragmented cRNA was hybridized on the Affymetrix rat array set for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Data was analyzed using Affymetrix GeneChip® version 3.0 and Expression Data Mining (EDMT) software (version 1.0), GeneExpress2000, and S-Plus.

[0186] Table 1 discloses a set of genes that are differentially expressed upon exposure to the named toxins and their corresponding GenBank Accession and Sequence Identification numbers, the gene names if known, and the sequence cluster titles (core set and alternate set gene fragments). The human homologues of the rat genes in Table 1 are indicated in Table 3. The identities of the metabolic pathways in which the genes of Table 1 function are indicated in Table 2. The model codes in Tables 1-3 represent the various toxicity or liver pathology states that differential expression of each gene is able to identify, as well as the individual toxin or toxin type associated with differential

expression of each gene. The model codes are defined in Table 4. The GLGC ID is the internal Gene Logic identification number.

[0187] Tables 5A-5WWW disclose a core or alternate set of genes, along with the summary statistics for each of the comparisons performed as indicated in these tables- *i.e.*, expression levels of a particular gene in toxicity group samples compared to non-toxicity group samples in response to exposure to a particular toxin, or as measured in a particular disease state. Each of these tables contains a set of predictive genes and creates a model for predicting the hepatotoxicity of an unknown, *i.e.*, untested compound. Each gene is identified by its Gene Logic identification number and can be cross-referenced to a gene name and representative SEQ ID NO. in Table 1 or in one more related applications, as mentioned on page 1. For each comparison of gene expression levels between samples in the toxicity group (samples affected by exposure to a toxin) and samples in the non-toxicity group (samples not affected by exposure to a toxin), the tox mean (for toxicity group samples) is the mean signal intensity, as normalized for the various chip parameters that are being assayed. The non-tox mean represents the mean signal intensity, as normalized for the various chip parameters that are being assayed, in non-toxicity group samples. For individual genes, an increase in the tox mean compared to the non-tox mean indicates up-regulation upon exposure to a toxin, while a decrease in the group mean compared to the non-group mean indicates down-regulation.

[0188] The mean values are derived from Average Difference (AveDiff) values for a particular gene, averaged across the corresponding samples. Each individual Average Difference value is calculated by integrating the intensity information from multiple probe pairs that are tiled for a particular fragment. The normalization multiplies each expression intensity for a given experiment (chip) by a global scaling factor. The intent of this normalization is to make comparisons of individual genes between chips possible. The scaling factor is calculated as follows:

1. From all the unnormalized expression values in the experiment, delete the largest 2% and smallest 2% of the values. That is, if the experiment yields 10,000 expression values, order the values and delete the smallest 200 and largest 200.
2. Compute the trimmed mean, which is equal to the mean of the remaining values.
3. Compute the scale factor $SF = 100/(\text{trimmed mean})$

[0189] The value of 100 used here is the standard target value used.

[0190] Values greater than $2.0 \times \text{SD noise}$ are assumed to come from expressors. For these values, the standard deviation SD log (signal) of the logarithms is calculated. The logarithms are then multiplied by a scale factor proportional to $1 / \text{SD log (signal)}$ and exponentiated. The resulting values are then multiplied by another scale factor, chosen so there will be no discontinuity in the normalized values from unscaled values on either side of $2.0 \times \text{SD noise}$. Some AveDiff values may be negative due to the general noise involved in nucleic acid hybridization experiments. Although many conclusions can be made corresponding to a negative value on the GeneChip platform, it is difficult to assess the meaning behind the negative value for individual fragments. Our observations show that, although negative values are observed at times within the predictive gene set, these values reflect a real biological phenomenon that is highly reproducible across all the samples from which the measurement was taken. For this reason, those genes that exhibit a negative value are included in the predictive set. It should be noted that other platforms of gene expression measurement may be able to resolve the negative numbers for the corresponding genes. The predictive ability of each of those genes should extend across platforms, however. Each mean value is accompanied by the standard deviation for the mean. The linear discriminant analysis score (discriminant score, or LDA), as disclosed in the tables, measures the ability of each gene to predict whether or not a sample is toxic. The discriminant score is calculated by the following steps:

Calculation of a discriminant score

[0191] Let X_i represent the AveDiff values for a given gene across the Group 1 samples, $i=1 \dots n$.

[0192] Let Y_i represent the AveDiff values for a given gene across the Group 2 samples, $i=1 \dots t$.

[0193] The calculations proceed as follows:

[0194] Calculate mean and standard deviation for X_i 's and Y_i 's, and denote these by m_X, m_Y, s_X, s_Y .

[0195] For all X_i 's and Y_i 's, evaluate the function $f(z) = ((1/s_Y) \cdot \exp(-.5 \cdot ((z - m_Y)/s_Y)^2)) / (((1/s_Y) \cdot \exp(-.5 \cdot ((z - m_Y)/s_Y)^2)) + ((1/s_X) \cdot \exp(-.5 \cdot ((z - m_X)/s_X)^2)))$.

[0196] The number of correct predictions, say P, is then the number of Y_i 's such that $f(Y_i) > .5$ plus the number of X_i 's such that $f(X_i) < .5$.

[0197] The discriminant score is then $P/(n+t)$.

[0198] Linear discriminant analysis (LDA) uses both the individual measurements of each gene and the calculated measurements of all combinations of genes to classify samples. For each gene a weight is derived from the mean and standard deviation of the tox and nontox groups. Every gene is multiplied by a weight and the sum of these values results in a collective discriminate score. This discriminant score is then compared against collective centroids of the tox and nontox groups. These centroids are the average of all tox and nontox samples respectively. Therefore, each gene contributes to the overall prediction. This contribution is dependent on weights that are large positive or negative numbers if the relative distances between the tox and nontox samples for that gene are large and small numbers if the relative distances are small. The discriminant score for each unknown sample and centroid values can be used to calculate a probability between zero and one as to the group in which the unknown sample belongs.

Example 2: General Toxicity Modeling

[0199] Samples were selected for grouping into tox-responding and non-tox-responding groups by examining each study individually with Principal Components Analysis (PCA) to determine which treatments had an observable response. Only groups where confidence of their tox-responding and non-tox-responding status was established were included in building a general tox model.

[0200] Linear discriminant models were generated to describe toxic and non-toxic samples. The top discriminant genes and/or EST's were used to determine toxicity by calculating each gene's contribution with homo and heteroscedastic treatment of variance and inclusion or exclusion of mutual information between genes. Prediction of samples within the database exceeded 80% true positives with a false positive rate of less than 5%. It was determined that combinations of genes and/or EST's generally provided a better predictive ability than individual genes and that the more genes and/or EST used the better predictive ability. Although the preferred embodiment includes fifty or more genes, many pairings or greater combinations of genes and/or EST can work better than individual genes. All combinations of two or more genes from the selected list could be used to predict toxicity. These combinations could be selected by pairing in an agglomerate, divisive, or random approach. Further, as yet undetermined genes and/or EST's could be combined with individual or combination of genes and/or EST's

described here to increase predictive ability. However, the genes and/or EST's described here would contribute most of the predictive ability of any such undetermined combinations.

[0201] Other variations on the above method can provide adequate predictive ability. These include selective inclusion of components via agglomerate, divisive, or random approaches or extraction of loading and combining them in agglomerate, divisive, or random approaches. Also the use of composite variables in logistic regression to determine classification of samples can also be accomplished with linear discriminate analysis, neural or Bayesian networks, or other forms of regression and classification based on categorical or continual dependent and independent variables.

Example 3: Modeling with Core Gene Set

[0202] As described in Examples 1 and 2, above, the data collected from microarray hybridization experiments were analyzed by LDA and by PCA. The genes in Tables 5A, 5C, 5D, 5E, 5F, 5G, 5I, 5K, 5L, 5M, 5N, 5O, 5Q, 5S, 5T, 5U, 5V, 5W, 5X, 5Z, 5BB, 5DD, 5FF, 5GG, 5HH, 5II, 5JJ, 5LL, 5MM, 5NN, 5PP, 5RR, 5SS, 5TT, 5UU, 5VV, 5WW, 5XX, 5ZZ, 5BBB, 5DDD, 5EEE, 5FFF, 5GGG, 5HHH, 5III, 5KKK, 5LLL, 5MMM, 5NNN, 5OOO, 5PPP, 5RRR, 5SSS, 5TTT, 5UUU and 5VVV constitute a core set of markers for predicting the hepatotoxicity of a compound. The genes in Tables 5B, 5H, 5J, 5P, 5R, 5Y, 5AA, 5CC, 5EE, 5KK, 5OO, 5QQ, 5YY, 5AAA, 5CCC, 5JJJ, 5QQQ, and 5WWW constitute an alternate set of markers which may also be used in the methods of the invention, although the core marker sets of Tables 5A, 5C, 5D, 5E, 5F, 5G, 5I, 5K, 5L, 5M, 5N, 5O, 5Q, 5S, 5T, 5U, 5V, 5W, 5X, 5Z, 5BB, 5DD, 5FF, 5GG, 5HH, 5II, 5JJ, 5LL, 5MM, 5NN, 5PP, 5RR, 5SS, 5TT, 5UU, 5VV, 5WW, 5XX, 5ZZ, 5BBB, 5DDD, 5EEE, 5FFF, 5GGG, 5HHH, 5III, 5KKK, 5LLL, 5MMM, 5NNN, 5OOO, 5PPP, 5RRR, 5SSS, 5TTT, 5UUU and 5VVV may be preferred in some embodiments of the invention because the core sets contain additional predictive genes. Each gene fragment in Tables 1-5WWW is assigned an LDA score, and those gene fragments in the core set are those with the highest LDA scores. The gene fragments in Tables 5A-5WWW were determined to give greater than 80% true positive results and less than 5% false positive results. Gene expression profiles prepared from expression data for these genes, in the presence and absence of toxin treatment, can be used as controls in assays of compounds whose toxic properties have not been examined. Comparison of data from

test compound-exposed and test compound-unexposed animals with the data in Tables 5A-5WWW, or with data from the core gene set controls, allows the prediction of toxic effects- or no toxic effects- upon exposure to the test compound. Thus, with a smaller gene set than in Table 1 and as described in Example 1, the core gene set can be used to examine the biological effects of a compound whose toxic properties following exposure are not known and to predict the toxicity in liver tissue of this compound.

Example 4: Modeling Methods

[0203] The above modeling methods provide broad approaches of combining the expression of genes to predict sample toxicity. One method uses each variable individually and weights them; the other combines variables as a composite measure and adds weights to them after combination into a new variable. One could also provide no weight in a simple voting method or determine weights in a supervised or unsupervised method using agglomerate, divisive, or random approaches. All or selected combinations of genes may be combined in ordered, agglomerate, or divisive, supervised or unsupervised clustering algorithms with unknown samples for classification. Any form of correlation matrix may also be used to classify unknown samples. The spread of the group distribution and discriminate score alone provide enough information to enable a skilled person to generate all of the above types of models with accuracy that can exceed discriminate ability of individual genes. Some examples of methods that could be used individually or in combination after transformation of data types include but are not limited to: Discriminant Analysis, Multiple Discriminant Analysis, logistic regression, multiple regression analysis, linear regression analysis, conjoint analysis, canonical correlation, hierarchical cluster analysis, k-means cluster analysis, self-organizing maps, multidimensional scaling, structural equation modeling, support vector machine determined boundaries, factor analysis, neural networks, bayesian classifications, and resampling methods.

Example 5: Grouping of Individual compound and Pathology Classes

[0204] Samples were grouped into individual pathology classes based on known toxicological responses and observed clinical chemical and pathology measurements or into early and late phases of observable toxicity within a compound (Tables 1-5WWW). The top 10, 25, 50, 100 genes based on individual discriminate scores were used in a model to ensure that combination of genes provided a better prediction than individual

genes. As described above, all combinations of two or more genes from this list could potentially provide better prediction than individual genes when selected in any order or by ordered, agglomerate, divisive, or random approaches. In addition, combining these genes with other genes could provide better predictive ability, but most of this predictive ability would come from the genes listed herein.

[0205] Samples may be considered toxic if they score positive in any pathological or individual compound class represented here or in any modeling method mentioned under general toxicology models based on combination of individual time and dose grouping of individual toxic compounds obtainable from the data. The pathological groupings and early and late phase models are preferred examples of all obtainable combinations of sample time and dose points. Most logical groupings with one or more genes and one or more sample dose and time points should produce better predictions of general toxicity, pathological specific toxicity, or similarity to known toxicant than individual genes.

[0206] Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
20	16901	AA799479	FF	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NUIM_HUMAN NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (Complex I-23KD) (CI-23KD) (TYKY subunit) [H.sapiens]
153	16756	AA818089	G, H	HHs:glycyl-tRNA synthetase	ESTs, Highly similar to SYG_HUMAN Glycyl-tRNA synthetase (Glycine--tRNA ligase) (GlyRS) [H.sapiens]
727	22847	AA923982	BBB, CCC	HHs:succinate-CoA ligase, ADP-forming, beta subunit	ESTs, Moderately similar to T12480 hypothetical protein DKFZp564P2062.1 - human (fragment) [H.sapiens]
905	22283	AA945172	LL	HHs:leucine aminopeptidase 3	ESTs, Highly similar to AMPL_HUMAN Cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Proline aminopeptidase) (Prolyl aminopeptidase) [H.sapiens]
1161	16625	AA998062	A, B, N	HHs:Alg5, S. cerevisiae, homolog of	ESTs, Highly similar to T51776 dolichyl-phosphate beta-glucosyltransferase (EC 2.4.1.117) [imported] - human [H.sapiens]
1196	3082	AA999172	C, UU, General Alternate	HHs:guanine monophosphate synthetase	ESTs, Highly similar to GUAA_HUMAN GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthetase) [H.sapiens]
1266	22056	AI008066	F	HHs:ubiquinol-cytochrome c reductase hinge protein	ESTs, Moderately similar to UCRH_HUMAN Ubiquinol-cytochrome C reductase complex 11 kDa protein, mitochondrial precursor (Mitochondrial hinge protein) (Cytochrome C1, nonheme 11 kDa protein) (Complex III subunit VIII) [H.sapiens]
1600	24374	AI045973	E	HHs:partner of RAC1 (arfaptin 2)	ESTs, Highly similar to S71627 Rac1-interacting protein por1 - human [H.sapiens]
2066	17027	AI170679	BBB, CCC, RRR	HHs:UDP-glucose pyrophosphorylase 2	ESTs, Highly similar to UDP-glucose pyrophosphorylase 2; UTP-glucose-1-phosphate uridylyltransferase; UDP-glucose diphosphorylase; UGPase 2 [Homo sapiens] [H.sapiens]

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2090	4428	AI171362	CCC	Hh:NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	ESTs, Moderately similar to S17854 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 75K chain precursor - human [H.sapiens]
2471	3099	AI229680	RRR	Hh:NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	ESTs, Moderately similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase) [Homo sapiens] [H.sapiens]
3429	23424	NM_021680	E	neurexophilin 4 (Nxph4), mRNA. 11/2002 Length = 1265	ESTs, Highly similar to SYA_HUMAN Alanine-tRNA synthetase (Alanine--tRNA ligase) (AlaRS) [H.sapiens]
789	16944	AA925541	SSS	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L
789	16945	AA925541	C, BBB, HHH	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L
791	17514	AA925554	VV, General Alternate	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
3097	20589	NM_012618	O, W, VV, EEE, MMM	S100 calcium-binding protein A4 (S100a4), mRNA. 10/2002 Length = 487	S100 calcium-binding protein A4
3253	6598	NM_017020	DD, EE, SS, WW, UUU	Interleukin 6 receptor (Il6r), mRNA. 11/2002 Length = 4614	Interleukin 6 receptor
3398	235	NM_019347	RR	solute carrier family 14, member 2 (Slc14a2), mRNA. 11/2002 Length = 3974	Urea transporter
3556	22282	NM_024394	Z, AA, MM, WW, TTT	5-hydroxytryptamine (serotonin) receptor 3a (Htr3a), mRNA. 11/2002 Length = 2230	5-Hydroxytryptamine (serotonin) receptor 3A
3638	12996	NM_031528	C, RR	Retinoic acid receptor, alpha (Rara), mRNA. 11/2002 Length = 2130	Retinoic acid receptor, alpha

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3683	13185	NM_031755	GG, RR	carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1), mRNA. 11/2002 Length = 1481	carcinoembryonic antigen-related cell adhesion molecule
3683	13186	NM_031755	L, RR	carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1), mRNA. 11/2002 Length = 1481	carcinoembryonic antigen-related cell adhesion molecule
3683	13187	NM_031755	GG, OO	carcinoembryonic antigen-related cell adhesion molecule 1 (Ceacam1), mRNA. 11/2002 Length = 1481	carcinoembryonic antigen-related cell adhesion molecule
3745	5175	NM_053297	O, P, NN, OO, VV, EEE, MMM	Pyruvate kinase, muscle (Pkm2), mRNA. 11/2002 Length = 1973	Pyruvate kinase 3
3921	17512	NM_130428	S, General Alternate	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) (Sdha), mRNA. 1/2002 Length = 2277	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
3999	15380	NM_139083	F	ribosomal protein L41 (Rpl41), mRNA. 11/2002 Length = 357	ribosomal protein L41
4173	1359	U78977	XX, YY	ATPase, Class II, type 9A	ATPase, Class II, type 9A
4290	1561	Z50052	E, I, J, BB, JJ, EEE, GGG, III, JJJ, MMM, SSS	Complement component 4 binding protein, beta	Complement component 4 binding protein, beta
7	16950	AA686164	S, VV, PPP, QQQ		ESTs, Highly similar to dendritic cell protein [Homo sapiens] [H.sapiens]
9	21815	AA686423	RRR, UUU		ESTs, Highly similar to T46390 hypothetical protein DKFZp434C1920.1 - human (fragment) [H.sapiens]

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Seq ID	GLCC ID No.	GeneBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
14	18299	AA799369	N, General Alternate		ESTs, Weakly similar to 2113200F ribosomal protein S9 [Homo sapiens] [H.sapiens]
18	23293	AA799472	Z, AA		ESTs, Moderately similar to AD16_HUMAN Protein AD-016 (Protein CGI-116) (x0009) [H.sapiens]
24	15303	AA799518	Q, R		ESTs, Highly similar to hypothetical protein FLJ13725; KIAA1930 protein [Homo sapiens] [H.sapiens]
36	16576	AA799570	Q, R		ESTs, Highly similar to hypothetical protein FLJ13725; KIAA1930 protein [Homo sapiens] [H.sapiens]
44	19472	AA799616	C, UU		ESTs, Moderately similar to PTTG_HUMAN Pituitary tumor-transforming gene 1 protein-interacting protein (Pituitary tumor-transforming gene protein binding factor) (PTTG-binding factor) (PBF) [H.sapiens]
45	20980	AA799633	BBB, CCC		ESTs, Moderately similar to hypothetical protein MGC13016 [Homo sapiens] [H.sapiens]
63	16730	AA799766	L, FFF, HHH, OOO		ESTs, Moderately similar to JTV1; hypothetical protein PRO0992 [Homo sapiens] [H.sapiens]
75	20811	AA799899	RR		ESTs, Highly similar to R5RT18 ribosomal protein L18a, cytosolic [validated] - rat [R.norvegicus]
82	3915	AA800029	N		ESTs, Highly similar to T14792 hypothetical protein DKFZp586G0322.1 - human (fragment) [H.sapiens]
93	22918	AA800243	LL, PPP, QQQ, RRR, UUU		ESTs, Highly similar to CIDA_MOUSE Cell death activator CIDE-A (Cell death-inducing DFFA-like effector A) [M.musculus]
95	17206	AA800296	Z, AA		ESTs, Highly similar to PAP_HUMAN Poly(A) polymerase alpha (PAP) (Polynucleotide adenylyltransferase alpha) [H.sapiens]

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
96	17187	AA800315	XX, YY, BBB, CCC		ESTs, Highly similar to peroxisomal farnesylated protein; Housekeeping gene, 33kD [Homo sapiens] [H.sapiens]
107	17997	AA800671	General Alternate		ESTs, Moderately similar to A54854 Ras GTPase activating protein-related protein - human [H.sapiens]
120	10320	AA800855	BB, CC		ESTs, ESTs, Highly similar to MLF2_MOUSE Myeloid leukemia factor 2 (Myelodysplasia-myeloid leukemia factor 2) [M.musculus]
161	3709	AA818192	UU		ESTs, Highly similar to transcriptional adaptor 3-like, isoform a [Homo sapiens] [H.sapiens]
176	6234	AA818612	F		ESTs, Highly similar to S3A3_MOUSE Splicing factor 3A subunit 3 (Spliceosome associated protein 61) (SAP 61) (SF3a60) [M.musculus]
211	7208	AA819337	F		ESTs, Highly similar to T47140 hypothetical protein DKFZp761K1115.1 - human (fragment) [H.sapiens]
219	6281	AA819517	U, SSS, UUU		ESTs, Weakly similar to JC5707 HYA22 protein - human [H.sapiens]
222	15117	AA819623	OO		ESTs, Highly similar to SNX4_HUMAN Sorting nexin 4 [H.sapiens]
231	20668	AA819749	PPP, QQQ		EST, Highly similar to T08750 hypothetical protein DKFZp586E1519.1 - human (fragment) [H.sapiens]
263	19412	AA849222	CC, PP, UU, III, KKK, NNN		ESTs, Weakly similar to T46904 hypothetical protein DKFZp761D081.1 - human [H.sapiens]
270	14024	AA849619	CCC		ESTs, Moderately similar to T08727 probable H ⁺ -transporting ATP synthase (EC 3.6.1.34) chain g - human [H.sapiens]
275	14608	AA849805	U		ESTs, Highly similar to HLA-B associated transcript-5; BAT5 protein [Homo sapiens] [H.sapiens]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
296	1867	AA850940	S, JJ, KK, FFF, GGG, General Alternate	ribosomal protein L4	ribosomal protein L4
311	19211	AA851329	KK, HHH		ESTs, Highly similar to S26846 modifier protein 2 - mouse [M.musculus]
318	4941	AA851650	CCC	rap7a	EST, rap7a
320	19269	AA851785	S		ESTs, Highly similar to eukaryotic translation initiation factor 3, subunit 8 (110kD) [Homo sapiens] [H.sapiens]
326	19158	AA851953	F		ESTs, Moderately similar to T12501 hypothetical protein DKFZp434O171.1 - human (fragment) [H.sapiens]
328	6676	AA851967	C		ESTs, Weakly similar to solute carrier family 16 (monocarboxylic acid transporters), member 6; monocarboxylate transporter 6 [Homo sapiens] [H.sapiens]
342	10517	AA858600	KKK, NNN		ESTs, Highly similar to I54388 LZTR-1 - human [H.sapiens]
348	12729	AA858677	XX		ESTs, Highly similar to CD81 partner 3 [Homo sapiens] [H.sapiens]
349	12829	AA858695	XX, YY, CCC		ESTs, Moderately similar to mitochondrial ribosomal protein S33; mitochondrial 28S ribosomal protein S33 [Homo sapiens] [H.sapiens]
369	18140	AA859240	JJ, KK		ESTs, Moderately similar to T46317 hypothetical protein DKFZp434A0612.1 - human [H.sapiens]
374	15160	AA859346	S		ESTs, Moderately similar to RP38_HUMAN Ribonuclease P protein subunit p38 (RNaseP protein p38) [H.sapiens]
376	4267	AA859412	V		ESTs, Highly similar to NICA_MOUSE Nicastrin precursor [M.musculus]
379	23340	AA859519	BBB, CCC		ESTs, Highly similar to JC6127 RNA-binding protein type 1 - human [H.sapiens]
379	23341	AA859519	CCC		ESTs, Highly similar to JC6127 RNA-binding protein type 1 - human [H.sapiens]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
427	15115	AA874928	V, W, BB, CC		ESTs, Highly similar to SNX4_HUMAN Sorting nexin 4 [H.sapiens]
427	15116	AA874928	NN, PP, QQ, ZZ, AAA		ESTs, Highly similar to SNX4_HUMAN Sorting nexin 4 [H.sapiens]
431	16215	AA874999	I, FF		ESTs, Highly similar to protein translocation complex beta; protein transport protein SEC61 beta subunit [Homo sapiens] [H.sapiens]
442	15339	AA875171	UU		ESTs, Weakly similar to T45062 hypothetical protein c316G12.3 [imported] - human [H.sapiens]
442	15340	AA875171	XX, YY		ESTs, Weakly similar to T45062 hypothetical protein c316G12.3 [imported] - human [H.sapiens]
444	15371	AA875205	N, MM, TTT, General Alternate		ESTs, Highly similar to IF39_HUMAN Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) [H.sapiens]
444	15372	AA875205	A, B, FFF, General Core Tox Markers, General Alternate		ESTs, Highly similar to IF39_HUMAN Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) [H.sapiens]
450	15410	AA875268	III, JJJ		ESTs, Highly similar to NUKM_HUMAN NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial precursor (Complex I-20KD) (CI-20KD) (PSST subunit) [H.sapiens]
462	11889	AA875641	SS		ESTs, Highly similar to A Chain A, The Sh3 Domain Of Eps8 Exists As A Novel Intertwined Dimer [M.musculus]
477	21952	AA891537	UU, ZZ, AAA		ESTs, Weakly similar to protein predicted by clone 23733 [Homo sapiens] [H.sapiens]
501	11966	AA891800	L, BB, CC, NNN, OOO, General Alternate		ESTs, Weakly similar to F22G12.5.p [Caenorhabditis elegans] [C.elegans], ESTs, Weakly similar to IPYR_HUMAN Inorganic pyrophosphatase (Pyrophosphate phosphohydrolase) (PPase) [H.sapiens]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
501	18128	AA891800	OOO, General Alternate		ESTs, Weakly similar to IPYR_HUMAN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) [H.sapiens]
515	17779	AA891914	Q, R, NNN		ESTs, Moderately similar to A47488 aminoacylase (EC 3.5.1.14) - human [H.sapiens]
537	15576	AA892132	DDD		ESTs, Moderately similar to uncharacterized hematopoietic stem/progenitor cells protein MDS032 [Homo sapiens] [H.sapiens]
541	8317	AA892234	A, B, X, Y, GG, NN, OO, GGG		ESTs, Moderately similar to microsomal glutathione S-transferase 3; microsomal glutathione S-transferase III [Homo sapiens] [H.sapiens]
545	22903	AA892250	P, VV		ESTs, Highly similar to SYK_HUMAN Lysyl-tRNA synthetase (Lysine--tRNA ligase) (LysRS) [H.sapiens]
552	4373	AA892310	T		ESTs, Highly similar to T08783 hypothetical protein DKFZp586O0120.1 - human (fragment) [H.sapiens]
553	17405	AA892313	G, H		ESTs, Moderately similar to beta-tubulin cofactor E [Homo sapiens] [H.sapiens]
555	22867	AA892353	III, JJJ, KKK, OOO, General Core Tox Markers, General Alternate		ESTs, Moderately similar to hypothetical protein FLJ22353 [Homo sapiens] [H.sapiens]
559	8159	AA892380	F		ESTs, Highly similar to LCB1_MOUSE Serine palmitoyltransferase 1 (Long chain base biosynthesis protein 1) (LCB 1) (Serine-palmitoyl-CoA transferase 1) (SPT 1) (SPT1) [M.musculus]
566	9074	AA892465	Z, AA		ESTs, Moderately similar to Y054_HUMAN Hypothetical protein KIAA0054 [H.sapiens]
599	17923	AA892843	H		ESTs, Moderately similar to hypothetical protein FLJ20917 [Homo sapiens] [H.sapiens]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
614	3439	AA893000	N, U, BBB		ESTs, Moderately similar to T00335 hypothetical protein KIAA0564 - human (fragment) [H.sapiens]
626	3879	AA893237	T, DDD		ESTs, Moderately similar to hypothetical protein MBC3205 [Homo sapiens] [H.sapiens]
648	19410	AA893667	PP, UU, III, KKK		ESTs, Weakly similar to T46904 hypothetical protein DKFZp761D081.1 - human [H.sapiens]
648	19411	AA893667	E, BB, NN, PP, QQ, EEE, III, JJJ, KKK, MMM, NNN		ESTs, Weakly similar to T46904 hypothetical protein DKFZp761D081.1 - human [H.sapiens]
652	4554	AA893749	UU		EST, Weakly similar to PDA2_HUMAN Protein disulfide isomerase A2 precursor (PDlp) [H.sapiens]
661	2192	AA894086	C, ZZ, AAA, General Alternate		ESTs, Highly similar to hypothetical protein MGC17552 [Homo sapiens] [H.sapiens]
687	4636	AA899491	NN, OO, EEE, MMM		ESTs, Highly similar to SYW_MOUSE Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS) [M.musculus]
705	10555	AA900198	General Core Tox Markers, General Alternate		ESTs, Highly similar to HLMSP3 poliovirus receptor homolog precursor - mouse [M.musculus]
733	4917	AA924140	General Alternate		ESTs, Weakly similar to Y193_HUMAN Hypothetical protein KIAA0193 [H.sapiens]
740	20797	AA924310	General Alternate		ESTs, Weakly similar to UBC3_HUMAN Ubiquitin-conjugating enzyme E2-32 kDa complementing (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2-CDC34) [H.sapiens]
743	4942	AA924396	Q, R		ESTs, Weakly similar to T43481 probable mucin DKFZp434C196.1 - human (fragment) [H.sapiens]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
754	11533	AA924716	MM, TTT		ESTs, Highly similar to CSL4_HUMAN 3'-5' exoribonuclease CSL4 homolog (CGI-108) [H.sapiens]
755	5009	AA924737	K		ESTs, Highly similar to T17237 hypothetical protein DKFZp434P106.1 - human (fragment) [H.sapiens]
762	23440	AA924881	General Alternate		ESTs, Weakly similar to T03030 hypothetical protein KIAA0365 - human (fragment) [H.sapiens]
774	22851	AA925204	FF		ESTs, Highly similar to T08747 hypothetical protein DKFZp586B0519.1 - human [H.sapiens]
781	5140	AA925391	UUU		ESTs, Highly similar to T46399 hypothetical protein DKFZp434N2420.1 - human (fragment) [H.sapiens]
784	12386	AA925450	LLL		ESTs, Moderately similar to T08732 hypothetical protein DKFZp566B0846.1 - human (fragment) [H.sapiens]
812	20866	AA926098	D		ESTs, Moderately similar to mitochondrial ribosomal protein L53 [Homo sapiens] [H.sapiens]
821	21798	AA926365	X, DDD		ESTs, Moderately similar to T43493 hypothetical protein DKFZp434C119.1 - human [H.sapiens]
824	9942	AA942697	SS		ESTs, Highly similar to hypothetical protein MGC3133 [Homo sapiens] [H.sapiens]
839	21993	AA943149	A, B		ESTs, Weakly similar to T00084 hypothetical protein KIAA0512 - human [H.sapiens]
842	7426	AA943494	MM, TTT		ESTs, Highly similar to A41784 tumor necrosis factor-alpha-induced protein B12 - human [H.sapiens]
848	21911	AA943610	JJ, KK		ESTs, Highly similar to T08795 hypothetical protein DKFZp586J1822.1 - human (fragment) [H.sapiens]
881	21522	AA944449	EEE, MMM		ESTs, Moderately similar to SR68_HUMAN Signal recognition particle 68 kDa protein (SRP68) [H.sapiens]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
886	22457	AA944572	PPP, QQQ		ESTs, Weakly similar to JC5511 TATA-binding protein-associated factor II 31 - rat [R.norvegicus]
931	21974	AA945769	Q, R		ESTs, Highly similar to T43483 translation initiation factor IF-2 homolog [similarity] - human (fragment) [H.sapiens]
952	18383	AA946421	MM, UU, TTT		ESTs, Highly similar to S59641 transcription factor TFEB - mouse (fragment) [M.musculus]
981	23561	AA955477	E		ESTs, Moderately similar to S78100 MAPK-activated protein kinase (EC 2.7.1.-) 2 - mouse (fragment) [M.musculus]
982	12407	AA955495	XX		ESTs, Moderately similar to T08802 hypothetical protein DKFZp586D0623.1 - human (fragment) [H.sapiens]
994	12427	AA955771	T		ESTs, Highly similar to T08683 hypothetical protein DKFZp564J2123.1 - human (fragment) [H.sapiens]
995	23272	AA955819	X, Y, WW		ESTs, Moderately similar to down-regulated in lung cancer [Homo sapiens] [H.sapiens]
1006	24366	AA956246	OOO, General Core Tox Markers, General Alternate		ESTs, Moderately similar to T46373 hypothetical protein DKFZp434B2119.1 - human (fragment) [H.sapiens]
1009	23762	AA956431	OO, PP, QQ		ESTs, Highly similar to LSM5_HUMAN U6 snRNA-associated Sm-like protein LSml5 [H.sapiens]
1017	23841	AA956693	K		ESTs, Weakly similar to C3X1_RAT CX3C CHEMOKINE RECEPTOR 1 (C-X3-C CKR-1) (CX3CR1) (FRACTALKINE RECEPTOR) (GPR13) (RBS11) [R.norvegicus]
1022	5989	AA956907	MM, WW, TTT		ESTs, Highly similar to IF3A_MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN) (CENTROSOMIN) [M.musculus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1022	5990	AA956907	L		ESTs, Highly similar to IF3A_MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN) (CENTROSOMIN) [M.musculus]
1046	5952	AA963102	I, J, WW, General Alternate	amino acid transporter system A2	amino acid transporter system A2
1084	24166	AA964630	WW		ESTs, Moderately similar to T02345 hypothetical protein KIAA0324 - human (fragment) [H.sapiens]
1095	2514	AA964944	UU, KKK		ESTs, Weakly similar to SYW_MOUSE Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS) [M.musculus]
1105	15885	AA965207	C		ESTs, Highly similar to T14795 hypothetical protein DKFZp434E171.1 - human (fragment) [H.sapiens]
1111	2809	AA996471	A, B, II		ESTs, Moderately similar to JM11 protein [Homo sapiens] [H.sapiens]
1128	23930	AA997182	TT		ESTs, Highly similar to S55370 RNA polymerase II chain hRPB17 - human [H.sapiens]
1142	21812	AA997588	CCC		ESTs, Highly similar to T46390 hypothetical protein DKFZp434C1920.1 - human (fragment) [H.sapiens]
1148	2354	AA997763	C, L, Z, GG, HH		ESTs, Moderately similar to T17239 hypothetical protein DKFZp434B027.1 - human (fragment) [H.sapiens]
1164	3367	AA998110	II, FFF		ESTs, Weakly similar to YCE3_HUMAN Hypothetical protein CGI-143 [H.sapiens]
1176	26116	AA998471	D		ESTs, Highly similar to I49668 binding protein - mouse [M.musculus]
1176	26117	AA998471	F, HH		ESTs, Highly similar to I49668 binding protein - mouse [M.musculus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1177	23770	AA998488	SS		ESTs, Weakly similar to atrophin-1 [Homo sapiens] [H.sapiens]
1180	26120	AA998619	D		ESTs, Weakly similar to T51776 dolichyl-phosphate beta-glucosyltransferase (EC 2.4.1.117) [imported] - human [H.sapiens]
1192	3710	AA999064	Q, R		ESTs, Highly similar to T47142 hypothetical protein DKFZp761P0724.1 - human (fragment) [H.sapiens]
1214	23417	AB022209	B, S, GGG, PPP, QQQ, General Alternate	ribonucleoprotein F	ribonucleoprotein F
1260	3148	AI007881	B		ESTs, Moderately similar to x 003 protein [Homo sapiens] [H.sapiens]
1264	17359	AI007981	GG		ESTs, Moderately similar to UCRX_HUMAN Ubiquinol-cytochrome C reductase complex 7.2 kDa protein (Cytochrome C1, nonheme 7 kDa protein) (Complex III subunit X) (7.2 kDa cytochrome c1-associated protein subunit) (HSPC119) [H.sapiens]
1268	3121	AI008160	N, U, NN, OO, III, LLL, RRR, SSS, UUU		ESTs, Moderately similar to T44603 hypothetical protein CGI-83 [imported] - human [H.sapiens]
1296	2193	AI009062	DD, EE, WW		ESTs, Highly similar to hypothetical protein MGC17552 [Homo sapiens] [H.sapiens]
1315	19275	AI009460	O, P		ESTs, Moderately similar to A37098 gelation factor ABP-280, long form - human [H.sapiens]
1317	11322	AI009492	CC, UUU		ESTs, Highly similar to hypothetical protein [Homo sapiens] [H.sapiens]
1348	16035	AI010295	L		ESTs, Highly similar to hypothetical protein MGC13010 [Homo sapiens] [H.sapiens]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1376	24022	AI011474	DDD		ESTs, Moderately similar to T00637 hypothetical protein H_GS541B18.1 - human (fragment) [H.sapiens]
1377	12629	AI011492	F		ESTs, Moderately similar to JC5707 HYA22 protein - human [H.sapiens]
1379	7060	AI011547	ZZ, AAA		ESTs, Highly similar to T47183 hypothetical protein DKFZp434K1822.1 - human (fragment) [H.sapiens]
1383	23768	AI011709	Y		ESTs, Moderately similar to S21977 Pm5 protein - human [H.sapiens]
1391	18684	AI011812	ZZ, AAA		ESTs, Highly similar to T12468 hypothetical protein DKFZp564O123.1 - human [H.sapiens]
1403	16783	AI012215	JJ, QQ, HHH		ESTs, Weakly similar to A61231 myosin heavy chain nonmuscle form A - human [H.sapiens]
1432	11197	AI012937	UU		ESTs, Moderately similar to T02246 hypothetical protein P1.11659_4 - human [H.sapiens]
1437	11191	AI013042	I, J, III, JJJ, KKK, General Alternate		ESTs, Highly similar to SRE1_RAT Sterol regulatory element binding protein-1 (SREBP-1) (Sterol regulatory element-binding transcription factor 1) (Adipocyte determination- and differentiation-dependent factor 1) (ADD1) [R.norvegicus]
1448	12794	AI013442	R		ESTs, Highly similar to T12539 hypothetical protein DKFZp434J154.1 - human [H.sapiens]
1452	7274	AI013715	U		ESTs, Moderately similar to BMP6_RAT BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6) (VG-1-RELATED PROTEIN) (VGR-1) [R.norvegicus]
1453	22592	AI013740	O, P, UUU		ESTs, Moderately similar to S32567 A4 protein - human [H.sapiens]
1461	9885	AI013878	LL		ESTs, Highly similar to T46332 hypothetical protein DKFZp434H0413.1 - human (fragment) [H.sapiens]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1486	7420	AI029291	U		ESTs, Highly similar to CLPX_MOUSE ATP-dependent CLP protease ATP-binding subunit ClpX-like, mitochondrial precursor [M.musculus]
1489	7451	AI029450	E, DD, UU, III, JJJ, KKK, NNN, General Alternate		ESTs, Moderately similar to SYEP_HUMAN Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRNA synthetase (Glutamate--tRNA ligase); Prolyl-tRNA synthetase (Proline--tRNA ligase)] [H.sapiens]
1518	23273	AI030738	VV, WW		ESTs, Moderately similar to down-regulated in lung cancer [Homo sapiens] [H.sapiens]
1593	5877	AI045768	UUU		ESTs, Moderately similar to T08692 hypothetical protein DKFZp564K112.1 - human (fragment) [H.sapiens]
1603	18172	AI058364	EE, WW		ESTs, Weakly similar to G02313 CDC37 homolog - human [H.sapiens]
1607	10069	AI058503	III, JJJ		ESTs, Moderately similar to Y247_HUMAN Hypothetical protein KIAA0247 [H.sapiens]
1636	8315	AI059389	SSS, UUU		ESTs, Highly similar to 2122208A adenylosuccinate synthetase:ISOTYPE=muscle [Mus musculus] [M.musculus]
1652	8132	AI060050	General Core Tox Markers, General Alternate		ESTs, Highly similar to NGP1_HUMAN Autoantigen NGP-1 [H.sapiens]
1671	18	AI070195	RR		ESTs, Highly similar to T42648 hypothetical protein DKFZp434C1415.1 - human [H.sapiens]
1678	22684	AI070323	VV		ESTs, Highly similar to AR34_HUMAN ARP2/3 complex 34 kDa subunit (P34-ARC) (Actin-related protein 2/3 complex subunit 2) [H.sapiens]
1686	514	AI070584	KKK	matrix metalloproteinase 14, membrane-inserted	matrix metalloproteinase 14, membrane-inserted

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1687	8944	AI070597	U		ESTs, Highly similar to YC97_HUMAN Hypothetical protein CGI-97 [H.sapiens]
1688	8950	AI070621	II		ESTs, Highly similar to S50852 cleavage stimulation factor 77K chain - human [H.sapiens]
1698	11596	AI071194	BB		ESTs, Weakly similar to S16506 hypothetical protein - human [H.sapiens]
1713	11125	AI071867	Z		ESTs, Weakly similar to PSS1_HUMAN Phosphatidylserine synthase I (Serine-exchange enzyme I) [H.sapiens]
1715	17673	AI071895	RR		EST, Moderately similar to I38937 DNA/RNA-binding protein - human (fragment) [H.sapiens]
1778	13261	AI101465	R		ESTs, Moderately similar to S24B_HUMAN Protein transport protein Sec24B (SEC24-related protein B) [H.sapiens]
1789	21691	AI102027	T		ESTs, Highly similar to hypothetical protein MGC10540 [Homo sapiens] [H.sapiens]
1854	6823	AI103793	EEE, MMM		ESTs, Highly similar to SSRB_HUMAN Translocon-associated protein, beta subunit precursor (TRAP-beta) (Signal sequence receptor beta subunit) (SSR-beta) [H.sapiens]
1863	3259	AI104245	SS, TT		ESTs, Weakly similar to T46363 hypothetical protein DKFZp434O0916.1 - human (fragment) [H.sapiens]
1869	21922	AI104376	SS		ESTs, Highly similar to HSPC142 protein [Homo sapiens] [H.sapiens]
1876	18509	AI104528	LL, RRR		ESTs, Weakly similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) [Homo sapiens] [H.sapiens]
1882	22957	AI104897	Q, R		ESTs, Moderately similar to MEA6_HUMAN Meningioma-expressed antigen 6/11 (MEA6) (MEA11) [H.sapiens]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1884	24375	AI104979	General Core Tox Markers		ESTs, Moderately similar to EBNA1 binding protein 2; nucleolar protein p40; homolog of yeast EBNA1-binding protein; nuclear FGF3 binding protein; EBNA1-binding protein 2 [Homo sapiens] [H.sapiens]
1959	7414	AI137586	R		ESTs, Highly similar to IMB3_HUMAN Importin beta-3 subunit (Karyopherin beta-3 subunit) (Ran-binding protein 5) [H.sapiens]
1962	12654	AI137864	QQQ		ESTs, Highly similar to MG15_HUMAN Transcription factor-like protein MRG15 (MORF-related gene 15 protein) (MSL3-1 protein) (Protein HSPC008/HSPC061) [H.sapiens]
1967	11588	AI138121	V, AA		ESTs, Moderately similar to hypothetical protein FLJ13222; likely ortholog of mouse testis expressed gene 27 [Homo sapiens] [H.sapiens]
1986	13167	AI145832	III, JJJ, OOO, General Core Tox Markers, General Alternate		ESTs, Moderately similar to YCD1_HUMAN Hypothetical protein CGI-131 [H.sapiens]
2014	20891	AI169337	A, B, HHH		ESTs, Moderately similar to CGB7_HUMAN Hypothetical protein CGI-117 (Protein HSPC111) [H.sapiens]
2023	23260	AI169617	MM, TTT		ESTs, Highly similar to Y124_HUMAN Hypothetical protein KIAA0124 [H.sapiens]
2025	18343	AI169648	WW		ESTs, Highly similar to RT25_MOUSE Mitochondrial 28S ribosomal protein S25 (MRP-S25) [M.musculus]
2026	24146	AI169668	R		ESTs, Weakly similar to ATP-binding cassette, sub-family F, member 2 [Homo sapiens] [H.sapiens]
2053	19884	AI170501	PP, QQ, YY		ESTs, Moderately similar to 0806162H protein URF3 [Mus musculus] [M.musculus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2058	24048	AI170570	S		ESTs, Moderately similar to COQ6_HUMAN Putative ubiquinone biosynthesis monooxygenase COQ6 (CGI-10) [H.sapiens]
2071	1923	AI170754	Q, R		ESTs, Highly similar to T50836 Yippee protein [imported] - human (fragment) [H.sapiens]
2081	5953	AI171231	C, I, MM, TTT	amino acid transporter system A2	amino acid transporter system A2
2085	3664	AI171289	GG		ESTs, Highly similar to JC2472 brain and reproductive organ-expressed protein - human [H.sapiens]
2093	22958	AI171374	Q, R, FF		ESTs, Moderately similar to MEA6_HUMAN Meningioma-expressed antigen 6/11 (MEA6) (MEA11) [H.sapiens]
2108	18994	AI171759	BB, CC		ESTs, Moderately similar to beta-tubulin cofactor E [Homo sapiens] [H.sapiens]
2110	15109	AI171768	UUU		ESTs, Highly similar to CGB0_HUMAN Hypothetical protein CGI-110 (Protein HSPC175) [H.sapiens]
2115	3266	AI171948	FFF, General Alternate		ESTs, Highly similar to T08675 hypothetical protein DKFZp564F0522.1 - human (fragment) [H.sapiens]
2117	18325	AI171953	Y	glutamate receptor, ionotropic	glutamate receptor, ionotropic
2123	23422	AI172034	O, P, CC		ESTs, Highly similar to T46333 hypothetical protein DKFZp434J1813.1 - human (fragment) [H.sapiens]
2130	6057	AI172102	E, DD, EE		ESTs, Highly similar to STXH_HUMAN Syntaxin 18 [H.sapiens]
2133	11416	AI172185	S, EEE, MMM		ESTs, Highly similar to mitochondrial ribosomal protein L49; chromosome 11 open reading frame 4 [Homo sapiens] [H.sapiens]
2135	20867	AI172214	F		ESTs, Moderately similar to mitochondrial ribosomal protein L53 [Homo sapiens] [H.sapiens]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2140	11525	AI172286	CCC, RRR, SSS		ESTs, Moderately similar to LPRC_HUMAN 130 kDa leucine-rich protein (LRP 130) (GP130) (Leucine-rich PPR-motif containing protein) [H.sapiens]
2143	15842	AI172325	FFF		ESTs, Highly similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1; DEAD/H box-1 [Homo sapiens] [H.sapiens]
2181	23311	AI176003	Z, AA		ESTs, Highly similar to PRLP_HUMAN Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein) [H.sapiens]
2195	19363	AI176247	A, Y, GGG, QQQ, General Core Tox Markers		ESTs, Moderately similar to SCO2_HUMAN SCO2 protein homolog, mitochondrial precursor [H.sapiens]
2203	20001	AI176396	LL		ESTs, Moderately similar to C560_HUMAN Succinate dehydrogenase cytochrome B560 subunit, mitochondrial precursor (QPS1) (CII-3) (Succinate dehydrogenase complex subunit C) (Succinate-ubiquinone oxidoreductase cytochrome B large subunit) (CYBL) [H.sapiens]
2205	17920	AI176422	II		ESTs, Highly similar to S41115 probable flavoprotein-ubiquinone oxidoreductase (EC 1.6.5.-) - human [H.sapiens]
2210	13678	AI176490	WW		ESTs, Weakly similar to T00065 hypothetical protein KIAA0442 - human (fragment) [H.sapiens]
2257	12958	AI177155	J, General Core Tox Markers, General Alternate		ESTs, Highly similar to NSDL_MOUSE NAD(P)-dependent steroid dehydrogenase [M.musculus]
2264	24049	AI177341	K, Y, DDD		ESTs, Moderately similar to COQ6_HUMAN Putative ubiquinone biosynthesis monooxygenase COQ6 (CGI-10) [H.sapiens]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2273	20669	AI177590	GG		EST, Highly similar to T08750 hypothetical protein DKFZp586E1519.1 - human (fragment) [H.sapiens], ESTs, Highly similar to T08750 hypothetical protein DKFZp586E1519.1 - human (fragment) [H.sapiens]
2274	6315	AI177645	VV		ESTs, Weakly similar to S69890 mitogen inducible gene mig-2 - human [H.sapiens]
2283	3834	AI177902	X, Y		ESTs, Highly similar to T14743 hypothetical protein DKFZp586F1524.1 - human (fragment) [H.sapiens]
2288	16739	AI178151	C, HH		ESTs, Highly similar to T46366 hypothetical protein DKFZp434C0118.1 - human (fragment) [H.sapiens]
2293	1050	AI178219	V	phosphatidylinositol glycan, class L	phosphatidylinositol glycan, class L
2322	11660	AI178944	HHH, General Alternate		ESTs, Highly similar to T03842 fission yeast Skb1 protein homolog - human [H.sapiens]
2326	13055	AI179100	Q, R, FFF		ESTs, Highly similar to CN01_HUMAN Protein C14orf1 (HSPC288) (Protein AD-011) (x0006) [H.sapiens]
2331	17358	AI179147	PP, QQ		ESTs, Highly similar to B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution [H.sapiens]
2357	12516	AI179651	UU		ESTs, Moderately similar to JC4760 SMT3 protein - human [H.sapiens]
2363	14586	AI179865	LLL		ESTs, Highly similar to T17270 hypothetical protein DKFZp434N241.1 - human (fragment) [H.sapiens]
2369	23989	AI179953	PP		ESTs, Highly similar to 1604368A gap junction protein Cx26 [Rattus norvegicus] [R.norvegicus]
2371	22569	AI179979	III, JJJ, General Core Tox Markers		ESTs, Moderately similar to hypothetical protein FLJ21634 [Homo sapiens] [H.sapiens]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2381	5481	AI180170	Z, AA		ESTs, Highly similar to S50853 translation releasing factor eRF-1 [validated] - human [H.sapiens]
2388	12556	AI180376	TT		ESTs, Weakly similar to Y310_HUMAN Hypothetical protein KIAA0310 [H.sapiens]
2390	7460	AI180413	N, HH, TT, XX, YY		ESTs, Highly similar to NBRT apolipoprotein H precursor - rat [R.norvegicus]
2432	21822	AI228642	D, BBB, CCC, RRR		ESTs, Highly similar to hypothetical protein MGC1936 [Homo sapiens] [H.sapiens]
2456	11527	AI229307	ZZ		ESTs, Highly similar to S27958 transcription factor BTF2 62K chain - human [H.sapiens]
2457	2615	AI229318	K, Q		ESTs, Moderately similar to nucleolar cysteine-rich protein; zinc finger autoantigen 330 [Homo sapiens] [H.sapiens]
2468	17245	AI229630	T		ESTs, Highly similar to S30034 translocating chain-associating membrane protein - human [H.sapiens]
2484	15862	AI230228	ZZ, AAA		ESTs, Weakly similar to SERC_HUMAN Phosphoserine aminotransferase (PSAT) [H.sapiens]
2490	7084	AI230362	HH		ESTs, Weakly similar to T46458 hypothetical protein DKFZp434M102.1 - human (fragment) [H.sapiens]
2495	7416	AI230458	MM, TTT		ESTs, Highly similar to S13293 KDEL receptor - human [H.sapiens]
2496	7881	AI230528	N		ESTs, Weakly similar to T17271 hypothetical protein DKFZp434B0335.1 - human [H.sapiens]
2510	8036	AI230884	F, LLL, SSS, UUU		ESTs, Highly similar to HMBA-inducible [Homo sapiens] [H.sapiens]
2514	13933	AI230991	I, J		EST, Weakly similar to T46347 hypothetical protein DKFZp434K0614.1 - human (fragment) [H.sapiens]
2521	14303	AI231159	PP, QQ		ESTs, Highly similar to KIAA1049 protein [Homo sapiens] [H.sapiens]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2530	13963	AI231388	JJ		ESTs, Highly similar to T17328 hypothetical protein DKFZp564K1964.1 - human [H.sapiens]
2536	13469	AI231479	W	UDP-glucose:ceramide glycosyltransferase	UDP-glucose:ceramide glycosyltransferase
2537	16073	AI231489	II		ESTs, Weakly similar to PCB3_MOUSE Poly(rC)-binding protein 3 (Alpha-CP3) [M.musculus]
2540	19271	AI231566	TT		ESTs, Highly similar to MAX_RAT MAX protein [R.norvegicus]
2553	24501	AI232006	General Alternate	translation elongation factor 1-delta subunit	translation elongation factor 1-delta subunit
2562	13056	AI232155	FFF		ESTs, Highly similar to CN01_HUMAN Protein C14orf1 (HSPC288) (Protein AD-011) (x0006) [H.sapiens]
2584	3661	AI232506	M		ESTs, Weakly similar to T46908 hypothetical protein DKFZp761G2423.1 - human [H.sapiens]
2585	11269	AI232510	E		ESTs, Highly similar to T08712 hypothetical protein DKFZp566C0424.1 - human (fragment) [H.sapiens]
2605	17240	AI233054	N, QQ, XX, YY		ESTs, Weakly similar to UCRQ_HUMAN Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C (Ubiquinol-cytochrome C reductase complex 9.5 kDa protein) (Complex III subunit VII) [H.sapiens]
2627	18900	AI233570	X, Y, LLL, SSS, UUU		ESTs, Highly similar to PSD8_HUMAN 26S proteasome non-ATPase regulatory subunit 8 (26S proteasome regulatory subunit S14) (p31) [H.sapiens]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2628	7888	AI233583	FFF, GGG, PPP, General Core Tox Markers		ESTs, Highly similar to SYR_HUMAN ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS) [H.sapiens], ESTs, Moderately similar to JC4365 arginine--trna ligase (EC 6.1.1.19) - human [H.sapiens]
2633	7243	AI233717	General Core Tox Markers		ESTs, Moderately similar to ERHUAH coatomer complex alpha chain homolog - human [H.sapiens]
2634	3816	AI233729	K, Q, UUU		ESTs, Moderately similar to PSD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 (26S proteasome subunit S5B) (26S protease subunit S5 basic) [H.sapiens]
2665	17537	AI234497	VV		ESTs, Highly similar to SNX6_HUMAN Sorting nexin 6 (TRAF4-associated factor 2) [H.sapiens]
2690	18484	AI235349	Z		ESTs, Highly similar to Y184_HUMAN HYPOTHETICAL PROTEIN KIAA0184 [H.sapiens]
2691	3645	AI235362	K		ESTs, Highly similar to mitochondrial ribosomal protein L49; chromosome 11 open reading frame 4 [Homo sapiens] [H.sapiens]
2695	11264	AI235493	HH		ESTs, Moderately similar to MAN1_HUMAN Inner nuclear membrane protein Man1 [H.sapiens]
2702	11164	AI235739	A, B		ESTs, Moderately similar to A56716 aromatic ester hydrolase (EC 3.1.1.-) - human [H.sapiens]
2736	15398	AI236566	General Alternate		ESTs, Moderately similar to T12473 hypothetical protein DKFZp564G1762.1 - human (fragment) [H.sapiens]
2762	17922	AI237007	M		ESTs, Highly similar to S41115 probable flavoprotein-ubiquinone oxidoreductase (EC 1.6.5.-) - human [H.sapiens]
2775	21653	AI237535	Q, R, DD, EE, CCC	LPS-induced TNF-alpha factor	LPS-induced TNF-alpha factor

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2818	14606	AI639342	WW		ESTs, Highly similar to YS64_HUMAN Hypothetical protein S164 [H.sapiens]
2824	2434	AI639411	WW, FFF		ESTs, Highly similar to T46344 hypothetical protein DKFZp434I1614.1 - human (fragment) [H.sapiens]
2824	2435	AI639411	C, FFF		ESTs, Highly similar to T46344 hypothetical protein DKFZp434I1614.1 - human (fragment) [H.sapiens]
2891	21864	H31144	MM, TTT, General Alternate		ESTs, Moderately similar to 1914275A non-receptor Tyr kinase [Homo sapiens] [H.sapiens]
2897	17913	H31707	BB, CC		ESTs, Moderately similar to T50621 hypothetical protein DKFZp762O076.1 - human (fragment) [H.sapiens]
2899	4360	H31813	B, I, J, XX, YY, PPP, QQQ		ESTs, Moderately similar to T14781 hypothetical protein DKFZp586B1621.1 - human (fragment) [H.sapiens]
2944	1336	L01267	PPP, QQQ	general transcription factor IIF, polypeptide 2 (30kD subunit)	general transcription factor IIF, polypeptide 2 (30kD subunit)
3011	4225	M31322	GG	sperm membrane protein (YWK-II)	sperm membrane protein (YWK-II)
3026	1586	M57728	BBB, CCC		Rat general mitochondrial matrix processing protease (MPP) mRNA, 3' end
3478	4940	NM_022526	U, BBB	rap7a (Rap7a), mRNA. 12/2000 Length = 1440	rap7a
3573	24648	NM_030985	F, LL, FFF	angiotensin receptor 1a (Agtr1a), mRNA. 11/2002 Length = 1450	Angiotensin II receptor, type 1 (AT1A)
3712	17734	NM_031970	Q, R	Heat shock 27 kDa protein (Hsp27), mRNA. 11/2002 Length = 787	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1
3712	17735	NM_031970	Q	Heat shock 27 kDa protein (Hsp27), mRNA. 11/2002 Length = 787	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3712	17736	NM_031970	Q, R, BBB, CCC	Heat shock 27 kDa protein (Hsp27), mRNA. 11/2002 Length = 787	ESTs, Moderately similar to hypothetical protein MGC10974 [Homo sapiens] [H.sapiens], heat shock 27kD protein 1
3789	22919	NM_053556	RR	maternal G10 transcript (G10), mRNA. 11/2001 Length = 816	maternal G10 transcript
3846	20939	NM_053884	FFF	ATPase, vacuolar, 14 kD (Atp6s14), mRNA. 11/2001 Length = 667	ATPase, vacuolar, 14 kD
3898	8820	NM_080399	S, LLL	Smhs1 protein (Smhs1), mRNA. 12/2001 Length = 1107	Smhs1 protein
3917	18027	NM_130407	K, GG, HH	UDP glycosyltransferase 1 family, polypeptide A7 (Ugt1a7), mRNA. 4/2002 Length = 2301	UDP glycosyltransferase 1 family, polypeptide A7
3935	17880	NM_133308	M	glutamate receptor, ionotropic, NMDA3B (Grin3b), mRNA. 5/2002 Length = 3178	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments) [H.sapiens]
3940	19099	NM_133417	FF	GCIP-interacting protein p29 (P29), mRNA. 3/2002 Length = 1292	GCIP-interacting protein p29
3943	21703	NM_133525	JJ, KK	putative c-Myc-responsive (Rcl), mRNA. 3/2002 Length = 564	putative c-Myc-responsive
3964	7166	NM_134406	UU	cytosolic sorting protein PACS-1 (Pacs1), mRNA. 3/2002 Length = 4198	cytosolic sorting protein PACS-1
3976	13563	NM_138530	O, P, GG, HH, EEE, GGG, MMM	MAWD binding protein (Mawbp), mRNA. 4/2002 Length = 1263	MAWD binding protein

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4012	22595	NM_139253	K	stem cell derived neuronal survival protein precursor (Sdnf), mRNA. 5/2002 Length = 1771	stem cell derived neuronal survival protein precursor
4015	9775	NM_139334	Z, WW	brain-enriched SH3-domain protein Besh3 (Besh3), mRNA. 11/2002 Length = 2362	brain-enriched SH3-domain protein Besh3
4015	9776	NM_139334	I, J	brain-enriched SH3-domain protein Besh3 (Besh3), mRNA. 11/2002 Length = 2362	brain-enriched SH3-domain protein Besh3
4015	9778	NM_139334	JJ, KK	brain-enriched SH3-domain protein Besh3 (Besh3), mRNA. 11/2002 Length = 2362	brain-enriched SH3-domain protein Besh3
4022	23251	NM_145085	PP, QQ	chloride ion pump-associated 55 kDa protein (Clp55), mRNA. 11/2002 Length = 3742	Rattus norvegicus chloride ion pump-associated 55 kDa protein (Clp55) mRNA, complete cds
4033	6824	NM_147138	G, H, X, Y, GGG, HHH, LLL, SSS, UUU, General Core Tox Markers	SNAP25 interacting protein 30 (Sip30), mRNA. 11/2002 Length = 1496	Rattus norvegicus SNAP25 interacting protein 30 (Sip30) mRNA, complete cds
4050	6365	NM_153628	OO	signal peptidase 21kDa subunit (Spc21), mRNA. 10/2002 Length = 679	Rattus norvegicus mRNA for signal peptidase 21kDa subunit, complete cds
4050	6366	NM_153628	CC, LL, NN, OO	signal peptidase 21kDa subunit (Spc21), mRNA. 10/2002 Length = 679	Rattus norvegicus mRNA for signal peptidase 21kDa subunit, complete cds
4059	18457	S45812	XX, YY		ESTs, Highly similar to 1903159A monoamine oxidase A [Rattus norvegicus] [R.norvegicus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4140	21654	U53184	Q, R, W	LPS-induced TNF-alpha factor	LPS-induced TNF-alpha factor
4177	23282	U90725	FF	lipoprotein-binding protein	lipoprotein-binding protein
4197	20810	X14181	EEE, MMM		ESTs, Highly similar to R5RT18 ribosomal protein L18a, cytosolic [validated] - rat [R.norvegicus]
4203	7459	X15551	V		ESTs, Highly similar to NBRT apolipoprotein H precursor - rat [R.norvegicus]
4209	23987	X51615	B, PP, QQ, HHH		ESTs, Highly similar to 1604368A gap junction protein Cx26 [Rattus norvegicus] [R.norvegicus]
4293	8664	Z75029	Q, ZZ, AAA		ESTs, Moderately similar to T17342 hypothetical protein DKFZp586K1924.1 - human (fragment) [H.sapiens], R.norvegicus hsp70.2 mRNA for heat shock protein 70
65	13683	AA799788	General Alternate	HHs:cell division cycle 34	ESTs, Moderately similar to I54552 hypothetical serine proteinase - rat [R.norvegicus]
87	4832	AA800190	ZZ, AAA	HHs:phosphorylase, glycogen; brain	ESTs, Highly similar to S37300 glycogen phosphorylase (EC 2.4.1.1), brain - rat [R.norvegicus]
187	13684	AA818770	H	HHs:cell division cycle 34	ESTs, Moderately similar to I54552 hypothetical serine proteinase - rat [R.norvegicus]
409	23336	AA859981	U, GG, HH, BBB, CCC, RRR	HHs:inositol(myo)-1(or 4)-monophosphatase 2	ESTs, Weakly similar to MYOP_RAT Myo-inositol-1(or 4)-monophosphatase (IMPase) (IMP) (Inositol monophosphatase) (Lithium-sensitive myo-inositol monophosphatase A1) [R.norvegicus]
794	21821	AA925664	LL	HHs:RAP1A, member of RAS oncogene family	ESTs, Highly similar to RAPA_HUMAN Ras-related protein RAP-1A (C21KG) (KREV-1 protein) (GTP-binding protein SMG-P21A) (G-22K) [R.norvegicus]
1304	4833	AI009178	E	HHs:phosphorylase, glycogen; brain	ESTs, Highly similar to S37300 glycogen phosphorylase (EC 2.4.1.1), brain - rat [R.norvegicus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1665	17506	AI070068	I, J, L, M, Z	HHs: growth arrest and DNA-damage-inducible, beta	ESTs, Weakly similar to 2104282A Gadd45 gene [Rattus norvegicus] [R.norvegicus]
1897	23596	AI105435	VV	HHs: glutaryl-Coenzyme A dehydrogenase	ESTs, Highly similar to GCDH_MOUSE Glutaryl-CoA dehydrogenase, mitochondrial precursor (GCD) [M.musculus]
2002	23152	AI169170	S	HHs: eukaryotic translation initiation factor 4A, isoform 2	ESTs, Highly similar to S00985 translation initiation factor eIF-4A II - mouse [M.musculus]
2062	15393	AI170663	FFF, General Alternate	HHs: sterol regulatory element binding transcription factor 2	ESTs, Weakly similar to A48085 transcription factor ADD1 - rat [R.norvegicus]
2973	13682	L38482	MM, FFF, TTT, General Alternate	HHs: cell division cycle 34	ESTs, Moderately similar to I54552 hypothetical serine proteinase - rat [R.norvegicus]
10	1600	AA686470	Q, R, EEE, MMM	DNA-damage inducible transcript 3	DNA-damage inducible transcript 3
37	1647	AA799575	G, H, II	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
57	14250	AA799729	W	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	ESTs, Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
58	18061	AA799735	I, J	RuvB-like protein 1	RuvB-like protein 1
133	1650	AA817825	II	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
145	2696	AA817997	F, G, H, FFF	ribosomal protein L24	ribosomal protein L24
203	576	AA819118	C, YY	S - adenosylmethionine synthetase	S - adenosylmethionine synthetase
204	6018	AA819140	BB, CC, PPP, QQQ	carbonic anhydrase 3	carbonic anhydrase 3
210	24654	AA819333	D, V	RAB3D, member RAS oncogene family	RAB3D, member RAS oncogene family
260	18673	AA849028	DDD	proteasome (prosome, macropain) subunit, alpha type 3	proteasome (prosome, macropain) subunit, alpha type 3

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
317	21713	AA851637	D	Lutheran blood group (Auberger b antigen included)	Lutheran blood group (Auberger b antigen included)
323	4048	AA851814	O, VV	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
416	17742	AA866302	HH, WW	4-hydroxyphenylpyruvic acid dioxygenase	4-hydroxyphenylpyruvic acid dioxygenase
465	1644	AA891068	G, II	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
505	21674	AA891828	SSS	procollagen, type I, alpha 2	procollagen, type I, alpha 2
509	3844	AA891857	U, FF, RRR, SSS, UUU	fractured callus expressed transcript 1	fractured callus expressed transcript 1
562	820	AA892395	B, PPP, QQQ	Aldolase B, fructose-biphosphate	Aldolase B, fructose-biphosphate
624	1552	AA893219	O, P, X, Y, WW	Glycine methyltransferase	Glycine methyltransferase
694	17906	AA899762	NNN	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1)	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1)
738	20711	AA924267	U, FF, LL, XX, BBB, CCC, RRR, SSS	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
742	17116	AA924339	X, Y	Thymus cell surface antigen	Thymus cell surface antigen
818	3817	AA926328	W	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
850	19069	AA943737	Z, General Core Tox Markers	endothelial differentiation sphingolipid G-protein-coupled receptor 1	endothelial differentiation sphingolipid G-protein-coupled receptor 1
857	867	AA943963	P	G protein-coupled receptor kinase 6	G protein-coupled receptor kinase 6

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
880	15476	AA944426	ZZ, AAA	Calmodulin III	Calmodulin III
901	402	AA945143	C, E, DD, SS, WW, KKK, NNN	tryptophan-2,3-dioxygenase	tryptophan-2,3-dioxygenase
903	4185	AA945169	V, EE, HH, TT	Transthyretin (prealbumin, amyloidosis type I)	Transthyretin (prealbumin, amyloidosis type I)
903	4186	AA945169	HH, TT	Transthyretin (prealbumin, amyloidosis type I)	Transthyretin (prealbumin, amyloidosis type I)
911	211	AA945453	General Alternate	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2
914	22604	AA945578	U, FF, KK, XX, RRR	putative peroxisomal 2,4-dienoyl-CoA reductase	putative peroxisomal 2,4-dienoyl-CoA reductase
923	1707	AA945698	OO	15-kDa selenoprotein	15-kDa selenoprotein
1151	20712	AA997806	FFF	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
1188	3062	AA998857	H, T, GG, PPP, QQQ	carboxypeptidase B2 (plasma)	carboxypeptidase B2 (plasma)
1202	1382	AB002406	UU, VV	RuvB-like protein 1	RuvB-like protein 1
1203	926	AB003042	O, P, VV	complement component 5, receptor 1	complement component 5, receptor 1
1212	22567	AB017544	W, DD, EE	peroxisomal membrane anchor protein	peroxisomal membrane anchor protein
1216	2016	AF000578	PPP, QQQ	CDC5 (cell division cycle 5, S. pombe, homolog)-like	CDC5 (cell division cycle 5, S. pombe, homolog)-like
1221	1597	AF014503	W, MM, TTT	nuclear proten 1	nuclear proten 1
1234	22602	AF044574	U, FF, BBB, CCC, RRR, SSS	putative peroxisomal 2,4-dienoyl-CoA reductase	putative peroxisomal 2,4-dienoyl-CoA reductase
1234	22603	AF044574	U, FF, LL, BBB, CCC, RRR, SSS	putative peroxisomal 2,4-dienoyl-CoA reductase	putative peroxisomal 2,4-dienoyl-CoA reductase

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1238	145	AF064541	N	arginine vasopressin receptor 1B	arginine vasopressin receptor 1B
1258	10108	AI007857	Q, R	HGF-regulated tyrosine kinase substrate	HGF-regulated tyrosine kinase substrate
1287	2853	AI008888	B, O, BB, CC, GG, NN, OO	Cystatin beta	Cystatin beta
1287	2854	AI008888	O	Cystatin beta	Cystatin beta
1347	11460	AI010293	K	HLA-B associated transcript 3	HLA-B associated transcript 3
1362	17524	AI010568	General Core Tox Markers	Growth hormone receptor	Growth hormone receptor
1384	21040	AI011734	K, L	aminolevulinic acid synthase 1	aminolevulinic acid synthase 1
1397	17654	AI012117	LL, XX	Uteroglobin (Clara cell secretory protein)	Uteroglobin (Clara cell secretory protein)
1415	2791	AI012429	ZZ, AAA	receptor (calcitonin) activity modifying protein 1	receptor (calcitonin) activity modifying protein 1
1424	3203	AI012595	Q, R, General Alternate	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
1430	1409	AI012802	A, B, M, HH, SS, UU, III, JJJ, KKK, OOO, General Core Tox Markers	Hydroxyacyl glutathione hydrolase	Hydroxyacyl glutathione hydrolase
1497	1114	AI029917	E, DD, KKK, NNN	Enolase 2, gamma, neuronal	Enolase 2, gamma, neuronal
1507	1876	AI030175	C, K, T, W, DD, EE, KKK, General Alternate	Sorbitol dehydrogenase	Sorbitol dehydrogenase
1586	6697	AI045340	MM, TTT	Kirsten rat sarcoma viral oncogene homologue 2 (active)	Kirsten rat sarcoma viral oncogene homologue 2 (active)
1808	2057	AI102579	UUU	cyclic AMP phosphoprotein, 19kD	cyclic AMP phosphoprotein, 19kD

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1814	17234	AI102741	RR	Tissue inhibitor of metalloproteinase 3	Tissue inhibitor of metalloproteinase 3
1842	18679	AI103496	AA	GDP-dissociation inhibitor 1	GDP-dissociation inhibitor 1
1850	3764	AI103651	C	ADP-ribosylarginine hydrolase	ADP-ribosylarginine hydrolase
1852	16884	AI103758	QQQ	aldehyde dehydrogenase family 9, subfamily A1	aldehyde dehydrogenase family 9, subfamily A1
1853	1649	AI103782	H	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1875	4235	AI104524	HHH, General Alternate	heterogeneous nuclear ribonucleoprotein A/B	heterogeneous nuclear ribonucleoprotein A/B
1890	16885	AI105188	PP, General Core Tox Markers	aldehyde dehydrogenase family 9, subfamily A1	aldehyde dehydrogenase family 9, subfamily A1
1908	4049	AI112012	O, VV	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
1944	24803	AI137065	MM, VV, TTT	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)
1968	961	AI138143	II	glutathione S-transferase, theta 2	glutathione S-transferase, theta 2
2017	7253	AI169378	RR	Myelin basic protein	Myelin basic protein
2018	4091	AI169417	X, Y, FFF, GGG, General Core Tox Markers, General Alternate	Phosphoglycerate mutase 1	Phosphoglycerate mutase 1
2019	24341	AI169421	GG	endosulfine alpha	endosulfine alpha
2021	3256	AI169479	H, K, LLL, SSS, UUU	proteasome (prosome, macropain) subunit, alpha type 5	proteasome (prosome, macropain) subunit, alpha type 5

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2088	14960	AI171319	G	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	ESTs, Highly similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1; integrase interactor 1 [Mus musculus] [M.musculus], guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
2160	21676	AI175101	SSS, UUU	procollagen, type I, alpha 2	procollagen, type I, alpha 2
2193	6782	AI176170	FFF	FK506-binding protein 1 (12kD)	FK506-binding protein 1 (12kD)
2218	3431	AI176595	C, D, W, BB, CC, FF, KKK, NNN, OOO, General Core Tox Markers, General Alternate	Cathepsin L	Cathepsin L
2266	14989	AI177366	HHH	Integrin, beta 1	Integrin, beta 1
2269	14977	AI177386	JJ, KK	Protein tyrosine phosphatase, receptor type, D	Protein tyrosine phosphatase, receptor type, D
2272	26258	AI177501	U	ribosomal protein S17	ribosomal protein S17
2291	659	AI178208	W	nuclear pore membrane glycoprotein 121 kD	nuclear pore membrane glycoprotein 121 kD
2309	6287	AI178652	RR	brain-specific angiogenesis inhibitor 1-associated protein 2	brain-specific angiogenesis inhibitor 1-associated protein 2
2353	16081	AI179610	B, E, Q, PP, EEE, MMM	Heme oxygenase	Heme oxygenase
2411	1651	AI228068	F	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
2437	4092	AI228723	K, DDD	Phosphoglycerate mutase 1	Phosphoglycerate mutase 1
2452	16203	AI229196	N	Synaptobrevin 1, Vesicle-associated membrane protein (synaptobrevin 2)	Synaptobrevin 1, Vesicle-associated membrane protein (synaptobrevin 2)

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2472	2088	AI229727	NN, OO	regulator of G-protein signaling 5	regulator of G-protein signaling 5
2485	4280	AI230247	LL	selenoprotein P, plasma, 1	selenoprotein P, plasma, 1
2527	24326	AI231292	X, Y	Cystatin C (cysteine proteinase inhibitor)	Cystatin C (cysteine proteinase inhibitor)
2552	4093	AI232001	S, GGG, LLL	Phosphoglycerate mutase 1	Phosphoglycerate mutase 1
2578	19287	AI232379	LLL, UUU	Platelet-derived growth factor receptor alpha	Platelet-derived growth factor receptor alpha
2615	17907	AI233224	U	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1)	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1)
2629	16709	AI233602	PP, QQ	Adenosin kinase	Adenosin kinase
2642	1653	AI233806	F, G, II, UUU	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
2659	21156	AI234248	N, PP, QQ, XX, YY	golgi SNAP receptor complex member 1	golgi SNAP receptor complex member 1
2660	1654	AI234258	X, Y, II	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
2677	2789	AI234949	MM, TTT	preimplantation protein 3	preimplantation protein 3
2688	2746	AI235291	Z, AA	casein kinase 1, alpha 1	casein kinase 1, alpha 1
2743	2855	AI236707	EEE, MMM	Cystatin beta	Cystatin beta
2763	1488	AI237016	DDD	H2A histone family, member Y	H2A histone family, member Y
2836	19703	AJ001517	E, BB, CC, II	hemochromatosis	hemochromatosis
2840	18686	D00729	B, I, J, U, FF, LL, XX, YY	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	Rat mRNA for delta3, delta2-enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
2843	1306	D10262	GG	Choline kinase	Choline kinase
2848	24797	D13667	MM, PP, QQ, RR, TTT	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)
2852	2515	D17512	E, GG, HH, GGG	cysteine-rich protein 2	cysteine-rich protein 2

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2855	16610	D28557	D, PP, QQ, HHH, General Alternate	cold shock domain protein A	cold shock domain protein A
2857	2005	D29646	NN, OO, VV	CD38 antigen (ADP-ribosyl cyclase / cyclic ADP-ribose hydrolase)	CD38 antigen (ADP-ribosyl cyclase / cyclic ADP-ribose hydrolase)
2858	3743	D30666	BBB	fatty acid Coenzyme A ligase, long chain 3	fatty acid Coenzyme A ligase, long chain 3
2859	1396	D30735	RR	augmenter of liver regeneration	augmenter of liver regeneration
2866	1531	D43964	OO, PP, QQ, PPP, QQQ	bile acid-Coenzyme A dehydrogenase: amino acid n-acyltransferase	bile acid-Coenzyme A dehydrogenase: amino acid n-acyltransferase
2871	811	D63704	B, L, III, JJJ, OOO, QQQ, General Core Tox Markers	dihydropyrimidinase	dihydropyrimidinase
2871	812	D63704	OOO, PPP, QQQ, General Core Tox Markers	dihydropyrimidinase	dihydropyrimidinase
2872	1125	D82071	OOO	prostaglandin D2 synthase 2, hematopoietic	prostaglandin D2 synthase 2, hematopoietic
2880	1414	D89514	VV	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP P cyclohydrolase	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
2882	24799	E01050	X, Y, MM, SS, TTT	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)
2884	1641	E03428	BB, CC, PP, QQ, EEE, MMM, UUU	Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
2929	1421	J04733	N, BBB, CCC, RRR	N-acylaminoacyl-peptide hydrolase	N-acylaminoacyl-peptide hydrolase

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2930	20429	J05035	F, T, GG, GGG, LLL	Steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	Steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
2930	20430	J05035	F, T, GG, GGG, General Alternate	Steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	Steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
2931	1247	J05181	Q, R, S	Glutamylcysteine gamma synthetase light chain	Glutamylcysteine gamma synthetase light chain
2932	1977	J05470	U, BBB, CCC, RRR, SSS	Carnitine palmitoyltransferase 2	Carnitine palmitoyltransferase 2
2940	20865	L00117	F, M, Y	Elastase 1	Elastase 1
2941	5616	L00191	C, E, LL, RRR, SSS	Fibronectin 1	Fibronectin 1
2969	1632	L27487	GG	Calcitonin receptor-like receptor	Calcitonin receptor-like receptor
2974	6405	L38615	G, H, JJ, KK, GGG	Glutathione synthetase gene	Glutathione synthetase gene
2974	6406	L38615	GGG	Glutathione synthetase gene	Glutathione synthetase gene
2975	1427	L38644	O, P, X, Y, VV	Importin beta	Importin beta
2983	21097	M12112	C, I, O, P, MM, NNN, TTT, General Core Tox Markers	Angiotensinogen	Angiotensinogen
2992	20714	M14972	I, J, U, FF, LL, XX, YY	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
2995	2505	M16235	B, F, G, NN, OO, GGG, LLL, General Core Tox Markers	Lipase, hepatic	Lipase, hepatic
3007	15571	M27207	M, II	procollagen, type I, alpha 1	procollagen, type I, alpha 1

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3018	1241	M35162	D, Z, AA	gamma-aminobutyric acid (GABA-A) receptor, subunit delta	gamma-aminobutyric acid (GABA-A) receptor, subunit delta
3022	16604	M37394	K, LLL, UUU	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1)	Epidermal growth factor receptor, formerly avian erythroblastic leukemia viral (v-erbB) oncogene homolog (ErbB1)
3025	20713	M57718	U, EE, FF, LL, RRR	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
3027	70	M58308	K, GG, OO, General Alternate	histidine ammonia lyase	histidine ammonia lyase
3031	457	M60666	VV	Tropomyosin 1 (alpha)	Tropomyosin 1 (alpha)
3047	1694	M84716	F, III, JJJ, General Alternate	ribosomal protein S3a	ribosomal protein S3a
3048	291	M88347	JJ	Cystathionine beta synthase	Cystathionine beta synthase
3055	1678	M96674	EEE, MMM, General Alternate	glucagon receptor	glucagon receptor
3058	23698	NM_012489	U, FF, HH, LL, XX, BBB, CCC, DDD, RRR, SSS, UUU	acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A (Acaa), mRNA. 11/2002 Length = 1619	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A 1, peroxisomal
3058	23699	NM_012489	U, FF, GG, HH, LL, DDD	acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A (Acaa), mRNA. 11/2002 Length = 1619	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A 1, peroxisomal
3060	7062	NM_012495	VV	Aldolase A, fructose-bisphosphate (Aldoa), mRNA. 11/2000 Length = 1442	Aldolase A, fructose-bisphosphate

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3060	7063	NM_012495	O, P, PP, QQ, UU, VV	Aldolase A, fructose-bisphosphate (Aldoa), mRNA. 11/2000 Length = 1442	Aldolase A, fructose-bisphosphate
3060	7064	NM_012495	II, VV, PPP, General Core Tox Markers	Aldolase A, fructose-bisphosphate (Aldoa), mRNA. 11/2000 Length = 1442	Aldolase A, fructose-bisphosphate
3061	17785	NM_012501	M, V	apolipoprotein C-3 (Apoc3), mRNA. 11/2002 Length = 306	Apolipoprotein C-III
3061	17787	NM_012501	S, DD, EE, HH, XX, YY	apolipoprotein C-3 (Apoc3), mRNA. 11/2002 Length = 306	Apolipoprotein C-III
3062	15675	NM_012504	H, DD, EE	ATPase, Na+K+ transporting, alpha 1 (Atp1a1), mRNA. 11/2002 Length = 3636	ATPase, Na+K+ transporting, alpha 1 polypeptide
3062	15677	NM_012504	N, RR, WW	ATPase, Na+K+ transporting, alpha 1 (Atp1a1), mRNA. 11/2002 Length = 3636	ATPase, Na+K+ transporting, alpha 1 polypeptide
3064	7427	NM_012515	O, P, NN, OO, VV, EEE, MMM	Benzodiazepin receptor (peripheral) (Bzrp), mRNA. 11/2000 Length = 781	Benzodiazepin receptor (peripheral)
3066	20518	NM_012518	R	Calmodulin III (Calm3), mRNA. 11/2000 Length = 691	Calmodulin III
3067	15740	NM_012520	LL	Catalase (Cat), mRNA. 11/2002 Length = 2495	Catalase
3067	15741	NM_012520	EEE, MMM	Catalase (Cat), mRNA. 11/2002 Length = 2495	Catalase
3069	24433	NM_012527	PP, QQ	cholinergic receptor, muscarinic 3 (Chrm3), mRNA. 11/2002 Length = 3578	Cholinergic receptor, muscarinic 3

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3071	11115	NM_012531	M	Catecholamine-O-methyltransferase (Comt), mRNA. 11/2000 Length = 1531	Catecholamine-O-methyltransferase
3071	11116	NM_012531	M	Catecholamine-O-methyltransferase (Comt), mRNA. 11/2000 Length = 1531	Catecholamine-O-methyltransferase
3073	488	NM_012540	A, C, L, GG, HH, DDD	cytochrome P450, 1a1 (Cyp1a1), mRNA. 10/2002 Length = 1575	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
3073	489	NM_012540	C, L, GG, HH	cytochrome P450, 1a1 (Cyp1a1), mRNA. 10/2002 Length = 1575	Cytochrome P450, subfamily I (aromatic compound-inducible), member A1 (C6, form c)
3073	20705	NM_012540	C, K, L, U, GG, HH, II, DDD, RRR	cytochrome P450, 1a1 (Cyp1a1), mRNA. 10/2002 Length = 1575	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
3074	20703	NM_012541	C, K, L, M, U, Y, GG, HH, II, RRR, SSS	cytochrome P450, 1a2 (Cyp1a2), mRNA. 11/2002 Length = 1542	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
3074	20704	NM_012541	C, K, L, T, GG, HH, DDD	cytochrome P450, 1a2 (Cyp1a2), mRNA. 11/2002 Length = 1542	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
3075	23868	NM_012551	A, BB, CC, NNN	Early growth response 1 (Egr1), mRNA. 11/2002 Length = 3112	Early growth response 1
3075	23869	NM_012551	A, BB, CC, NNN	Early growth response 1 (Egr1), mRNA. 11/2002 Length = 3112	Early growth response 1
3075	23871	NM_012551	W	Early growth response 1 (Egr1), mRNA. 11/2002 Length = 3112	Early growth response 1
3075	23872	NM_012551	A, OO, NNN	Early growth response 1 (Egr1), mRNA. 11/2002 Length = 3112	Early growth response 1

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3078	17676	NM_012556	N, HH	Fatty acid binding protein 1, liver (Fabp1), mRNA. 11/2002 Length = 493	Fatty acid binding protein 1, liver
3082	4573	NM_012570	XX, YY	Glutamate dehydrogenase (Glud1), mRNA. 11/2002 Length = 2874	Glutamate dehydrogenase
3082	4574	NM_012570	GG, OO, DDD	Glutamate dehydrogenase (Glud1), mRNA. 11/2002 Length = 2874	Glutamate dehydrogenase
3084	16024	NM_012578	WW, ZZ, AAA	Histone H1-0 (H1f0), mRNA. 11/2000 Length = 1779	Histone H1-0
3084	16025	NM_012578	WW, ZZ, AAA	Histone H1-0 (H1f0), mRNA. 11/2000 Length = 1779	Histone H1-0
3084	16026	NM_012578	ZZ, AAA	Histone H1-0 (H1f0), mRNA. 11/2000 Length = 1779	Histone H1-0
3085	16080	NM_012580	E, OO, PP, EEE, MMM	Heme oxygenase (Hmox1), mRNA. 10/2002 Length = 870	Heme oxygenase
3087	20313	NM_012585	D, E	5-hydroxytryptamine (serotonin) receptor 1A (Htr1a), mRNA. 11/2002 Length = 1269	5-Hydroxytryptamine (serotonin) receptor 1A
3088	15097	NM_012588	Z	insulin-like growth factor binding protein 3 (Igfbp3), mRNA. 11/2002 Length = 2352	Insulin-like growth factor-binding protein (IGF-BP3)
3088	15098	NM_012588	GG, II	insulin-like growth factor binding protein 3 (Igfbp3), mRNA. 11/2002 Length = 2352	Insulin-like growth factor-binding protein (IGF-BP3)
3089	21162	NM_012591	W	Interferon regulatory factor 1 (Irf1), mRNA. 11/2002 Length = 2078	Interferon regulatory factor 1

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Seq. ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3090	4449	NM_012592	F, V, Z, AA, XX, YY, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3090	4450	NM_012592	A, B, V, BB, CC, II, OOO, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3090	4451	NM_012592	VV, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3090	4452	NM_012592	VV, General Alternate	Isovaleryl Coenzyme A dehydrogenase (Ivd), mRNA. 11/2002 Length = 2104	Isovaleryl Coenzyme A dehydrogenase
3094	2629	NM_012603	W	v-myc avian myelocytomatosis viral oncogene homolog (Myc), mRNA. 11/2002 Length = 2168	Avian myelocytomatosis viral (v-myc) oncogene homolog
3096	23522	NM_012615	A	Ornithine decarboxylase (Odc1), mRNA. 11/2000 Length = 2442	Ornithine decarboxylase
3096	23523	NM_012615	B, H, I, J	Ornithine decarboxylase (Odc1), mRNA. 11/2000 Length = 2442	Ornithine decarboxylase
3098	6055	NM_012619	WW, LLL, RRR, SSS, UUU	Phenylalanine hydroxylase (Pah), mRNA. 11/2002 Length = 1998	Phenylalanine hydroxylase
3100	20798	NM_012639	V, X, Y	v-raf-1 murine leukemia viral oncogene homolog 1 (Raf1), mRNA. 11/2002 Length = 2524	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3100	20799	NM_012639	I	v-raf-1 murine leukemia viral oncogene homolog 1 (Raf1), mRNA. 11/2002 Length = 2524	Murine leukemia viral (v-raf-1) oncogene homolog 1 (3611-MSV)
3103	9423	NM_012649	I, J, L, U, W, EE, NNN, OOO, General Alternate	syndecan 4 (Sdc4), mRNA. 11/2002 Length = 2462	Ryudocan/syndecan 4
3103	9424	NM_012649	C, L, W, DD, WW, NNN	syndecan 4 (Sdc4), mRNA. 11/2002 Length = 2462	Ryudocan/syndecan 4
3104	16332	NM_012651	Z, AA	Solute carrier family 4, member 1, anion exchange protein 1 (kidney band 3) (Slc4a1), mRNA. 11/2000 Length = 2547	Solute carrier family 4, member 1, anion exchange protein 1 (kidney band 3)
3105	16217	NM_012656	G, H, M, EE, II, LLL, SSS, UUU	Secreted acidic cystein-rich glycoprotein (osteonectin) (Sparc), mRNA. 11/2000 Length = 2025	Secreted acidic cystein-rich glycoprotein (osteonectin)
3105	16221	NM_012656	M, QQ	Secreted acidic cystein-rich glycoprotein (osteonectin) (Sparc), mRNA. 11/2000 Length = 2025	Secreted acidic cystein-rich glycoprotein (osteonectin)
3109	24825	NM_012668	C, D, I, J, NNN	tyrosine aminotransferase (Tat), mRNA. 11/2002 Length = 2362	Tyrosine aminotransferase

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3110	24427	NM_012669	UU	Transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1); albumin proximal factor, also TCF1 (Tcf1), mRNA. 11/2000 Length = 3538	Transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1); albumin proximal factor, also TCF1
3111	17117	NM_012673	K	Thymus cell surface antigen (Thy1), mRNA. 11/2000 Length = 650	Thymus cell surface antigen
3114	20776	NM_012680	XX, YY	Tuberous sclerosis 2, (renal carcinoma) (Tsc2), mRNA. 11/2000 Length = 5573	Tuberous sclerosis 2, (renal carcinoma)
3115	24453	NM_012690	A	P-glycoprotein 3/ multidrug resistance 2 (Pgy3), mRNA. 11/2002 Length = 3912	ATP-binding cassette, sub-family B (MDR/TAP), member 4 (P-glycoprotein 3/ multidrug resistance 2
3118	139	NM_012694	SS, UU	Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA. 11/2002 Length = 3404	Solute carrier family 6 (neurotransmitter transporter, dopamine), member 3
3120	1850	NM_012696	D, E, M, BB, CC, III, JJJ	T-kininogen (Kng), mRNA. 11/2002 Length = 1417	T-kininogen, see also D11Elh1 and D11Mit8
3120	1854	NM_012696	D, E, M, BB	T-kininogen (Kng), mRNA. 11/2002 Length = 1417	T-kininogen, see also D11Elh1 and D11Mit8
3123	4002	NM_012708	KKK	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2) (Psemb9), mRNA. 11/2002 Length = 880	Low molecular mass polypeptide 2

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3123	4003	NM_012708	I, J, KKK	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2) (Psm9), mRNA. 11/2002 Length = 880	Low molecular mass polypeptide 2
3125	20888	NM_012716	CC, BBB, CCC	Solute carrier 16 (monocarboxylic acid transporter), member 1 (Slc16a1), mRNA. 11/2000 Length = 3320	Solute carrier 16 (monocarboxylic acid transporter), member 1
3125	20889	NM_012716	BB, CC, LL, TT	Solute carrier 16 (monocarboxylic acid transporter), member 1 (Slc16a1), mRNA. 11/2000 Length = 3320	Solute carrier 16 (monocarboxylic acid transporter), member 1
3126	22294	NM_012720	AA, SS	Myelin-associated/Oligodendrocytic Basic Protein-81 (Mbp81), mRNA. 11/2002 Length = 3442	myelin-associated oligodendrocytic basic protein
3127	24722	NM_012725	F, G, U, WW	kallikrein B, plasma 1 (Klk3), mRNA. 11/2002 Length = 2583	Plasma kallikrein
3130	1371	NM_012734	D, V, GG	Hexokinase 1 (Hk1), mRNA. 11/2002 Length = 3653	Hexokinase 1
3131	11839	NM_012735	Z, AA, NNN	Hexokinase 2 (Hk2), mRNA. 11/2002 Length = 3635	Hexokinase 2
3132	5318	NM_012737	PP, QQ	Apolipoprotein A-IV (Apoa4), mRNA. 5/2002 Length = 1423	Apolipoprotein A-IV, ESTs, Moderately similar to APA4_RAT APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) [R.norvegicus]
3132	18236	NM_012737	V	Apolipoprotein A-IV (Apoa4), mRNA. 5/2002 Length = 1423	ESTs, Moderately similar to APA4_RAT APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) [R.norvegicus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3139	11938	NM_012783	X, Y, EE	basigin (Bsg), mRNA. 11/2002 Length = 1443	Basigin (Ox47 antigen or CE-9) (EMMPRIN in human) (neurothelin, HT7 or 5A11 in avian)
3142	16947	NM_012793	N, T, HHH, PPP, QQQ, General Alternate	Guanidinoacetate methyltransferase (Gamt), mRNA. 11/2002 Length = 924	Guanidinoacetate methyltransferase
3142	16948	NM_012793	PPP, QQQ	Guanidinoacetate methyltransferase (Gamt), mRNA. 11/2002 Length = 924	Guanidinoacetate methyltransferase
3143	960	NM_012796	V, DD, EE, UU, III, JJJ, General Alternate	glutathione S-transferase, theta 2 (Gstt2), mRNA. 9/2002 Length = 1258	glutathione S-transferase, theta 2
3148	835	NM_012813	SS	Sialyltransferase 8a (Siat8a), mRNA. 10/2002 Length = 1223	Sialyltransferase 8 A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase) GenBank no: U53883
3149	15032	NM_012816	X, Y	alpha-methylacyl-CoA racemase (Amacr), mRNA. 11/2002 Length = 1504	alpha-methylacyl-CoA racemase
3150	6780	NM_012819	U, RRR	Acyl Coenzyme A dehydrogenase, long chain (Acadl), mRNA. 11/2000 Length = 1451	Acyl Coenzyme A dehydrogenase, long chain
3150	6781	NM_012819	HH	Acyl Coenzyme A dehydrogenase, long chain (Acadl), mRNA. 11/2000 Length = 1451	Acyl Coenzyme A dehydrogenase, long chain
3151	23670	NM_012824	S, V	Apolipoprotein C1 (Apoc1), mRNA. 11/2000 Length = 435	Apolipoprotein C1
3152	20587	NM_012826	O, P, VV	alpha-2 - glycoprotein 1, zinc (Azgp1), mRNA. 11/2002 Length = 1250	Zn - alpha2 - glycoprotein

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TABLE 1					
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Seq. ID No.	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3153	373	NM_012833	NN, UU, KKK, NNN	ATP-binding cassette, sub-family C (CFTR/MRP), member 2 (Abcc2), mRNA. 11/2002 Length = 4918	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
3155	20885	NM_012842	II	epidermal growth factor (Egf), mRNA. 11/2002 Length = 4801	Epidermal growth factor
3156	17541	NM_012844	F, N, S, CC, II, NN, OO, PP, QQ, TT, DDD, EEE, LLL, MMM, SSS, UUU, General Alternate	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase) (Ephx1), mRNA. 10/2002 Length = 1242	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)
3157	20819	NM_012847	W, General Alternate	Farnesyltransferase, subunit alpha (Fnta), mRNA. 11/2000 Length = 1680	Farnesyltransferase, subunit alpha
3161	17306	NM_012876	EE, MM, YY, TTT	Ribosomal protein S29 (Rps29), mRNA. 11/2002 Length = 318	Ribosomal protein S29
3162	15872	NM_012879	U, FF, MM, NN, OO, EEE, LLL, MMM, RRR, SSS, TTT, UUU	Solute carrier family 2 A2 (gkucose transporter, type 2) (Slc2a2), mRNA. 11/2000 Length = 2573	Solute carrier family 2 A2 (gkucose transporter, type 2)
3163	494	NM_012880	General Alternate	Superoxide dismutase 3 (Sod3), mRNA. 12/2001 Length = 1729	Superoxide dismutase 3
3165	4282	NM_012883	R, General Alternate	sulfotransferase, estrogen preferring (Ste), mRNA. 11/2002 Length = 1309	Estrogen sulfotransferase, selenoprotein P, plasma, 1

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3166	16871	NM_012887	T, EE, KKK, NNN	Thymopoietin (lamina associated polypeptide 2) (Tmpe), mRNA. 11/2000 Length = 3508	Thymopoietin (lamina associated polypeptide 2)
3167	24857	NM_012888	RR, SS	Thyroid stimulating hormone receptor (Tshr), mRNA. 11/2002 Length = 5270	Thyroid stimulating hormone receptor
3169	16708	NM_012895	UU, WW	Adenosin kinase (Adk), mRNA. 11/2002 Length = 1123	Adenosin kinase
3170	16274	NM_012898	M, S, SS, TT	alpha 2 HS-glycoprotein alpha 2 (fetuin) (Ahsg), mRNA. 11/2002 Length = 1490	alpha-2-HS-glycoprotein
3170	16275	NM_012898	S, FF, HH, SS, NNN	alpha 2 HS-glycoprotein alpha 2 (fetuin) (Ahsg), mRNA. 11/2002 Length = 1490	alpha-2-HS-glycoprotein
3171	18564	NM_012899	L, CC, DD, EE, III, JJJ, KKK, OOO, General Core Tox Markers, General Alternate	aminolevulinate,delta-dehydratase (Alad), mRNA. 10/2001 Length = 1116	aminolevulinate,delta-dehydratase
3172	7897	NM_012901	V, SS, NNN	Alpha-1 microglobulin/bikunin (Ambp), mRNA. 1/2002 Length = 1162	Alpha-1 microglobulin/bikunin
3172	7898	NM_012901	NNN	Alpha-1 microglobulin/bikunin (Ambp), mRNA. 1/2002 Length = 1162	Alpha-1 microglobulin/bikunin
3172	7899	NM_012901	UUU	Alpha-1 microglobulin/bikunin (Ambp), mRNA. 1/2002 Length = 1162	Alpha-1 microglobulin/bikunin

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3173	7197	NM_012904	O, P, VV	Annexin 1 (p35) (Lipocortin 1) (Anx1), mRNA. 11/2002 Length = 1402	Annexin 1 (p35) (Lipocortin 1)
3176	18119	NM_012913	VV	ATPase, Na+K+ transporting, beta polypeptide 3 (Atp1b3), mRNA. 11/2000 Length = 1818	ATPase, Na+K+ transporting, beta polypeptide 3
3181	191	NM_012940	GG	Cytochrome P450 1b1 (Cyp1b1), mRNA. 11/2000 Length = 4964	Cytochrome P450 1b1
3182	20928	NM_012941	T	Cytochrom P450 Lanosterol 14 alpha-demethylase (Cyp51), mRNA. 11/2002 Length = 2260	Cytochrom P450 Lanosterol 14 alpha-demethylase
3182	20931	NM_012941	G, H, I, J, FF, General Alternate	Cytochrom P450 Lanosterol 14 alpha-demethylase (Cyp51), mRNA. 11/2002 Length = 2260	Cytochrom P450 Lanosterol 14 alpha-demethylase
3184	5033	NM_012966	L, PPP, QQQ	Heat shock 10 kD protein 1 (chaperonin 10) (Hspe1), mRNA. 11/2000 Length = 680	Heat shock 10 kD protein 1 (chaperonin 10)
3184	5034	NM_012966	RR	Heat shock 10 kD protein 1 (chaperonin 10) (Hspe1), mRNA. 11/2000 Length = 680	Heat shock 10 kD protein 1 (chaperonin 10)
3185	2554	NM_012967	W	Intercellular adhesion molecule 1 (Icam1), mRNA. 11/2000 Length = 2602	Intercellular adhesion molecule 1
3185	2555	NM_012967	W, BB, CC, NN, OO, PP	Intercellular adhesion molecule 1 (Icam1), mRNA. 11/2000 Length = 2602	Intercellular adhesion molecule 1

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3188	763	NM_012988	KK	Nuclear Factor IA (Nfia), mRNA. 11/2000 Length = 3368	Nuclear Factor IA
3189	17393	NM_012992	D, JJ, HHH	Nucleoplasmin-related protein (Nuclear protein B23 (Npm1), mRNA. 11/2000 Length = 1232	Nucleoplasmin-related protein (Nuclear protein B23
3189	17394	NM_012992	FFF, General Alternate	Nucleoplasmin-related protein (Nuclear protein B23 (Npm1), mRNA. 11/2000 Length = 1232	Nucleoplasmin-related protein (Nuclear protein B23
3193	1640	NM_013000	II, LLL, UUU	Peptidylglycine alpha-amidating monooxygenase (Pam), mRNA. 11/2002 Length = 3770	Peptidylglycine alpha-amidating monooxygenase
3195	3404	NM_013011	A, B, P, VV	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (Ywhaz), mRNA. 11/2002 Length = 1687	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
3195	25279	NM_013011	O, P, R, VV	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (Ywhaz), mRNA. 11/2002 Length = 1687	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
3197	11904	NM_013016	E, BB, PP, EEE, III, MMM	Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1) (Ptpns1), mRNA. 11/2002 Length = 3709	Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1)

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3198	1588	NM_013026	T, U, LLL, SSS	Syndecan (Synd1), mRNA. 11/2002 Length = 2410	Syndecan 1
3199	17894	NM_013027	A, HHH, III, JJJ, General Alternate	Selenoprotein W muscle 1 (Sepw1), mRNA. 7/2001 Length = 664	Selenoprotein W muscle 1
3205	16683	NM_013052	W, SS, HHH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (Ywhah), mRNA. 11/2002 Length = 1689	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
3205	16684	NM_013052	W, JJ, GGG, HHH	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (Ywhah), mRNA. 11/2002 Length = 1689	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
3207	12371	NM_013055	C	Zipper (leucine) protein kinase (Zpk), mRNA. 11/2002 Length = 3754	Mitogen activated protein kinase 12 (Zipper (leucine) protein kinase)
3210	21287	NM_013065	N	Protein phosphatase 1, catalytic subunit, beta isoform (Ppp1cb), mRNA. 11/2002 Length = 2706	Protein phosphatase 1, catalytic subunit, beta isoform
3214	13282	NM_013078	WW, FFF, General Alternate	Ornithine carbamoyltransferase (Otc), mRNA. 11/2000 Length = 1519	Ornithine carbamoyltransferase
3214	13283	NM_013078	A, B, NN, OO	Ornithine carbamoyltransferase (Otc), mRNA. 11/2000 Length = 1519	Ornithine carbamoyltransferase
3220	15295	NM_013102	P, HH, JJ	FK506-binding protein 1 (12kD) (Fkbp1a), mRNA. 11/2000 Length = 554	FK506-binding protein 1 (12kD)

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3220	15296	NM_013102	O, P, HH	FK506-binding protein 1 (12kD) (Fkbp1a), mRNA. 11/2000 Length = 554	FK506-binding protein 1 (12kD)
3222	19949	NM_013106	L, HHH	Guanine nucleotide binding, protein, alpha inhibiting polypeptide 3 (Gnai3), mRNA. 11/2000 Length = 3072	Guanine nucleotide binding, protein, alpha inhibiting polypeptide 3
3226	650	NM_013134	Q	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (Hmgcr), mRNA. 11/2002 Length = 2664	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
3226	651	NM_013134	Q	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (Hmgcr), mRNA. 11/2002 Length = 2664	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
3226	652	NM_013134	Q, R	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (Hmgcr), mRNA. 11/2002 Length = 2664	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
3228	21681	NM_013154	D, GG, HH	CCAAT/enhancer binding, protein (C/EBP) delta (Cebpd), mRNA. 11/2000 Length = 1200	CCAAT/enhancer binding, protein (C/EBP) delta
3229	3430	NM_013156	C, Q, W, MM, OOO, TTT	Cathepsin L (Ctsl), mRNA. 11/2002 Length = 1386	Cathepsin L
3234	20854	NM_013200	Z, AA	Carnitine palmitoyltransferase 1, muscle (Cpt1b), mRNA. 11/2002 Length = 2826	Carnitine palmitoyltransferase 1 beta, muscle isoform
3234	20855	NM_013200	BBB	Carnitine palmitoyltransferase 1, muscle (Cpt1b), mRNA. 11/2002 Length = 2826	Carnitine palmitoyltransferase 1 beta, muscle isoform

TABLE 1					
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Seq ID	GLCG ID No.	Genbank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3237	23362	NM_013216	JJ, GGG	Ras homolog enriched in brain (Rheb), mRNA. 11/2000 Length = 1088	Ras homolog enriched in brain
3240	21078	NM_016986	T, U, X, TT, XX, YY, III, JJJ, RRR	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain (Acadm), mRNA. 11/2000 Length = 1866	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain
3241	15610	NM_016987	Z, AA	ATP citrate lyase (Acly), mRNA. 11/2002 Length = 4269	ATP citrate lyase
3241	15612	NM_016987	BB, CC, JJJ, OOO	ATP citrate lyase (Acly), mRNA. 11/2002 Length = 4269	ATP citrate lyase
3241	15613	NM_016987	E, J, WW, OOO, General Core Tox Markers, General Alternate	ATP citrate lyase (Acly), mRNA. 11/2002 Length = 4269	ATP citrate lyase
3243	17972	NM_016989	Y	adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA. 11/2002 Length = 2681	adenylate cyclase activating polypeptide 1
3244	24869	NM_016992	Z, AA	arginine vasopressin (Avp), mRNA. 11/2002 Length = 602	Arginine vasopressin (Diabetes insipidus)
3248	15621	NM_017005	MM, XX, YY, TTT	Fumarate hydratase (Fh), mRNA. 11/2000 Length = 1589	Fumarate hydratase
3249	1399	NM_017006	G, FF	Glucose-6-phosphate dehydrogenase (G6pd), mRNA. 11/2002 Length = 2324	Glucose-6-phosphate dehydrogenase

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3252	17815	NM_017015	NNN	Glucuronidase, beta (Gusb), mRNA. 11/2002 Length = 2472	Glucuronidase, beta
3255	17807	NM_017025	C, U, FF, HH, YY	Lactate dehydrogenase A (Ldha), mRNA. 11/2002 Length = 1609	Lactate dehydrogenase A
3257	3202	NM_017039	B, Q, R, WW, General Alternate	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (Ppp2ca), mRNA. 11/2002 Length = 1804	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
3258	24596	NM_017040	Q, R, PP, QQ, SS, VV	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb), mRNA. 11/2002 Length = 1843	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
3258	24597	NM_017040	B, II	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (Ppp2cb), mRNA. 11/2002 Length = 1843	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
3259	21580	NM_017041	ZZ, AAA	protein phosphatase 3, catalytic subunit, alpha isoform (Ppp3ca), mRNA. 11/2002 Length = 2337	Calcineurin subunit A alpha
3260	24771	NM_017047	A, B, G, JJ, KK, CCC, EEE, FFF, GGG, HHH, MMM, General Core Tox Markers	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1 (Slc10a1), mRNA. 11/2002 Length = 1663	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3261	20876	NM_017050	N, UUU	Superoxide dismutase 1, soluble (Sod1), mRNA. 12/2001 Length = 650	Superoxide dismutase 1, soluble
3261	20877	NM_017050	M	Superoxide dismutase 1, soluble (Sod1), mRNA. 12/2001 Length = 650	Superoxide dismutase 1, soluble
3265	6653	NM_017068	LL, XX, YY, LLL	Lysosomal-associated membrane protein 2 (Lamp2), mRNA. 11/2000 Length = 1548	Lysosomal-associated membrane protein 2
3265	6654	NM_017068	LL	Lysosomal-associated membrane protein 2 (Lamp2), mRNA. 11/2000 Length = 1548	Lysosomal-associated membrane protein 2
3266	24719	NM_017071	RR	insulin receptor (Insr), mRNA. 11/2002 Length = 5397	Insulin receptor
3267	20649	NM_017072	L, WW	Carboamyl-phosphate synthetase 1 (Cps1), mRNA. 11/2000 Length = 4503	Carboamyl-phosphate synthetase 1
3270	18956	NM_017075	BBB	Acetyl-Co A acetyltransferase 1, mitochondrial (Acat1), mRNA. 11/2000 Length = 1715	Acetyl-Co A acetyltransferase 1, mitochondrial
3270	18957	NM_017075	D, U, GG, XX, YY, BBB, CCC	Acetyl-Co A acetyltransferase 1, mitochondrial (Acat1), mRNA. 11/2000 Length = 1715	Acetyl-Co A acetyltransferase 1, mitochondrial
3270	18958	NM_017075	U, FF, XX, BBB, CCC, RRR, SSS	Acetyl-Co A acetyltransferase 1, mitochondrial (Acat1), mRNA. 11/2000 Length = 1715	Acetyl-Co A acetyltransferase 1, mitochondrial

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3273	1550	NM_017084	F, N, O, P, X, Y, EEE, GGG, MMM	Glycine methyltransferase (Gnmt), mRNA. 11/2000 Length = 988	Glycine methyltransferase
3273	1551	NM_017084	F, O, P, X, GGG, LLL, UUU	Glycine methyltransferase (Gnmt), mRNA. 11/2000 Length = 988	Glycine methyltransferase
3274	10886	NM_017094	B, H, S, LLL, PPP, QQQ, General Core Tox Markers, General Alternate	growth hormone receptor (Ghr), mRNA. 11/2002 Length = 2950	Growth hormone receptor
3274	10887	NM_017094	A, B, T, FF, NN, OO, General Alternate	growth hormone receptor (Ghr), mRNA. 11/2002 Length = 2950	Growth hormone receptor
3275	6013	NM_017096	DD, KKK, NNN, PPP, QQQ	C-reactive protein (Crp), mRNA. 10/2002 Length = 693	C-reactive protein
3276	2149	NM_017097	H, U, GGG, General Core Tox Markers, General Alternate	Cathepsin C (dipeptidyl peptidase I) (Ctsc), mRNA. 11/2000 Length = 1850	Cathepsin C (dipeptidyl peptidase I)
3276	2150	NM_017097	LL, FFF, GGG, OOO, RRR, SSS, UUU, General Core Tox Markers, General Alternate	Cathepsin C (dipeptidyl peptidase I) (Ctsc), mRNA. 11/2000 Length = 1850	Cathepsin C (dipeptidyl peptidase I)

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence/Cluster Title
3277	15517	NM_017099	NN, OO	potassium inwardly-rectifying channel, subfamily J, member 8 (Kcnj8), mRNA. 11/2002 Length = 1580	Inwardly rectifying potassium channel gene, subfamily J-8 (ATP sensitive)
3279	15776	NM_017108	SS	potassium voltage-gated channel, subfamily H (eag-related), member 3 (Kcnh3), mRNA. 11/2002 Length = 3715	potassium voltage-gated channel, subfamily H (eag-related), member 3
3280	20745	NM_017113	C, O, P	granulin (Grn), mRNA. 11/2002 Length = 2113	granulin
3280	20746	NM_017113	O, P	granulin (Grn), mRNA. 11/2002 Length = 2113	granulin
3281	21538	NM_017116	P	calpain 2 (Capn2), mRNA. 11/2002 Length = 3252	calpain 2
3282	21663	NM_017126	E, BBB, CCC	ferredoxin 1 (Fdx1), mRNA. 11/2002 Length = 838	ferredoxin 1
3283	24693	NM_017134	C, General Alternate	arginase 1 (Arg1), mRNA. 11/2002 Length = 1386	arginase 1, liver
3284	16681	NM_017136	A, B	squalene epoxidase (Sqle), mRNA. 11/2002 Length = 2199	squalene epoxidase
3285	24885	NM_017138	F, G, H, General Alternate	laminin receptor 1 (67kD, ribosomal protein SA) (Lamr1), mRNA. 11/2002 Length = 1018	laminin receptor 1
3285	24886	NM_017138	F, G, H, VV	laminin receptor 1 (67kD, ribosomal protein SA) (Lamr1), mRNA. 11/2002 Length = 1018	laminin receptor 1
3286	24107	NM_017141	PP, QQ	DNA polymerase beta (Polb), mRNA. 11/2002 Length = 3298	DNA polymerase beta

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3289	15365	NM_017147	VV, FFF, General Alternate	cofilin 1 (Cf1), mRNA. 11/2002 Length = 1039	cofilin 1, non-muscle
3292	21643	NM_017152	CC, II, EEE, MMM	ribosomal protein S17 (Rps17), mRNA. 11/2002 Length = 466	ribosomal protein S17
3295	17104	NM_017160	G, H, II, JJ, KK, DDD, FFF, HHH, General Alternate	ribosomal protein S6 (Rps6), mRNA. 11/2002 Length = 801	ribosomal protein S6
3295	17105	NM_017160	H, II, General Alternate	ribosomal protein S6 (Rps6), mRNA. 11/2002 Length = 801	ribosomal protein S6
3295	17107	NM_017160	XX, YY	ribosomal protein S6 (Rps6), mRNA. 11/2002 Length = 801	ribosomal protein S6
3298	14498	NM_017169	EE	peroxiredoxin 2 (Prdx2), mRNA. 11/2002 Length = 877	peroxiredoxin 2
3301	19031	NM_017180	Q, R	T-cell death associated gene (Tdag), mRNA. 11/2002 Length = 1353	T-cell death associated gene
3303	24670	NM_017189	L	asialoglycoprotein receptor 2 (Asgr2), mRNA. 11/2002 Length = 1290	asialoglycoprotein receptor 2
3305	16269	NM_017196	V, X, Y	allograft inflammatory factor 1 (Aif1), mRNA. 11/2002 Length = 653	allograft inflammatory factor 1, balloon angioplasty responsive transcript
3307	20779	NM_017201	I, J, HH	S-adenosylhomocysteine hydrolase (Ahcy), mRNA. 11/2002 Length = 2029	S-adenosylhomocysteine hydrolase

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3308	14696	NM_017202	LL	cytochrome c oxidase, subunit 4a (Cox4a), mRNA. 11/2002 Length = 696	cytochrome c oxidase, subunit IVa
3314	17740	NM_017233	L, S, EE, TT, WW	4-hydroxyphenylpyruvic acid dioxygenase (Hpd), mRNA. 11/2002 Length = 1361	4-hydroxyphenylpyruvic acid dioxygenase
3315	15598	NM_017236	V	phosphatidylethanolamine binding protein (Pbp), mRNA. 11/2002 Length = 1075	phosphatidylethanolamine binding protein
3315	15599	NM_017236	I, J, GG	phosphatidylethanolamine binding protein (Pbp), mRNA. 11/2002 Length = 1075	phosphatidylethanolamine binding protein
3318	18750	NM_017257	II, EEE, MMM	protease (prosome, macropain) 28 subunit, beta (Psme2), mRNA. 11/2002 Length = 806	protease (prosome, macropain) 28 subunit, beta
3319	15299	NM_017259	W, II, KKK, OOO, General Core Tox Markers	B-cell translocation gene 2 (Btg2), mRNA. 11/2002 Length = 2519	Early induced gene, B-cell translocation gene 2
3319	15300	NM_017259	W, II	B-cell translocation gene 2 (Btg2), mRNA. 11/2002 Length = 2519	Early induced gene, B-cell translocation gene 2
3319	15301	NM_017259	A, B, W, II	B-cell translocation gene 2 (Btg2), mRNA. 11/2002 Length = 2519	Early induced gene, B-cell translocation gene 2
3320	15224	NM_017264	N, LL	protease (prosome, macropain) 28 subunit, alpha (Psme1), mRNA. 11/2002 Length = 921	protease (prosome, macropain) 28 subunit, alpha

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Seq. ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3320	15225	NM_017264	N	protease (prosome, macropain) 28 subunit, alpha (Psme1), mRNA. 11/2002 Length = 921	protease (prosome, macropain) 28 subunit, alpha
3320	15227	NM_017264	HH	protease (prosome, macropain) 28 subunit, alpha (Psme1), mRNA. 11/2002 Length = 921	protease (prosome, macropain) 28 subunit, alpha
3321	20600	NM_017268	G, H, FF, JJ, KK, FFF, General Alternate	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (Hmgcs1), mRNA. 11/2002 Length = 3275	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
3321	20601	NM_017268	G, H, J, JJ, KK, FFF, KKK, OOO, General Alternate	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (Hmgcs1), mRNA. 11/2002 Length = 3275	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
3323	15141	NM_017278	A, D, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 1 (Psma1), mRNA. 11/2002 Length = 1174	proteasome (prosome, macropain) subunit, alpha type 1
3324	5747	NM_017279	D, General Alternate	proteasome (prosome, macropain) subunit, alpha type 2 (Psma2), mRNA. 11/2002 Length = 852	proteasome (prosome, macropain) subunit, alpha type 2
3324	5748	NM_017279	X, Y	proteasome (prosome, macropain) subunit, alpha type 2 (Psma2), mRNA. 11/2002 Length = 852	proteasome (prosome, macropain) subunit, alpha type 2

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3324	5749	NM_017279	D, LL, YY, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 2 (Psm2), mRNA. 11/2002 Length = 852	proteasome (prosome, macropain) subunit, alpha type 2
3325	3987	NM_017280	GGG, HHH	proteasome (prosome, macropain) subunit, alpha type 3 (Psm3), mRNA. 11/2002 Length = 897	proteasome (prosome, macropain) subunit, alpha type 3
3326	1447	NM_017281	A, BBB, CCC, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 4 (Psm4), mRNA. 11/2002 Length = 1121	proteasome (prosome, macropain) subunit, alpha type 4
3327	3253	NM_017282	ZZ, AAA	proteasome (prosome, macropain) subunit, alpha type 5 (Psm5), mRNA. 11/2002 Length = 970	proteasome (prosome, macropain) subunit, alpha type 5
3327	3254	NM_017282	TT, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 5 (Psm5), mRNA. 11/2002 Length = 970	proteasome (prosome, macropain) subunit, alpha type 5
3329	8956	NM_017284	PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 2 (Psm2), mRNA. 11/2002 Length = 792	proteasome (prosome, macropain) subunit, beta type, 2
3329	8957	NM_017284	PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 2 (Psm2), mRNA. 11/2002 Length = 792	proteasome (prosome, macropain) subunit, beta type, 2

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3332	16839	NM_017291	AA	gamma-aminobutyric acid A receptor, rho 1 (Gabrr1), mRNA. 11/2002 Length = 4183	gamma-aminobutyric acid (GABA-A) receptor, subunit rho 1
3333	23825	NM_017299	KK, EEE, MMM	solute carrier family 19, member 1 (Slc19a1), mRNA. 11/2002 Length = 2402	solute carrier family 19 (sodium/hydrogen exchanger), member 1
3333	23826	NM_017299	D, Z, AA	solute carrier family 19, member 1 (Slc19a1), mRNA. 11/2002 Length = 2402	solute carrier family 19 (sodium/hydrogen exchanger), member 1
3334	14003	NM_017305	Q, R, S, X, Y, NN, OO, General Alternate	Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (Glcrl), mRNA. 11/2002 Length = 1382	glutamate-cysteine ligase, modifier subunit
3334	14004	NM_017305	Q, R, T, KKK	Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (Glcrl), mRNA. 11/2002 Length = 1382	glutamate-cysteine ligase, modifier subunit
3335	18687	NM_017306	A, B, E, I, J, U, FF, LL, XX, YY	dodecenoyl-coenzyme A delta isomerase (Dci), mRNA. 11/2002 Length = 987	Rat mRNA for delta3, delta2-enoyl-CoA isomerase, dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
3342	20809	NM_017326	K	Calmodulin 2 (phosphorylase kinase, delta) (Calm2), mRNA. 5/2002 Length = 1112	Calmodulin 2 (phosphorylase kinase, delta)
3352	455	NM_019131	H, VV	tropomyosin 1, alpha (Tpm1), mRNA. 11/2002 Length = 1004	Tropomyosin 1 (alpha)
3355	16227	NM_019137	SS, XX, YY	early growth response 4 (Egr4), mRNA. 11/2002 Length = 2145	Zinc-finger transcription factor NGFI-C (early response gene)

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3356	14971	NM_019140	JJ, KK	protein tyrosine phosphatase, receptor type, D (Ptprd), mRNA. 11/2002 Length = 6469	Protein tyrosine phosphatase, receptor type, D
3356	14973	NM_019140	JJ, KK, General Alternate	protein tyrosine phosphatase, receptor type, D (Ptprd), mRNA. 11/2002 Length = 6469	Protein tyrosine phosphatase, receptor type, D
3356	14974	NM_019140	T	protein tyrosine phosphatase, receptor type, D (Ptprd), mRNA. 11/2002 Length = 6469	Protein tyrosine phosphatase, receptor type, D
3357	5617	NM_019143	RR, SS, UU	Fibronectin 1 (Fn1), mRNA. 11/2002 Length = 8329	Fibronectin 1
3357	5619	NM_019143	N, PP, QQ, RR, WW, SSS, UUU	Fibronectin 1 (Fn1), mRNA. 11/2002 Length = 8329	Fibronectin 1
3357	5621	NM_019143	T, PPP, QQQ	Fibronectin 1 (Fn1), mRNA. 11/2002 Length = 8329	Fibronectin 1
3357	5622	NM_019143	E, S, U, V, X, Y, BB, CC, LL, III, JJJ, LLL, RRR, SSS, UUU	Fibronectin 1 (Fn1), mRNA. 11/2002 Length = 8329	Fibronectin 1
3359	20373	NM_019145	D, Z, AA	cholinergic receptor, nicotinic, gamma polypeptide (Chrng), mRNA. 11/2002 Length = 1832	Cholinergic receptor, nicotinic, gamma polypeptide
3360	20863	NM_019152	D	calpain 1 (Capn1), mRNA. 11/2002 Length = 2917	calpain 1
3362	21090	NM_019158	KKK	aquaporin 8 (Aqp8), mRNA. 11/2002 Length = 1463	aquaporin 8

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3363	20256	NM_019163	JJ, KK	presenilin 1 (Psen1), mRNA. 11/2002 Length = 1407	presenilin 1
3365	23481	NM_019185	Y	GATA-binding protein 6 (Gata6), mRNA. 3/2001 Length = 1844	GATA-binding protein 6
3366	24019	NM_019186	Q, R, General Alternate	ADP-ribosylation-like 4 (Arl4), mRNA. 11/2002 Length = 1067	ADP-ribosylation-like 4
3367	15242	NM_019191	O, P, EE	MAD homolog 2 (Drosophila) (Madh2), mRNA. 11/2002 Length = 2113	MAD homolog 2 (Drosophila)
3368	22062	NM_019195	CCC	integrin-associated protein (Cd47), mRNA. 11/2002 Length = 1053	integrin-associated protein
3368	22063	NM_019195	BBB, CCC	integrin-associated protein (Cd47), mRNA. 11/2002 Length = 1053	integrin-associated protein
3369	18573	NM_019201	A, B, KK, HHH	C-terminal binding protein 1 (Ctbp1), mRNA. 11/2002 Length = 2430	C-terminal binding protein 1
3370	20435	NM_019202	UU	phospholipase A2, group 2C (Pla2g2c), mRNA. 11/2002 Length = 4372	phospholipase A2, group IIC
3371	19241	NM_019206	O	Serine/threonine kinase 10 (Stk10), mRNA. 11/2002 Length = 4301	Serine/threonine kinase 10
3373	2078	NM_019220	S, V	amino-terminal enhancer of split (Aes), mRNA. 1/2002 Length = 1356	amino-terminal enhancer of split
3373	2079	NM_019220	General Alternate	amino-terminal enhancer of split (Aes), mRNA. 1/2002 Length = 1356	amino-terminal enhancer of split

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3375	20938	NM_019223	V, EE	NADH dehydrogenase Fe-S protein 6 (Ndufs6), mRNA. 11/2002 Length = 351	NADH dehydrogenase Fe-S protein 6
3376	16285	NM_019229	JJ, KK	solute carrier family 12, member 4 (Slc12a4), mRNA. 11/2002 Length = 3726	solute carrier family 12, member 4
3378	16449	NM_019238	SS, KKK, OOO, General Alternate	farnesyl diphosphate farnesyl transferase 1 (Fdt1), mRNA. 11/2002 Length = 1662	farnesyl diphosphate farnesyl transferase 1
3378	16450	NM_019238	C, I, J, FF, OOO, General Alternate	farnesyl diphosphate farnesyl transferase 1 (Fdt1), mRNA. 11/2002 Length = 1662	farnesyl diphosphate farnesyl transferase 1
3380	21109	NM_019243	PP, QQ, BBB, CCC	prostaglandin F2 receptor negative regulator (Ptgfrn), mRNA. 11/2002 Length = 5825	prostaglandin F2 receptor negative regulator
3381	23419	NM_019257	I, J	splicing factor, arginine/serine-rich 5 (Sfrs5), mRNA. 11/2002 Length = 2781	splicing factor, arginine/serine-rich 5 (SRp40, HRS)
3382	15259	NM_019259	QQ, General Alternate	complement component 1, q subcomponent binding protein (C1qbp), mRNA. 11/2002 Length = 1124	complement component 1, q subcomponent binding protein
3384	23625	NM_019269	BBB, CCC	solute carrier family 22, member 5 (Slc22a5), mRNA. 11/2002 Length = 3037	solute carrier family 22 (organic cation transporter), member 5
3385	1143	NM_019280	Z, AA	gap junction membrane channel protein alpha 5 (Gja5), mRNA. 11/2002 Length = 3115	gap junction membrane channel protein alpha 5 (connexin 40)

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Seq ID	GLGC ID No.	GenBank Acc. or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3386	20734	NM_019283	QQQ, General Core Tox Markers	solute carrier family 3, member 2 (Slc3a2), mRNA. 11/2002 Length = 1940	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
3386	20735	NM_019283	G, H, L, R, II, UU, KKK, OOO, General Core Tox Markers	solute carrier family 3, member 2 (Slc3a2), mRNA. 11/2002 Length = 1940	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
3389	6017	NM_019292	A, B, S, X, Y, GGG, HHH, General Core Tox Markers	carbonic anhydrase 3 (Ca3), mRNA. 11/2002 Length = 988	carbonic anhydrase 3
3401	23491	NM_019359	C, E, DD, JJ, MM, HHH, TTT	calponin 3, acidic (Cnn3), mRNA. 5/2002 Length = 1932	calponin 3, acidic
3403	18820	NM_019367	D, V	palmitoyl-protein thioesterase 2 (Ppt2), mRNA. 11/2002 Length = 1660	palmitoyl-protein thioesterase 2
3408	24626	NM_019381	HHH, PPP, QQQ	Testis enhanced gene transcript (Tegt), mRNA. 11/2002 Length = 940	Testis enhanced gene transcript
3414	18713	NM_020075	C, FFF	eukaryotic initiation factor 5 (eIF-5) (Eif5), mRNA. 11/2000 Length = 3504	eukaryotic initiation factor 5 (eIF- 5)
3414	18715	NM_020075	R, UU, FFF	eukaryotic initiation factor 5 (eIF-5) (Eif5), mRNA. 11/2000 Length = 3504	eukaryotic initiation factor 5 (eIF- 5)
3415	20493	NM_020076	W	3-hydroxyanthranilate 3,4-dioxygenase (HaaO), mRNA. 11/2002 Length = 1254	3-hydroxyanthranilate 3,4- dioxygenase

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3422	21336	NM_021266	UUU	frizzled homolog 1 (Drosophila) (Fzd1), mRNA. 11/2002 Length = 4540	Drosophila polarity gene (frizzled) homologue
3431	22916	NM_021740	HHH	prothymosin alpha (Ptma), mRNA. 11/2002 Length = 1182	prothymosin alpha
3433	19712	NM_021745	A, B, General Core Tox Markers, General Alternate	nuclear receptor subfamily 1, group H, member 4 (Nr1h4), mRNA. 5/2002 Length = 2070	nuclear receptor subfamily 1, group H, member 4
3435	20090	NM_021757	E, TT, ZZ, JJJ	pleiotropic regulator 1 (Plrg1), mRNA. 11/2002 Length = 1545	pleiotropic regulator 1
3437	17936	NM_021766	Y	progesterone receptor membrane component 1 (Pgrmc1), mRNA. 11/2002 Length = 1885	progesterone receptor membrane component 1
3438	22352	NM_021835	I, J, II	Avian sarcoma virus 17 (v-jun) oncogene homolog (Jun), mRNA. 4/2002 Length = 2573	Avian sarcoma virus 17 (v-jun) oncogene homolog
3441	20114	NM_021842	BB, CC, PP, QQ	endosulfine alpha (Ensa), mRNA. 11/2002 Length = 366	endosulfine alpha
3442	20187	NM_021869	M	syntaxin 7 (Stx7), mRNA. 11/2002 Length = 786	syntaxin 7
3443	243	NM_021989	EE	tissue inhibitor of metalloproteinase 2 (Timp2), mRNA. 11/2002 Length = 1009	ESTs, tissue inhibitor of metalloproteinase 2
3452	20450	NM_022239	Z, AA, SS	neuromedin (Nmu), mRNA. 11/2002 Length = 832	neuromedin U
3457	10509	NM_022268	B, I, J, V, GGG, OOO, General Core Tox Markers	liver glycogen phosphorylase (Pygl), mRNA. 11/2002 Length = 2715	liver glycogen phosphorylase

TABLE 1					
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Seq. ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3457	25814	NM_022268	I, FF, General Alternate	liver glycogen phosphorylase (Pygl), mRNA. 11/2002 Length = 2715	liver glycogen phosphorylase
3459	4561	NM_022278	GG, HH	glutaredoxin 1 (thioltransferase) (Glr1), mRNA. 5/2002 Length = 1255	glutaredoxin 1 (thioltransferase)
3460	10562	NM_022280	General Alternate	lecithin-retinol acyltransferase (Lrat), mRNA. 11/2002 Length = 5358	lecithin retinol acyltransferase
3462	1914	NM_022380	M, Z, AA	signal transducer and activator of transcription 5b (Stat5b), mRNA. 12/2000 Length = 2671	signal transducer and activator of transcription 5b
3463	11454	NM_022381	VV	Proliferating cell nuclear antigen (Pcna), mRNA. 11/2002 Length = 1160	Proliferating cell nuclear antigen
3463	11455	NM_022381	VV, General Alternate	Proliferating cell nuclear antigen (Pcna), mRNA. 11/2002 Length = 1160	Proliferating cell nuclear antigen
3472	20915	NM_022407	F, U, LL, TT, BBB, CCC, EEE, LLL, MMM, RRR, SSS, UUU	Aldehyde dehydrogenase 1, subfamily A1 (Aldh1a1), mRNA. 10/2001 Length = 2012	Aldehyde dehydrogenase 1, subfamily A1
3483	8983	NM_022539	D	methionine aminopeptidase 2 (Metap2), mRNA. 5/2002 Length = 1944	methionine aminopeptidase 2

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3483	8984	NM_022539	B, K, GGG, HHH, PPP, QQQ, General Alternate	methionine aminopeptidase 2 (Metap2), mRNA. 5/2002 Length = 1944	methionine aminopeptidase 2
3491	21076	NM_022584	QQ	thioredoxin reductase 2 (Txnrd2), mRNA. 11/2002 Length = 1999	thioredoxin reductase 2
3492	21062	NM_022585	DD, EE, MM, UU, TTT	ornithine decarboxylase antizyme inhibitor (Oazi), mRNA. 11/2002 Length = 4269	ornithine decarboxylase antizyme inhibitor
3492	21063	NM_022585	C, MM, UU, TTT	ornithine decarboxylase antizyme inhibitor (Oazi), mRNA. 11/2002 Length = 4269	ornithine decarboxylase antizyme inhibitor
3503	17567	NM_022672	III, JJJ	ribosomal protein S14 (Rps14), mRNA. 11/2002 Length = 492	ribosomal protein S14
3509	17729	NM_022697	F, DDD, FFF	ribosomal protein L28 (Rpl28), mRNA. 11/2002 Length = 466	ribosomal protein L28
3512	24345	NM_022701	N, PP, QQ	flotillin 1 (Flot1), mRNA. 11/2002 Length = 2157	flotillin 1
3513	24434	NM_022704	H, S, HH, FFF, GGG, General Core Tox Markers	mannose-binding protein C (liver) (Mbl2), mRNA. 2/2002 Length = 1037	mannose-binding protein C (liver)
3519	24838	NM_022924	PPP, QQQ	coagulation factor 2 (F2), mRNA. 11/2002 Length = 2045	coagulation factor II

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3523	19669	NM_022944	ZZ	inositol polyphosphate phosphatase-like 1 (Inpp1), mRNA. 11/2002 Length = 4828	SH2-containing inositol phosphatase 2
3532	4228	NM_023950	V	RAB7, member RAS oncogene family (Rab7), mRNA. 11/2002 Length = 861	RAB7, member RAS oncogene family
3534	21238	NM_024125	I, J, MM, TTT	CCAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA. 11/2002 Length = 1408	Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)
3534	21239	NM_024125	MM, TTT, General Alternate	CCAAT/enhancer binding protein (C/EBP), beta (Cebpb), mRNA. 11/2002 Length = 1408	Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)
3535	351	NM_024127	C	growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = 711	DNA-damage-inducible transcript 1
3535	353	NM_024127	C, HH, PP, QQ	growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = 711	DNA-damage-inducible transcript 1
3535	354	NM_024127	C, FF, II, PP, NNN	growth arrest and DNA-damage-inducible 45 alpha (Gadd45a), mRNA. 11/2002 Length = 711	DNA-damage-inducible transcript 1
3536	17226	NM_024131	Q, R, Y	D-dopachrome tautomerase (Ddt), mRNA. 11/2002 Length = 628	D-dopachrome tautomerase
3536	17227	NM_024131	F, N	D-dopachrome tautomerase (Ddt), mRNA. 11/2002 Length = 628	D-dopachrome tautomerase

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3537	20801	NM_024148	FFF, QQQ	apurinic/apurimidinic endonuclease 1 (Apex), mRNA. 5/2002 Length = 1213	apurinic/apurimidinic endonuclease 1
3543	22079	NM_024157	BBB, CCC	complement factor I (Cfi), mRNA. 2/2001 Length = 2021	complement factor I
3547	10980	NM_024349	Z, AA	adenylate kinase 1 (Ak1), mRNA. 10/2002 Length = 585	Adenylate kinase 1
3548	17764	NM_024351	Z, AA, FF	Heat shock cognate protein 70 (Hsc70), mRNA. 11/2002 Length = 2073	heat shock 70kD protein 8
3548	17765	NM_024351	GG	Heat shock cognate protein 70 (Hsc70), mRNA. 11/2002 Length = 2073	heat shock 70kD protein 8
3549	15350	NM_024356	L	GTP cyclohydrolase 1 (Gch), mRNA. 11/2002 Length = 1016	GTP cyclohydrolase 1
3550	20772	NM_024363	A	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae) (Hrmt1l2), mRNA. 11/2002 Length = 1201	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae)
3551	767	NM_024365	UU	5-hydroxytryptamine (serotonin) receptor 6 (Htr6), mRNA. 11/2002 Length = 1929	5-hydroxytryptamine (serotonin) receptor 6
3554	20380	NM_024381	HHH, General Core Tox Markers, General Alternate	glycerol kinase (Gyk), mRNA. 11/2002 Length = 2989	Glycerol kinase
3557	19992	NM_024398	L, Z, AA, WW, LLL, RRR, SSS, UUU	mitochondrial aconitase (nuclear aco2 gene) (Aco2), mRNA. 1/2002 Length = 2744	mitochondrial aconitase (nuclear aco2 gene)

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3557	19993	NM_024398	Z, AA, GGG	mitochondrial aconitase (nuclear aco2 gene) (Aco2), mRNA. 1/2002 Length = 2744	mitochondrial aconitase (nuclear aco2 gene)
3557	19994	NM_024398	WW	mitochondrial aconitase (nuclear aco2 gene) (Aco2), mRNA. 1/2002 Length = 2744	mitochondrial aconitase (nuclear aco2 gene)
3560	1835	NM_024483	HH	adrenergic receptor, alpha 1d (Adra1d), mRNA. 11/2002 Length = 2939	adrenergic receptor, alpha 1d
3561	21038	NM_024484	TT	aminolevulinic acid synthase 1 (Alas1), mRNA. 11/2002 Length = 2052	aminolevulinic acid synthase 1
3561	21039	NM_024484	K, QQ, TT	aminolevulinic acid synthase 1 (Alas1), mRNA. 11/2002 Length = 2052	aminolevulinic acid synthase 1
3563	24798	NM_030656	F, N, MM, SS, BBB, CCC, TTT	Serine-pyruvate aminotransferase (Spat), mRNA. 11/2002 Length = 1595	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)
3563	24800	NM_030656	MM, RR, SS, TTT	Serine-pyruvate aminotransferase (Spat), mRNA. 11/2002 Length = 1595	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)
3563	24801	NM_030656	MM, VV, TTT	Serine-pyruvate aminotransferase (Spat), mRNA. 11/2002 Length = 1595	Alanine-glyoxylate aminotransferase (Serine-pyruvate aminotransferase)
3574	17050	NM_030986	UU	Adenylate kinase 2 (Ak2), mRNA. 11/2002 Length = 889	Adenylate kinase 2
3576	17377	NM_030989	CC, NN, OO	Tumor protein p53 (Li Fraumeni syndrome) (Tp53), mRNA. 4/2001 Length = 1786	Tumor protein p53 (Li-Fraumeni syndrome)
3579	1792	NM_030996	K, KKK	opioid receptor, sigma 1 (Oprs1), mRNA. 11/2002 Length = 1590	opioid receptor, sigma 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3581	15683	NM_031011	MM, TTT	S-Adenosylmethionine decarboxylase 1A (Amd1a), mRNA. 11/2002 Length = 3102	S-Adenosylmethionine decarboxylase 1
3582	15700	NM_031013	VV, FFF, GGG, III, JJJ, KKK, OOO, General Core Tox Markers	liver multidrug resistance-associated protein 6 (Abcc6), mRNA. 4/2001 Length = 5775	liver multidrug resistance-associated protein 6
3594	11849	NM_031065	A, B, G, H, RR, EEE, MMM, UUU, General Alternate	ribosomal protein L10a (Rpl10a), mRNA. 11/2002 Length = 710	ribosomal protein L10a
3602	20462	NM_031102	G, H, EEE, MMM	ribosomal protein L18 (Rpl18), mRNA. 11/2002 Length = 607	ribosomal protein L18
3609	24615	NM_031112	JJ, KK, FFF	ribosomal protein S24 (Rps24), mRNA. 11/2002 Length = 466	ribosomal protein S24
3622	12313	NM_031241	JJ, KK, HHH	cytochrome P450, 8b1, sterol 12 alpha-hydrolase (Cyp8b1), mRNA. 11/2002 Length = 1965	cytochrome P450, 8b1, sterol 12 alpha-hydrolase
3623	1857	NM_031315	FF, LL	cytosolic acyl-CoA thioesterase 1 (Cte1), mRNA. 11/2002 Length = 1591	acyl-CoA thioesterase 1, cytosolic
3624	15662	NM_031318	P, ZZ, AAA	t-complex testis expressed 1 (Tctex1), mRNA. 11/2002 Length = 698	t-complex testis expressed 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3626	4234	NM_031330	A, B, I, L, Y, MM, HHH, KKK, OOO, TTT, General Alternate	heterogeneous nuclear ribonucleoprotein A/B (Hnnpab), mRNA. 11/2002 Length = 3061	heterogeneous nuclear ribonucleoprotein A/B
3633	24645	NM_031502	GCG, OOO, General Core Tox Markers	Amylase 1 (Amy1), mRNA. 11/2002 Length = 1574	Amylase 1
3637	9369	NM_031527	E	Protein phosphatase type 1 alpha, catalytic subunit (Ppp1ca), mRNA. 5/2001 Length = 1392	Protein phosphatase type 1 alpha, catalytic subunit
3637	9370	NM_031527	RR, SS	Protein phosphatase type 1 alpha, catalytic subunit (Ppp1ca), mRNA. 5/2001 Length = 1392	Protein phosphatase type 1 alpha, catalytic subunit
3642	16048	NM_031541	NN, OO	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (Cd36l1), mRNA. 10/2002 Length = 2497	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 (scavenger receptor class B type 1)
3644	18389	NM_031545	PP, UU, III	natriuretic peptide precursor type B (Nppb), mRNA. 11/2002 Length = 628	Brain natriuretic factor
3645	28	NM_031546	H, I, J, FF, FFF, OOO, SSS, UUU, General Core Tox Markers, General Alternate	Regucalcin (Rgn), mRNA. 11/2002 Length = 1605	Regucalcin

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3646	15411	NM_031559	J	carnitine palmitoyltransferase 1 (Cpt1a), mRNA. 11/2002 Length = 4377	Carnitine palmitoyltransferase 1 alpha, liver isoform
3647	18315	NM_031561	A, B, FF, BBB, CCC, RRR, SSS	cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3647	18316	NM_031561	A, B, II, BBB, CCC, RRR	cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3647	18318	NM_031561	BBB, HHH, RRR	cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3647	18319	NM_031561	BBB, CCC	cd36 antigen (Cd36), mRNA. 11/2002 Length = 2436	CD36 antigen (collagen type I receptor, thrombospondin receptor)
3648	16163	NM_031563	MM, TTT	nuclease sensitive element binding protein 1 (Nsep1), mRNA. 11/2002 Length = 1489	nuclease sensitive element binding protein 1
3648	16164	NM_031563	RR, VV	nuclease sensitive element binding protein 1 (Nsep1), mRNA. 11/2002 Length = 1489	nuclease sensitive element binding protein 1
3648	16165	NM_031563	D	nuclease sensitive element binding protein 1 (Nsep1), mRNA. 11/2002 Length = 1489	nuclease sensitive element binding protein 1
3652	24219	NM_031579	B, I, J, DD, EE, NN, OO, SS, III, JJJ	protein tyrosine phosphatase 4a1 (Ptp4a1), mRNA. 11/2002 Length = 2638	protein tyrosine phosphatase 4a1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3653	5496	NM_031589	U, W, TT, WW, EEE, LLL, MMM, RRR, SSS, UUU, General Alternate	glucose-6-phosphatase, transport protein 1 (G6pt1), mRNA. 11/2002 Length = 1930	glucose-6-phosphatase, transport protein 1
3653	5497	NM_031589	L, U, OO, TT, WW, CCC, LLL, SSS, UUU	glucose-6-phosphatase, transport protein 1 (G6pt1), mRNA. 11/2002 Length = 1930	glucose-6-phosphatase, transport protein 1
3656	19340	NM_031603	HH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide (Ywhae), mRNA. 11/2002 Length = 1771	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
3657	24234	NM_031614	G, H, Q, II	thioredoxin reductase 1 (Txnrd1), mRNA. 11/2002 Length = 3360	thioredoxin reductase 1
3657	24235	NM_031614	Q, HH, ZZ, AAA, HHH	thioredoxin reductase 1 (Txnrd1), mRNA. 11/2002 Length = 3360	thioredoxin reductase 1
3660	20940	NM_031629	G, H, X, Y, SSS	proteasome (prosome, macropain) subunit, beta type 4 (Psmb4), mRNA. 11/2002 Length = 831	proteasome (prosome, macropain) subunit, beta type, 4
3660	20942	NM_031629	UUU	proteasome (prosome, macropain) subunit, beta type 4 (Psmb4), mRNA. 11/2002 Length = 831	proteasome (prosome, macropain) subunit, beta type, 4

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3661	6554	NM_031640	V, II, RRR, General Core Tox Markers	plasma glutamate carboxypeptidase (Pgcp), mRNA. 11/2002 Length = 1778	plasma glutamate carboxypeptidase
3663	18368	NM_031648	F, General Alternate	FXD domain-containing ion transport regulator 1 (Fxd1), mRNA. 11/2002 Length = 279	FXD domain-containing ion transport regulator 1
3663	18369	NM_031648	S, General Alternate	FXD domain-containing ion transport regulator 1 (Fxd1), mRNA. 11/2002 Length = 279	FXD domain-containing ion transport regulator 1
3667	15175	NM_031682	A, B, P, U, BBB, CCC, RRR, SSS, General Alternate	hydroxysteroid (17-beta) dehydrogenase 10 (Hsd17b10), mRNA. 11/2002 Length = 917	hydroxysteroid (17-beta) dehydrogenase 10
3670	21575	NM_031698	V, FF	ribophorin 2 (Rpn2), mRNA. 10/2002 Length = 2234	ribophorin II
3672	20404	NM_031700	K, HH, TT	claudin 3 (Cldn3), mRNA. 11/2002 Length = 1192	claudin 3
3673	16204	NM_031706	JJ, KK, FFF, GGG, HHH, General Core Tox Markers, General Alternate	ribosomal protein S8 (Rps8), mRNA. 11/2002 Length = 696	ribosomal protein S8
3673	16205	NM_031706	V, Z, KK, GGG, HHH, General Alternate	ribosomal protein S8 (Rps8), mRNA. 11/2002 Length = 696	ribosomal protein S8
3675	21693	NM_031714	A, B, RRR, SSS, UUU, General Alternate	heat-responsive protein 12 (Hrsp12), mRNA. 11/2002 Length = 917	heat-responsive protein 12

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3676	19048	NM_031719	RR, SS	chloride channel, nucleotide-sensitive, 1A (Clns1a), mRNA. 11/2002 Length = 1399	chloride channel, nucleotide-sensitive, 1A
3678	23884	NM_031731	U	aldehyde dehydrogenase family 3, subfamily A2 (Aldh3a2), mRNA. 11/2002 Length = 2977	alcohol dehydrogenase family 3, subfamily A2
3679	24810	NM_031732	A, G, II, GGG, PPP, QQQ, General Alternate	sulfotransferase family 1A, phenol-preferring, member 2 (Sult1a2), mRNA. 11/2002 Length = 1363	sulfotransferase family 1A, phenol preferring, member 2
3679	24811	NM_031732	A, B, G, S, VV, GGG, PPP, QQQ, General Core Tox Markers, General Alternate	sulfotransferase family 1A, phenol-preferring, member 2 (Sult1a2), mRNA. 11/2002 Length = 1363	sulfotransferase family 1A, phenol preferring, member 2
3684	11611	NM_031756	C, FF	gamma-glutamyl carboxylase (Ggcx), mRNA. 11/2002 Length = 2754	gamma-glutamyl carboxylase
3686	14953	NM_031774	UU, XX, YY	rab acceptor 1 (prenylated) (Rabac1), mRNA. 5/2001 Length = 861	rab acceptor 1 (prenylated)
3691	15864	NM_031797	WW, OOO	kangai 1 (Kai1), mRNA. 11/2002 Length = 1740	ESTs, Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))
3693	17941	NM_031812	T, XX, YY, PPP, QQQ	CD164 antigen (Cd164), mRNA. 11/2002 Length = 2836	endolyn
3694	17194	NM_031814	ZZ, AAA	G protein-coupled receptor kinase-interactor 1 (Git1), mRNA. 11/2002 Length = 3236	G protein-coupled receptor kinase associated ADP ribosylation factor GTPase-activating protein (GIT1)

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3697	15840	NM_031817	WW	osteomodulin (osteoaderin) (Omd), mRNA. 5/2001 Length = 1536	osteomodulin (osteoaderin)
3699	10167	NM_031830	PP, QQ	flotillin 2 (Flot2), mRNA. 11/2002 Length = 2629	flotillin 2
3700	22321	NM_031832	O, BB, PP, VV, EEE, MMM, General Alternate	lectin, galactose binding, soluble 3 (Lgals3), mRNA. 5/2002 Length = 948	lectin, galactose binding, soluble 3
3710	16726	NM_031855	A, B, BB, CC, HH, OO, EEE, GGG, III, JJJ, MMM, General Core Tox Markers	Ketohexokinase (Khk), mRNA. 11/2002 Length = 1342	Ketohexokinase
3711	19191	NM_031969	O, P	Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/2002 Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
3711	25802	NM_031969	EEE, MMM	Calmodulin 1 (phosphorylase kinase, delta) (Calm1), mRNA. 11/2002 Length = 3513	Calmodulin 1 (phosphorylase kinase, delta)
3716	17601	NM_031976	K, U, X, Y, LLL, SSS	protein kinase, AMP-activated, beta 1 non-catalytic subunit (Prkab1), mRNA. 11/2002 Length = 1978	5'-AMP-activated protein kinase, beta subunit
3717	15469	NM_031978	Q, R	26S proteasome, subunit p112 (PSMD1), mRNA. 5/2001 Length = 3089	26S proteasome, subunit p112

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3722	20554	NM_031987	U, LL, BBB, CCC, RRR, SSS	carnitine O-octanoyltransferase (Crot), mRNA. 11/2002 Length = 2681	carnitine O-octanoyltransferase
3722	20555	NM_031987	U, FF, BBB, CCC, RRR	carnitine O-octanoyltransferase (Crot), mRNA. 11/2002 Length = 2681	carnitine O-octanoyltransferase
3723	18640	NM_032057	C, I, J, TT, OOO	Inositol (myo)-1(or 4)-monophosphatase 1 (Impa1), mRNA. 11/2002 Length = 2075	Inositol (myo)-1(or 4)-monophosphatase 1
3726	21809	NM_032067	ZZ, AAA	RalA binding protein 1 (Ralbp1), mRNA. 5/2001 Length = 3622	RalA binding protein 1
3726	21810	NM_032067	ZZ, AAA	RalA binding protein 1 (Ralbp1), mRNA. 5/2001 Length = 3622	RalA binding protein 1
3730	17474	NM_032614	F	thioredoxin-like 2 (Txnl2), mRNA. 11/2002 Length = 1089	thioredoxin-like 2
3730	17475	NM_032614	F	thioredoxin-like 2 (Txnl2), mRNA. 11/2002 Length = 1089	thioredoxin-like 2
3736	12363	NM_033351	N	Fc receptor, IgG, alpha chain transporter (Fcgrt), mRNA. 11/2002 Length = 1552	Fc fragment immunoglobulin G receptor
3736	12365	NM_033351	F	Fc receptor, IgG, alpha chain transporter (Fcgrt), mRNA. 11/2002 Length = 1552	Fc fragment immunoglobulin G receptor
3737	23895	NM_033485	A, B, HHH	PRKC, apoptosis, WT1, regulator (Pawr), mRNA. 11/2002 Length = 2122	Prostate apoptosis response protein 4

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3739	25431	NM_052807	D, SS	Insulin-like growth factor 1 receptor (Igf1r), mRNA. 10/2001 Length = 4696	Insulin-like growth factor 1 receptor
3740	15028	NM_052809	A, B, T, LLL	cytosolic cysteine dioxygenase 1 (Cdo1), mRNA. 5/2002 Length = 1458	cytosolic cysteine dioxygenase 1
3740	25024	NM_052809	A, YY	cytosolic cysteine dioxygenase 1 (Cdo1), mRNA. 5/2002 Length = 1458	cytosolic cysteine dioxygenase 1
3741	12577	NM_052981	A, D, V, BB, III, JJJ	cyclin H (Ccnh), mRNA. 11/2002 Length = 1116	cyclin H
3743	4090	NM_053290	JJ, KK, GGG, HHH	Phosphoglycerate mutase 1 (Pgam1), mRNA. 10/2002 Length = 1754	Phosphoglycerate mutase 1
3743	25499	NM_053290	G, H, X, Y	Phosphoglycerate mutase 1 (Pgam1), mRNA. 10/2002 Length = 1754	Phosphoglycerate mutase 1
3744	1524	NM_053293	V, General Alternate	Glutathione S-transferase 1 (theta) (Gstt1), mRNA. 11/2001 Length = 914	Glutathione S-transferase 1 (theta)
3747	17473	NM_053319	GGG	dynein, cytoplasmic, light chain 1 (Pin), mRNA. 11/2002 Length = 505	dynein, cytoplasmic, light chain 1
3749	21977	NM_053329	G, BB, CC, GGG, III, JJJ, KKK, LLL, NNN, OOO, PPP, QQQ, SSS, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. 11/2002 Length = 1812	insulin-like growth factor binding protein, acid labile subunit

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3749	21978	NM_053329	BB, PPP, QQQ, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. 11/2002 Length = 1812	insulin-like growth factor binding protein, acid labile subunit
3749	25480	NM_053329	G, S, CC, GGG, III, JJJ, KKK, OOO, PPP, QQQ, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit (Igfals), mRNA. 11/2002 Length = 1812	insulin-like growth factor binding protein, acid labile subunit
3751	14934	NM_053337	T, OO	Msx-interacting-zinc finger (Miz1), mRNA. 11/2002 Length = 1858	Msx-interacting-zinc finger
3754	6155	NM_053356	G, M, II	procollagen, type I, alpha 2 (Col1a2), mRNA. 11/2002 Length = 4474	procollagen, type I, alpha 2
3754	6156	NM_053356	M	procollagen, type I, alpha 2 (Col1a2), mRNA. 11/2002 Length = 4474	procollagen, type I, alpha 2
3754	6157	NM_053356	S	procollagen, type I, alpha 2 (Col1a2), mRNA. 11/2002 Length = 4474	procollagen, type I, alpha 2
3756	3842	NM_053371	BBB, CCC	fractured callus expressed transcript 1 (Fxc1), mRNA. 5/2002 Length = 780	fractured callus expressed transcript 1
3760	17252	NM_053402	O, P, PP, QQ	wingless-type MMTV integration site family, member 4 (Wnt4), mRNA. 11/2001 Length = 1213	wingless-type MMTV integration site family, member 4
3762	19322	NM_053409	GG	melanoma antigen, family D, 1 (Maged1), mRNA. 11/2002 Length = 2824	melanoma antigen, family D, 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3770	22586	NM_053469	L, M	hepcidin antimicrobial peptide (Hamp), mRNA. 11/2002 Length = 367	hepcidin antimicrobial peptide
3771	21866	NM_053472	V, RR, UU	cytochrome c oxidase, subunit 4b (Cox4b), mRNA. 11/2002 Length = 704	cytochrome c oxidase, subunit IVb
3791	9267	NM_053567	OO, PP, TT	formiminotransferase cyclodeaminase (Ftcd), mRNA. 11/2002 Length = 1942	formiminotransferase cyclodeaminase
3793	19252	NM_053576	G, H, L, N, HH	peroxiredoxin 5 (Prdx5), mRNA. 10/2002 Length = 1414	peroxiredoxin 5
3793	19253	NM_053576	G, H	peroxiredoxin 5 (Prdx5), mRNA. 10/2002 Length = 1414	peroxiredoxin 5
3793	19254	NM_053576	G, H, L	peroxiredoxin 5 (Prdx5), mRNA. 10/2002 Length = 1414	peroxiredoxin 5
3794	21153	NM_053584	T	golgi SNAP receptor complex member 1 (Gosr1), mRNA. 11/2002 Length = 2412	golgi SNAP receptor complex member 1
3802	20725	NM_053602	Q, R	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6 (Atp5j), mRNA. 11/2001 Length = 573	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6
3802	20726	NM_053602	LL	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6 (Atp5j), mRNA. 11/2001 Length = 573	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3803	15925	NM_053607	B	fatty acid Coenzyme A ligase, long chain 5 (FACL5), mRNA. 10/2002 Length = 2454	long-chain fatty acid coenzyme A ligase 5
3803	15926	NM_053607	I, J, General Alternate	fatty acid Coenzyme A ligase, long chain 5 (FACL5), mRNA. 10/2002 Length = 2454	long-chain fatty acid coenzyme A ligase 5
3804	20243	NM_053615	VV	casein kinase 1, alpha 1 (Csnk1a1), mRNA. 11/2001 Length = 978	casein kinase 1, alpha 1
3809	15090	NM_053638	B, HHH	isocitrate dehydrogenase 3 (NAD+) alpha (Idh3a), mRNA. 11/2002 Length = 2449	isocitrate dehydrogenase 3 (NAD+) alpha
3809	23305	NM_053638	KK, WW, HHH	isocitrate dehydrogenase 3 (NAD+) alpha (Idh3a), mRNA. 11/2002 Length = 2449	isocitrate dehydrogenase 3 (NAD+) alpha
3817	13368	NM_053742	T, PP, QQ	phosphatidylinositol transfer protein, beta (Pitpnb), mRNA. 11/2002 Length = 2680	phosphatidylinositol transfer protein, beta
3817	13369	NM_053742	C, UU, HHH, General Alternate	phosphatidylinositol transfer protein, beta (Pitpnb), mRNA. 11/2002 Length = 2680	phosphatidylinositol transfer protein, beta
3818	15376	NM_053747	Q, R, T	ubiquitin 1 (Ubqln1), mRNA. 11/2002 Length = 2131	ubiquitin 1
3822	24621	NM_053764	Z, AA	regulator of G-protein signaling 14 (Rgs14), mRNA. 11/2001 Length = 2854	regulator of G-protein signaling 14

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3823	7927	NM_053765	I, U, X, Y, DDD, LLL	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase (Uae1), mRNA. 11/2002 Length = 2508	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase
3825	15995	NM_053769	I, J, Q, R	protein tyrosine phosphatase, non-receptor type 16 (Ptpn16), mRNA. 11/2002 Length = 1908	protein tyrosine phosphatase, non-receptor type 16
3825	15996	NM_053769	C, I, J, R, LLL	protein tyrosine phosphatase, non-receptor type 16 (Ptpn16), mRNA. 11/2002 Length = 1908	protein tyrosine phosphatase, non-receptor type 16
3825	15997	NM_053769	I, J, R	protein tyrosine phosphatase, non-receptor type 16 (Ptpn16), mRNA. 11/2002 Length = 1908	protein tyrosine phosphatase, non-receptor type 16
3844	11405	NM_053866	Q, R, PPP, QQQ	phospholipase A2, activating protein (Plaa), mRNA. 11/2001 Length = 2451	phospholipase A2, activating protein
3854	15857	NM_053948	ZZ, AAA	polymerase (RNA) II (DNA directed) polypeptide G (Polr2g), mRNA. 11/2001 Length = 864	polymerase (RNA) II (DNA directed) polypeptide G
3875	22849	NM_057099	G, H	proteasome (prosome, macropain) subunit, beta type 6 (Psmb6), mRNA. 11/2002 Length = 760	proteasome (prosome, macropain) subunit, beta type 6
3875	25253	NM_057099	B, G, H, PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 6 (Psmb6), mRNA. 11/2002 Length = 760	proteasome (prosome, macropain) subunit, beta type 6

TABLE 1					
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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3878	9527	NM_057104	E, Y, CC, HH, General Alternate	ectonucleotide pyrophosphatase/phosphodiesterase 2 (Enpp2), mRNA. 11/2002 Length = 3216	ectonucleotide pyrophosphatase/phosphodiesterase 2
3878	9528	NM_057104	HH, General Alternate	ectonucleotide pyrophosphatase/phosphodiesterase 2 (Enpp2), mRNA. 11/2002 Length = 3216	ectonucleotide pyrophosphatase/phosphodiesterase 2
3879	5492	NM_057105	G, K, GG, HH, WW, DDD	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	ESTs, UDP glycosyltransferase 1 family, polypeptide A6
3879	5493	NM_057105	G, K, GG, HH, TT, WW, DDD	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	ESTs, UDP glycosyltransferase 1 family, polypeptide A6
3879	15124	NM_057105	J, K, L, N, S, U, FF, GG, HH, TT, LLL, UUU	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7, UDP-glucuronosyltransferase 1 family, member 1
3879	15125	NM_057105	K, L, M, N, U, FF, GG, PP, QQ, TT, LLL, SSS, UUU	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7
3879	15126	NM_057105	I, J, K, L, M, N, U, X, Y, GG, HH, LLL, SSS, UUU	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 1/2002 Length = 1593	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7, UDP-glucuronosyltransferase 1 family, member 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3879	15127	NM_057105	I, J, K, L, M, S, U, X, GG, HH, TT, LLL, SSS, UUU	UDP glycosyltransferase 1 family, polypeptide A6 (Ugt1a6), mRNA. 11/2002 Length = 1593	UDP glycosyltransferase 1 family, polypeptide A6, UDP glycosyltransferase 1 family, polypeptide A7, UDP-glucuronosyltransferase 1 family, member 1
3886	19833	NM_057139	GG	transporter protein; system N1 Na ⁺ and H ⁺ -coupled glutamine transporter (Hnrpu), mRNA. 11/2001 Length = 3563	transporter protein; system N1 Na ⁺ and H ⁺ -coupled glutamine transporter
3889	6613	NM_057186	A, U	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (Hadhsc), mRNA. 11/2002 Length = 1660	hydroxylacyl-Coenzyme A dehydrogenase, short chain
3891	15408	NM_057197	M, U, FF, XX, YY, BBB, CCC	2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. 11/2002 Length = 1109	2,4-dienoyl CoA reductase 1, mitochondrial
3891	15409	NM_057197	J, U, FF, VV, SSS	2,4-dienoyl CoA reductase 1, mitochondrial (Decr1), mRNA. 11/2002 Length = 1109	2,4-dienoyl CoA reductase 1, mitochondrial
3897	21562	NM_078623	S	enoyl Coenzyme A hydratase, short chain 1 (Echs1), mRNA. 11/2002 Length = 1454	Enoyl-CoA hydratase, short chain 1, mitochondrial
3901	17956	NM_080583	JJ, KK, HHH	adaptor-related protein complex 2, beta 1 subunit (Ap2b1), mRNA. 11/2002 Length = 5413	adaptor-related protein complex 2, beta 1 subunit

TABLE 1					
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Seq ID	CLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3902	16108	NM_080585	Z, AA	N-ethylmaleimide sensitive fusion protein attachment protein alpha (Napa), mRNA. 1/2002 Length = 1505	N-ethylmaleimide sensitive fusion protein attachment protein alpha
3902	16109	NM_080585	RR, SS	N-ethylmaleimide sensitive fusion protein attachment protein alpha (Napa), mRNA. 1/2002 Length = 1505	N-ethylmaleimide sensitive fusion protein attachment protein alpha
3906	25252	NM_080767	O, P, HH	proteasome (prosome, macropain) subunit, beta type, 8 (low molecular mass polypeptide 7) (Psm8), mRNA. 10/2002 Length = 1018	Proteasome (prosome, macropain) subunit, beta type, 8 (low molecular mass polypeptide 7)
3907	19831	NM_080781	U	coatomer protein complex, subunit beta 1 (Copb1), mRNA. 1/2002 Length = 3073	coatomer protein complex, subunit beta 1
3909	21842	NM_080886	I, J, II, XX, FFF	sterol-C4-methyl oxidase-like (Sc4mol), mRNA. 3/2002 Length = 1712	sterol-C4-methyl oxidase-like
3920	21391	NM_130416	X, Y	annexin A7 (Anxa7), mRNA. 1/2002 Length = 2912	annexin A7
3924	14959	NM_130734	A, B, JJ, KK, FFF, GGG, HHH, General Alternate	guanine nucleotide binding protein, beta polypeptide 2-like 1 (Gnb2l1), mRNA. 11/2002 Length = 1089	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
3927	9268	NM_130756	U, LL, BBB, CCC, LLL, RRR, SSS, UUU	4,8-dimethylnonanoyl-CoA thioesterase (Pte1), mRNA. 10/2002 Length = 1145	peroxisomal acyl-CoA thioesterase 1

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3933	20879	NM_133295	D, V, NN, OO, FFF	carboxylesterase 3 (Ces3), mRNA. 11/2002 Length = 1935	carboxylesterase 3
3933	20880	NM_133295	LL	carboxylesterase 3 (Ces3), mRNA. 11/2002 Length = 1935	carboxylesterase 3
3934	19456	NM_133298	O, P, VV	glycoprotein (transmembrane) nmb (Gpnmb), mRNA. 2/2002 Length = 2320	glycoprotein (transmembrane) nmb
3948	15524	NM_133556	V	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2 (Atp5g2), mRNA. 11/2002 Length = 593	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
3968	21098	NM_134432	C, L, DD, NNN	angiotensinogen (Agt), mRNA. 11/2002 Length = 1434	Angiotensinogen
3972	12215	NM_138502	K, BBB	monoglyceride lipase (Mgl1), mRNA. 11/2002 Length = 912	monoglyceride lipase
3973	16180	NM_138508	L, LL, DDD	Sterol carrier protein 2, liver (Scp2), mRNA. 11/2002 Length = 2599	Sterol carrier protein 2, liver
3981	14822	NM_138708	Q, R, JJ, KK, MM, FFF, TTT	Rab geranylgeranyl transferase component, subunit beta (Rabggtb), mRNA. 4/2002 Length = 996	Rab geranylgeranyl transferase component, subunit beta
3983	16400	NM_138828	S	apolipoprotein E (ApoE), mRNA. 11/2002 Length = 936	Apolipoprotein E,
4002	17203	NM_139099	RRR	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit (Atp5e), mRNA. 5/2002 Length = 404	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4003	17549	NM_139100	G, H, WW, FFF, GGG, HHH, General Alternate	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3 (Slc25a3), mRNA. 11/2002 Length = 1263	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3
4026	9096	NM_145771	RRR	aldehyde reductase (aldose reductase) like 6 (Aldrl6), mRNA. 11/2002 Length = 1006	hypothetical protein LOC56728
4053	11850	R46985	G	ribosomal protein L10a	ribosomal protein L10a
4055	18356	R47042	D	decorin	decorin
4056	5624	R47122	Z, AA	Fibronectin 1	Fibronectin 1
4057	16223	R47128	PP, QQ	Secreted acidic cystein-rich glycoprotein (osteonectin)	Secreted acidic cystein-rich glycoprotein (osteonectin)
4069	1471	S68809	RR	S100 calcium binding protein A1	ESTs, Highly similar to S10A_RAT S-100 protein, alpha chain [R.norvegicus]
4087	40	U02096	II, MM, XX, YY, FFF, TTT	fatty acid binding protein 7, brain	fatty acid binding protein 7, brain
4089	313	U03120	JJ, KK	Solute carrier family 5, member alpha 1 (Na ⁺ /glucose cotransporter)	Solute carrier family 5, member alpha 1 (Na ⁺ /glucose cotransporter)
4097	1928	U10357	II, General Alternate	pyruvate dehydrogenase kinase 2 subunit p45 (PDK2)	pyruvate dehydrogenase kinase 2 subunit p45 (PDK2)
4101	1424	U14746	W	von Hippel-Lindau syndrome	von Hippel-Lindau syndrome
4113	1340	U25651	SS	phosphofructokinase, muscle	phosphofructokinase, muscle
4115	317	U29339	RR, XX, YY	avian erythroblastosis oncogene B 3	avian erythroblastosis oncogene B 3
4125	368	U38379	XX, YY	Gamma-glutamyl hydrolase	Gamma-glutamyl hydrolase
4130	15851	U42719	BBB, CCC	Complement component 4	Complement component 4
4131	19543	U44948	General Alternate	cysteine-rich protein 2	cysteine-rich protein 2

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4138	1960	U52102	FF	Collapsin response mediator protein 1	Collapsin response mediator protein 1
4155	871	U66479	BB, CC	MAD (mothers against decapentaplegic, Drosophila) homolog 3	MAD (mothers against decapentaplegic, Drosophila) homolog 3
4158	794	U68168	B, G, M, GG, HH, NN, OO, FFF, GGG, III, JJJ, General Core Tox Markers	kynureninase (L-kynurenine hydrolase)	kynureninase (L-kynurenine hydrolase)
4162	851	U72497	A, B, III, JJJ, KKK, OOO, PPP, QQQ, General Core Tox Markers	fatty acid amide hydrolase	fatty acid amide hydrolase
4166	2153	U75404	W, BB, CC, ZZ, AAA	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein (gravin) 12
4171	1520	U77777	V	interleukin 18	interleukin 18
4178	1401	U93692	ZZ, AAA	preimplantation protein 2	preimplantation protein 2
4181	412	V01216	D, E, BB, CC, III, JJJ	Orosomucoid 1	Orosomucoid 1
4183	818	X02291	HH, SS	Aldolase B, fructose-biphosphate	Aldolase B, fructose-biphosphate
4188	614	X04070	General Alternate	gap junction membrane channel protein beta 1	gap junction membrane channel protein beta 1
4192	20715	X07259	J, U, DD, FF, LL, XX, QQQ, RRR, SSS	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
4194	20597	X12459	C, YY, BBB	Arginosuccinate synthetase 1	Arginosuccinate synthetase 1
4199	644	X14232	X, Y	Fibroblast growth factor 1 (heparin binding)	Fibroblast growth factor 1 (heparin binding)

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
4201	21152	X14848	F, S, FF, HH, SS, WW	golgi SNAP receptor complex member 1	golgi SNAP receptor complex member 1
4205	575	X15734	F, L, T, RR, SS, WW, SSS, UUU	S - adenosylmethionine synthetase	S - adenosylmethionine synthetase
4206	15626	X17665	F, H, BB, CC, EEE, MMM	ribosomal protein S16	ESTs, Highly similar to R3RT16 ribosomal protein S16, cytosolic [validated] - rat [R.norvegicus]
4207	1893	X51529	NN, EEE, MMM	phospholipase A2, group IIA (platelets, synovial fluid)	phospholipase A2, group IIA (platelets, synovial fluid)
4215	20427	X53378	FFF, HHH, General Alternate	ribosomal protein S13	ribosomal protein S13
4218	492	X53944	RR	dopamine receptor 3	dopamine receptor 3
4219	670	X54096	XX, YY, CCC, PPP, QQQ	Lecithin-cholesterol acyltransferase	Lecithin-cholesterol acyltransferase
4221	21122	X56228	R, DDD, PPP, QQQ	Thiosulfate sulphurtransferase (rhodanese)	Thiosulfate sulphurtransferase (rhodanese)
4221	21123	X56228	Q, R, SS, DDD, PPP, QQQ, General Alternate	Thiosulfate sulphurtransferase (rhodanese)	Thiosulfate sulphurtransferase (rhodanese)
4228	10109	X58465	G, H, II, VV, DDD, EEE, FFF, GGG, III, JJJ, MMM, General Core Tox Markers	Ribosomal protein S5	Ribosomal protein S5

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4228	25702	X58465	X, Y, JJ, KK, FFF, GGG, HHH, III, JJJ, General Core Tox Markers	Ribosomal protein S5	Ribosomal protein S5
4229	1719	X59267	Z, AA, SS	drebrin 1	drebrin 1
4245	515	X63854	UU	Transporter 2, ABC (ATP binding cassette)	Transporter 2, ABC (ATP binding cassette)
4253	405	X70223	O, P, FFF, General Alternate	peroxisomal membrane protein 2, 22 kDa	peroxisomal membrane protein 2, 22 kDa
4260	1877	X74593	W, DD, EE, SS, WW, XX, YY, General Core Tox Markers	Sorbitol dehydrogenase	Sorbitol dehydrogenase
4266	447	X79208	RR	Cholecystokinin B receptor	Cholecystokinin B receptor
4269	570	X82445	BBB, CCC	nuclear distribution gene C homolog (Aspergillus)	nuclear distribution gene C homolog (Aspergillus)
4273	764	X84210	F, HH, JJ, KK	Nuclear Factor IA	Nuclear Factor IA
4277	420	X90710	U, RRR, SSS	alcohol dehydrogenase 4 (class II), pi polypeptide	alcohol dehydrogenase 4 (class II), pi polypeptide
4284	1146	Y09507	WW	hypoxia inducible factor 1, alpha subunit	hypoxia inducible factor 1, alpha subunit
4288	442	Z22867	Z, AA	phosphodiesterase 3B, cGMP-inhibited	phosphodiesterase 3B, cGMP-inhibited
8	6050	AA686190	N, V		ESTs, Highly similar to T30827 nascent polypeptide-associated complex alpha chain, non-muscle splice form - mouse [M.musculus]
22	15654	AA799501	KK, GGG, HHH, General Alternate	NADH ubiquinone oxidoreductase subunit B13	NADH ubiquinone oxidoreductase subunit B13

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
25	16942	AA799520	T, MM, PPP, QQQ, TTT		ESTs, Highly similar to ITMB_MOUSE Integral membrane protein 2B (E25B protein) [M.musculus]
27	21120	AA799526	S		ESTs, Highly similar to RIKEN cDNA 1700043E15 [Mus musculus] [M.musculus]
33	16959	AA799550	HHH		ESTs, Moderately similar to RIKEN cDNA 9130413I22 [Mus musculus] [M.musculus]
46	20093	AA799637	UUU		ESTs, Weakly similar to A55071 hydrogen peroxide-inducible protein hic-5 - mouse [M.musculus]
47	18227	AA799641	Z, AA		ESTs, Moderately similar to I53063 testicular tumor overexpressed protein - mouse [M.musculus]
66	18880	AA799801	D		ESTs, Moderately similar to predicted gene ICRFP703B1614Q5.6; ICRFP703N2430Q5.6; C11orf17 [Mus musculus] [M.musculus]
74	15011	AA799893	R, MM, TTT		ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
78	18883	AA799992	Z, AA		ESTs, ESTs, Moderately similar to predicted gene ICRFP703B1614Q5.6; ICRFP703N2430Q5.6; C11orf17 [Mus musculus] [M.musculus]
79	2098	AA799995	Q, R, QQQ	ribosomal protein L14	ribosomal protein L14
86	21064	AA800175	II, ZZ, AAA		ESTs, Highly similar to JC7136 peptidylprolyl isomerase (EC 5.2.1.8) - mouse [M.musculus]
90	15659	AA800199	P		ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]
94	18442	AA800258	ZZ, AAA		ESTs, Moderately similar to low density lipoprotein B [Mus musculus] [M.musculus]
117	9092	AA800814	Z, AA	HMm:tumor necrosis factor (ligand) superfamily, member 13	ESTs, Highly similar to tumor necrosis factor (ligand) superfamily, member 13 [Mus musculus] [M.musculus]
118	22025	AA800849	S, TT		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
122	21416	AA800962	O, X, Y		ESTs, Highly similar to S11661 talin - mouse [M.musculus]
124	23115	AA801165	II	Testis-specific histone 2a	Testis-specific histone 2a
126	11166	AA801346	UU		ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]
148	2845	AA818026	UUU		ESTs, Weakly similar to PSD7_MOUSE 26S proteasome non-ATPase regulatory subunit 7 (26S proteasome regulatory subunit S12) (Proteasome subunit p40) (Mov34 protein) [M.musculus]
180	4245	AA818692	GG, RR		ESTs, Highly similar to RIKEN cDNA 0610009M10; RIKEN cDNA 0610009M10 gene [Mus musculus] [M.musculus]
189	4491	AA818798	O, P, V, VV		Rattus norvegicus mRNA for cathepsin Y, partial cds
191	7690	AA818875	HHH	uroguanylin	uroguanylin
197	22175	AA818999	WW		ESTs, Moderately similar to MBNL_MOUSE Muscleblind-like protein (Triplet-expansion RNA-binding protein) [M.musculus]
206	6329	AA819259	XX, YY		ESTs, Moderately similar to S31799 apolipoprotein C2 precursor - mouse [M.musculus]
212	17824	AA819362	LL		ESTs, Highly similar to hypothetical protein MGC7474 [Mus musculus] [M.musculus]
218	17097	AA819501	F, II		ESTs, Highly similar to R3RT27 ribosomal protein S27, cytosolic [validated] - rat [R.norvegicus]
236	230	AA819870	YY, PPP, QQQ		Rattus norvegicus complement C8 beta (C8b) mRNA, partial cds
237	320	AA819905	U	stearoyl-Coenzyme A desaturase 1	stearoyl-Coenzyme A desaturase 1
258	21171	AA848979	D	MAP-kinase activating death domain	MAP-kinase activating death domain
274	17179	AA849797	GGG	Protein-L-isoaspartate (D-aspartate) O-methyltransferase	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
277	23981	AA850040	O, P	cyclase-associated protein homologue	cyclase-associated protein homologue
279	22027	AA850060	V, OOO		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935823.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
279	22028	AA850060	CCC		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
285	16329	AA850542	JJ, KK, FFF		ESTs, Highly similar to Tnf receptor associated factor 4 [Mus musculus] [M.musculus]
287	14507	AA850618	RRR		ESTs, Highly similar to T09123 hybrid receptor SorLA precursor - mouse (fragment) [M.musculus]
289	22797	AA850733	LL	HMm:ring-box 1	ESTs, Highly similar to ring-box 1; ring-box protein 1 [Mus musculus] [M.musculus]
292	22721	AA850781	V		ESTs, Highly similar to peptidylprolyl isomerase D (cyclophilin D) [Mus musculus] [M.musculus]
294	16132	AA850885	E, S, T, HH, NNN	unknown Glu-Pro dipeptide repeat protein	unknown Glu-Pro dipeptide repeat protein
299	3924	AA851017	W, DDD, LLL		ESTs, Highly similar to molybdenum cofactor synthesis 2 [Mus musculus] [M.musculus]
299	3925	AA851017	Q, R, WW, LLL		ESTs, Highly similar to molybdenum cofactor synthesis 2 [Mus musculus] [M.musculus]
302	2103	AA851135	YY	ribosomal protein S27	ribosomal protein S27
303	4490	AA851184	O, P, VV, HHH		Rattus norvegicus mRNA for cathepsin Y, partial cds
312	883	AA851347	O, P		ESTs, Highly similar to SNX5_MOUSE Sorting nexin 5 [M.musculus]
315	21489	AA851443	GG		ESTs, Weakly similar to I49523 tumor necrosis factor alpha-induced protein 2 - mouse [M.musculus]
321	14292	AA851791	R		ESTs, Weakly similar to CBP_MOUSE CREB-binding protein [M.musculus]
337	15284	AA858551	BB, CC		ESTs, Highly similar to UB6B_MOUSE Ubiquitin-conjugating enzyme E2-23 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein) [M.musculus]
338	13523	AA858552	NN, OO	HMm:leukotriene A4 hydrolase	ESTs, Highly similar to S20444 leukotriene-A4 hydrolase (EC 3.3.2.6) - rat [R.norvegicus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
340	18001	AA858573	LL, EEE, MMM, UUU	spp-24 precursor	spp-24 precursor
350	17334	AA858704	A, B, I, J, SS, General Core Tox Markers		ESTs, Highly similar to EXT1_MOUSE Exostosin-1 (Multiple exostoses protein 1 homolog) [M.musculus]
351	6380	AA858758	FF, LL		ESTs, Weakly similar to RIKEN cDNA 1500031O19 [Mus musculus] [M.musculus]
356	6403	AA858879	A, B, G, H, S, PPP, QQQ		ESTs, Highly similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 13; 26S proteasome subunit p40.5 [Mus musculus] [M.musculus]
366	6440	AA859130	Q, R, General Alternate		ESTs, Weakly similar to JC2524 phosphoprotein phosphatase (EC 3.1.3.16) 1A-beta - rat [R.norvegicus]
371	14124	AA859305	VV, HHH		R.norvegicus mRNA for tropomyosin isoform 6, Rattus norvegicus nonmuscle tropomyosin 5 (Tpm5) isoforms NM 5 and NM 6 mRNA, partial cds
372	15149	AA859327	PPP, QQQ		ESTs, Highly similar to UBPA_MOUSE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 10 (UBIQUITIN THIOLESTERASE 10) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 10) (DEUBIQUITINATING ENZYME 10) [M.musculus]
375	15172	AA859362	XX, YY		ESTs, Highly similar to BAG3_MOUSE BAG-family molecular chaperone regulator-3 (BCL-2 binding athanogene-3) (BAG-3) (Bcl-2-binding protein Bis) [M.musculus]
386	17142	AA859612	J, LL		EST, Moderately similar to 0806162J protein URF4 [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
389	11635	AA859645	A, B, F, G, S, FFF, GGG, III, JJJ, OOO, General Core Tox Markers	attractin	attractin
393	14138	AA859700	E, General Alternate	HMm:protoporphyrinogen oxidase	ESTs, Highly similar to PPOX_MOUSE PROTOPORPHYRINOGEN OXIDASE (PPO) [M.musculus]
393	14139	AA859700	E, III, JJJ, NNN, General Alternate	HMm:protoporphyrinogen oxidase	ESTs, Highly similar to PPOX_MOUSE PROTOPORPHYRINOGEN OXIDASE (PPO) [M.musculus]
396	22374	AA859804	P		ESTs, Highly similar to SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [M.musculus]
410	4222	AA860024	KK		ESTs, Highly similar to EF1G_MOUSE Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [M.musculus]
411	13974	AA860030	O, P, VV		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
415	15884	AA866276	O, P, PP		ESTs, Weakly similar to A60543 protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain - rat (fragment) [R.norvegicus]
424	16013	AA866482	Q, R, PPP, QQQ		ESTs, Highly similar to FGD1_MOUSE Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (Faciogenital dysplasia protein homolog) [M.musculus]
426	22781	AA874926	V, RR, SS		ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus]
428	16167	AA874941	C		ESTs, Moderately similar to ADFP_MOUSE ADIPOPHILIN (ADIPOSE DIFFERENTIATION-RELATED PROTEIN) (ADRP) [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
430	17303	AA874990	UU		ESTs, Weakly similar to RIKEN cDNA 6330407G11 [Mus musculus] [M.musculus]
447	15887	AA875225	PP, QQ	GTP-binding protein (G-alpha-i2)	GTP-binding protein (G-alpha-i2)
447	15888	AA875225	O, P, X, NN, OO, VV, ZZ, AAA	GTP-binding protein (G-alpha-i2)	GTP-binding protein (G-alpha-i2)
455	24470	AA875523	GG		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
461	2846	AA875639	V		ESTs, Weakly similar to FAS_RAT FATTY ACID SYNTHASE [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14] [R.norvegicus]
464	5384	AA891041	W, BB, CC, DD, EE, PP, QQ, III, NNN	jun B proto-oncogene	jun B proto-oncogene
476	21951	AA891535	MM, ZZ, AAA, TTT		ESTs, Highly similar to hippocampus abundant gene transcript 1 [Mus musculus] [M.musculus]
480	17225	AA891553	General Core Tox Markers		ESTs, Moderately similar to IF37_MOUSE Eukaryotic translation initiation factor 3 subunit 7 (eIF-3 zeta) (eIF3 p66) [M.musculus]
483	22858	AA891591	D	programmed cell death 8 (apoptosis-inducing factor)	programmed cell death 8 (apoptosis-inducing factor)
485	22860	AA891681	N, MM, TTT		ESTs, Highly similar to UNRI_MOUSE UNR-interacting protein (Serine-threonine kinase receptor-associated protein) [M.musculus]
487	9091	AA891690	VV	HMM:tumor necrosis factor (ligand) superfamily, member 13	ESTs, Highly similar to tumor necrosis factor (ligand) superfamily, member 13 [Mus musculus] [M.musculus]
502	6967	AA891810	S		ESTs, Moderately similar to g1-related zinc finger protein [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
502	6968	AA891810	M		ESTs, Moderately similar to g1-related zinc finger protein [Mus musculus] [M.musculus]
504	7050	AA891824	SS		Rattus norvegicus clone ZG52 mRNA sequence
510	16023	AA891872	OOO		ESTs, Highly similar to NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) [M.musculus]
519	17333	AA891940	EEE, MMM		ESTs, Highly similar to RHOC_MOUSE TRANSFORMING PROTEIN RHOC [M.musculus]
527	16836	AA892005	BBB, CCC		ESTs, Weakly similar to PGC1_RAT Membrane associated progesterone receptor component 1 (Acidic 25 kDa protein) (25-DX) [R.norvegicus]
534	19469	AA892112	V, NN, EEE, MMM		ESTs, Weakly similar to PROD_MOUSE PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR (PROLINE DEHYDROGENASE) [M.musculus]
543	3427	AA892246	C, HH		ESTs, Weakly similar to serine/threonine kinase 25 (yeast); Ste20-like kinase; serine/threonine kinase 25 (Ste20, yeast homolog); Yeast Sps1/Ste20-related kinase 1 [Mus musculus] [M.musculus]
550	7226	AA892297	D	histone deacetylase 2	histone deacetylase 2
554	18209	AA892318	WW		ESTs, Highly similar to JC7219 nuclear protein SR-25 - mouse [M.musculus]
564	23194	AA892417	I, J, W	ephrin A1	ephrin A1
572	15154	AA892532	I, J, K, FF, OOO		R.norvegicus (Wistar) CaBP1 mRNA
573	17468	AA892545	E, I, J, KKK, NNN, OOO		ESTs, Moderately similar to organic cationic transporter-like 2 [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
594	11997	AA892828	MM, DDD, TTT	HMm:pyruvate dehydrogenase (lipoamide) beta	ESTs, Highly similar to S15892 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - rat [R.norvegicus]
594	11998	AA892828	MM, TTT	HMm:pyruvate dehydrogenase (lipoamide) beta	ESTs, Highly similar to S15892 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - rat [R.norvegicus]
597	17581	AA892835	DDD		ESTs, Moderately similar to BTF3_MOUSE Transcription factor BTF3 (RNA polymerase B transcription factor 3) [M.musculus]
608	24280	AA892919	V	nucleolar phosphoprotein p130	nucleolar phosphoprotein p130
612	3381	AA892993	X, CCC, SSS, UUU		ESTs, Moderately similar to high mobility group protein 20 B; BRCA2-associated factor 35 [Mus musculus] [M.musculus]
617	3865	AA893065	ZZ, AAA		ESTs, Weakly similar to THDE_RAT Thyrotropin-releasing hormone degrading ectoenzyme (TRH-degrading ectoenzyme) (TRH-DE) (TRH-specific aminopeptidase) (Thyroliberinase) (Pyroglutamyl-peptidase II) (PAP-II) [R.norvegicus]
630	3880	AA893247	LL	MAP/microtubule affinity-regulating kinase 3	MAP/microtubule affinity-regulating kinase 3
631	16168	AA893280	C		ESTs, Moderately similar to ADFP_MOUSE ADIPOPHILIN (ADIPOSE DIFFERENTIATION-RELATED PROTEIN) (ADRP) [M.musculus]
633	4242	AA893325	A, B, F, H, X, Y, LLL	ornithine aminotransferase	ornithine aminotransferase
634	11935	AA893328	LL		ESTs, Moderately similar to C54354 calnexin precursor - rat [R.norvegicus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
639	13088	AA893495	A, G, BB, CC, TT, FFF, GGG, HHH, General Core Tox Markers		ESTs, Highly similar to A40066 corticosteroid-binding globulin precursor - rat [R.norvegicus]
650	16912	AA893690	I, J, Z, AA, LL		ESTs, Highly similar to neuronal protein 15.6 [Mus musculus] [M.musculus]
651	19171	AA893699	C		ESTs, Moderately similar to maternal inhibition of differentiation; maternal inhibition of differentiation; stage specific embryonic cDNA-8 [Mus musculus] [M.musculus]
667	16434	AA894174	BBB, CCC		ESTs, Highly similar to A31568 electron transfer flavoprotein alpha chain precursor - rat [R.norvegicus]
667	16435	AA894174	J, M, U		ESTs, Highly similar to A31568 electron transfer flavoprotein alpha chain precursor - rat [R.norvegicus]
669	24473	AA894200	Z, AA		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
669	24474	AA894200	GG		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
670	22783	AA894207	SS		ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus]
686	22981	AA899455	Z, AA, SS		ESTs, Weakly similar to JC4863 homeobox protein zhx-1 - mouse [M.musculus]
715	3944	AA900688	JJ, KK, MM, TTT		ESTs, Weakly similar to A45988 dentin matrix acidic phosphoprotein AG1 - rat [R.norvegicus]
720	16465	AA901042	OOO, General Core Tox Markers, General Alternate		ESTs, Highly similar to RAN binding protein 16 [Mus musculus] [M.musculus]

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Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
723	4857	AA901237	RR		ESTs, Weakly similar to CYCK_MOUSE Cyclin K [M.musculus]
732	22578	AA924105	X, Y		ESTs, Weakly similar to SY03_RAT Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha) [R.norvegicus]
744	4944	AA924405	KK, HHH, General Core Tox Markers		ESTs, Weakly similar to NFH_MOUSE Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament heavy polypeptide) (NF-H) [M.musculus]
768	23173	AA925057	O, VV		ESTs, Highly similar to GYRTI cysteine-rich intestinal protein - rat [R.norvegicus]
778	23159	AA925318	General Alternate	I-kappa-B-beta	I-kappa-B-beta
815	11691	AA926193	M, X, Y	sulfotransferase family, cytosolic, 1C, member 2	sulfotransferase family, cytosolic, 1C, member 2
817	1897	AA926292	HH	trans-golgi network protein 1	trans-golgi network protein 1
826	22677	AA942718	C, F, W, HH, II	B cell lymphoma 2 like	B cell lymphoma 2 like
829	12247	AA942812	General Alternate		ESTs, Moderately similar to putative homeodomain transcription factor [Mus musculus] [M.musculus]
838	24262	AA943116	X, Y, UUU	HMm:thymidylate kinase	ESTs, Highly similar to KTHY_MOUSE Thymidylate kinase (dTMP kinase) [M.musculus]
841	15319	AA943307	D	tyrosine protein kinase pp60-c-src	tyrosine protein kinase pp60-c-src
859	24369	AA944011	H		ESTs, Highly similar to NUB2_MOUSE Nucleotide binding protein 2 (NBP 2) [M.musculus]
865	2762	AA944165	General Core Tox Markers		ESTs, Highly similar to C10_MOUSE Putative C10 protein (B-cell receptor-associated protein 37) [M.musculus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
866	22017	AA944209	III, JJJ		ESTs, Moderately similar to PIM1_RAT Proto-oncogene serine/threonine-protein kinase pim-1 [R.norvegicus]
870	22392	AA944269	RRR		ESTs, Weakly similar to ML64_MOUSE MLN 64 protein (ES 64 protein) [M.musculus]
885	22452	AA944542	L, T, KKK		ESTs, Moderately similar to Pxmp4; PMP24 protein; 24 kDa intrinsic membrane protein [Mus musculus] [M.musculus]
904	16635	AA945171	D		ESTs, Highly similar to APC4_RAT APOLIPOPROTEIN C-IV PRECURSOR (APO-CIV) (APOLIPOPROTEIN E-LINKED) (ECL) [R.norvegicus]
908	22029	AA945284	K, N		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
909	7683	AA945320	ZZ, AAA		ESTs, Highly similar to IMA3_MOUSE Importin alpha-3 subunit (Karyopherin alpha-3 subunit) (Importin alpha Q2) [M.musculus]
912	1798	AA945569	E, Y, MM, NNN, TTT		R.norvegicus alpha-1-macroglobulin mRNA, complete cds
916	4207	AA945591	FF		ESTs, Weakly similar to JC5105 stromal cell-derived factor 2 - mouse [M.musculus]
917	12314	AA945596	G, GG, HH, VV		ESTs, Moderately similar to LCT2_MOUSE Leukocyte cell-derived chemotaxin 2 precursor (Chondromodulin II) (ChM-II) [M.musculus]
921	24521	AA945636	DDD		ESTs, Highly similar to R5RT12 acidic ribosomal protein P1, cytosolic [validated] - rat [R.norvegicus]
924	13751	AA945699	HH	synaptosomal-associated protein, 23 kD	synaptosomal-associated protein, 23 kD
944	20832	AA946040	F		ESTs, Highly similar to COXG_MOUSE Cytochrome c oxidase polypeptide VIb (AED) [M.musculus]
951	19044	AA946379	BBB		ESTs, Moderately similar to methyl-CpG binding domain protein 2 [Mus musculus] [M.musculus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
961	1809	AA946503	E, V, W, BB, CC, VV, EEE, III, JJJ, MMM	lipocalin 2	lipocalin 2
998	17540	AA955914	A, B		EST, EST, Moderately similar to FBRL_MOUSE Fibrillarin (Nucleolar protein 1) [M.musculus], ESTs, Highly similar to S38342 fibrillarin - mouse [M.musculus]
1004	22576	AA955983	G, H, NNN		ESTs, Weakly similar to FLAP_RAT 5-lipoxygenase activating protein (FLAP) (MK-886 binding protein) [R.norvegicus]
1021	23463	AA956794	Q, R		ESTs, Weakly similar to I58376 hypothetical protein unip - mouse [M.musculus]
1025	22251	AA957037	EE		ESTs, Highly similar to RIKEN cDNA 2310011M22 [Mus musculus] [M.musculus]
1028	12000	AA957319	MM, TTT	HMm:pyruvate dehydrogenase (lipoamide) beta	ESTs, Highly similar to S15892 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - rat [R.norvegicus]
1036	22358	AA957624	T, V		Rattus norvegicus hypothetical RNA binding protein RDA288 mRNA, complete cds
1039	24135	AA957736	S		ESTs, Weakly similar to FBL5_RAT Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing protein) (EVEC) [R.norvegicus]
1047	20827	AA963185	T		ESTs, Highly similar to R3RT28 ribosomal protein S28, cytosolic [validated] - rat [R.norvegicus]
1060	8430	AA964033	HHH		Rattus norvegicus NonO/p54nrb homolog mRNA, partial cds
1062	2588	AA964080	UUU		ESTs, Highly similar to LSM4_MOUSE U6 snRNA-associated Sm-like protein LSM4 [M.musculus]
1090	24233	AA964756	General Alternate		ESTs, Weakly similar to CALM_HUMAN Calmodulin [R.norvegicus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1093	2492	AA964866	W, QQ		ESTs, Moderately similar to A49947 interferon gamma receptor beta subunit - mouse [M.musculus]
1097	2542	AA965035	HH		ESTs, Moderately similar to RIKEN cDNA 1700030G05 [Mus musculus] [M.musculus]
1112	2828	AA996529	UUU		ESTs, Highly similar to CLN3_MOUSE CLN3 PROTEIN (BATTENIN) [M.musculus]
1121	2939	AA996885	BB, CC, UU, DDD		ESTs, Moderately similar to SY19_MOUSE Small inducible cytokine A19 precursor (CCL19) (Epstein-Barr virus induced molecule 1 ligand chemokine) (EBI1-ligand chemokine) (ELC) [M.musculus]
1125	8786	AA996993	K		EST, Moderately similar to RED_MOUSE Red protein (RER protein) [M.musculus], ESTs, Highly similar to RED_MOUSE Red protein (RER protein) [M.musculus]
1127	3112	AA997122	NN, OO	adrenomedullin receptor	ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus], adrenomedullin receptor
1133	3496	AA997304	F		ESTs, Highly similar to ribosomal protein, mitochondrial, S22 [Mus musculus] [M.musculus]
1135	16883	AA997345	A, B, General Core Tox Markers		ESTs, Highly similar to RIKEN cDNA 1190017B19 [Mus musculus] [M.musculus]
1137	3172	AA997406	AA		ESTs, Highly similar to PSA7_RAT Proteasome subunit alpha type 7 (Proteasome subunit RC6-1) [R.norvegicus]
1154	3458	AA997861	KK	stromal cell derived factor 4	stromal cell derived factor 4
1166	14149	AA998172	GG	platelet-activating factor acetylhydrolase alpha 2 subunit (PAF-AH alpha 2)	platelet-activating factor acetylhydrolase alpha 2 subunit (PAF-AH alpha 2)
1175	24094	AA998435	XX		ESTs, Highly similar to RIKEN cDNA 2210412K09 [Mus musculus] [M.musculus]

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1198	1557	AB000216	General Alternate	Cca3 protein	Cca3 protein
1199	1291	AB000491	H, S	for proteasomal ATPase (SUG1)	for proteasomal ATPase (SUG1)
1200	1201	AB000929	D	zona pellucida 2 glycoprotein	zona pellucida 2 glycoprotein
1206	16304	AB008424	PP, QQ, EEE, FFF, MMM		Rat cytochrome P-450 IID3 mRNA, complete cds
1208	13973	AB011679	O, P		Rattus norvegicus mRNA for class I beta-tubulin, complete cds
1217	1058	AF003835	B, XX, YY	isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
1230	4292	AF034896	Z, AA		Rattus norvegicus olfactory receptor-like protein (SCR D-8) mRNA, complete cds
1232	8426	AF036335	JJ, KK, HHH		Rattus norvegicus NonO/p54nrb homolog mRNA, partial cds
1232	8427	AF036335	B, HHH		Rattus norvegicus NonO/p54nrb homolog mRNA, partial cds
1235	17597	AF051943	O, P	nucleoside diphosphate kinase type 6	nucleoside diphosphate kinase type 6
1236	16762	AF059530	UU	protein arginine N-methyltransferase 3(hnRNP methyltransferase S. cerevisiae)-like 3	protein arginine N-methyltransferase 3(hnRNP methyltransferase S. cerevisiae)-like 3
1237	18675	AF061947	A, B, DD, EE	cain	cain
1246	20236	AF091570	Z, AA, RR	olfactory receptor 41	olfactory receptor 41
1255	15848	AI007820	J, K, FF		ESTs, ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
1259	4032	AI007875	Z, AA	x-ray repair cross-complementing group 1 protein	x-ray repair cross-complementing group 1 protein
1267	15849	AI008074	XX, YY		ESTs, ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
1271	22018	AI008309	III, JJJ, KKK		ESTs, Moderately similar to PIM1_RAT Proto-oncogene serine/threonine-protein kinase pim-1 [R.norvegicus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1277	22126	AI008511	RR	ribosomal protein S27	ribosomal protein S27
1285	16701	AI008838	U, FF, TT, UU, DDD, SSS, UUU, General Core Tox Markers		ESTs, Highly similar to RIKEN cDNA 1300002A08 [Mus musculus] [M.musculus]
1292	410	AI008974	UU, OOO, General Alternate	low density lipoprotein receptor-related protein associated protein 1	low density lipoprotein receptor-related protein associated protein 1
1293	1830	AI009002	T	cell division cycle 25B	cell division cycle 25B
1306	9150	AI009198	A, B, Q, R		ESTs, Highly similar to UNRI_MOUSE UNR-interacting protein (Serine-threonine kinase receptor-associated protein) [M.musculus]
1309	24249	AI009273	I, J, BB, CC	fatty acid synthase	fatty acid synthase
1313	3665	AI009376	A, B, HHH		ESTs, Moderately similar to A34168 nucleolar phosphoprotein B23.2 - rat [R.norvegicus]
1314	12071	AI009456	U, X, Y, LLL, UUU		ESTs, Weakly similar to ABC2_MOUSE ATP-BINDING CASSETTE TRANSPORTER 2 [M.musculus]
1319	19092	AI009501	KKK		ESTs, Highly similar to SUI1_MOUSE Protein translation factor SUI1 homolog [M.musculus]
1320	3828	AI009601	V	transmembrane 4 superfamily member 4	transmembrane 4 superfamily member 4
1330	8431	AI009761	L		Rattus norvegicus NonO/p54nrb homolog mRNA, partial cds
1333	15627	AI009810	CCC		ESTs, Highly similar to R3RT16 ribosomal protein S16, cytosolic [validated] - rat [R.norvegicus]
1343	3882	AI010191	D, U	MAP/microtubule affinity-regulating kinase 3	MAP/microtubule affinity-regulating kinase 3
1344	15644	AI010256	C, L, W, WW	H3 histone, family 3B	H3 histone, family 3B
1356	15624	AI010449	K	folistatin-related protein precursor	folistatin-related protein precursor

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1363	21659	AI010584	LL		Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
1369	13296	AI011020	YY		ESTs, Moderately similar to MTM1_MOUSE Myotubularin [M.musculus]
1371	22030	AI011177	N, BB, CC		ESTs, Moderately similar to 0806162L protein URF5 [Mus musculus] [M.musculus]
1381	3995	AI011678	GGG, General Core Tox Markers	Ryudocan/syndecan 2	Ryudocan/syndecan 2
1385	14267	AI011738	U, FF		ESTs, Highly similar to P044_RAT 0-44 protein [R.norvegicus]
1388	15033	AI011754	SSS, UUU		ESTs, Weakly similar to RIKEN cDNA 0610008N23 [Mus musculus] [M.musculus]
1392	2516	AI011843	W		ESTs, Moderately similar to SELX_MOUSE Selenoprotein X 1 (Selenoprotein R) [M.musculus]
1393	4286	AI011920	V		ESTs, Moderately similar to WDR1_MOUSE WD-repeat protein 1 (Actin interacting protein 1) [M.musculus]
1401	13093	AI012177	T		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
1402	6547	AI012181	E, JJ, KK		ESTs, Highly similar to 2206297A folypoly-gamma-Glu synthetase [Mus musculus] [M.musculus]
1417	15443	AI012480	D		ESTs, Highly similar to EXT2_MOUSE Exostosin-2 (Multiple exostoses protein 2 homolog) [M.musculus]
1418	12766	AI012505	SSS		ESTs, Highly similar to diacylglycerol O-acyltransferase 2; diacylglycerol acyltransferase 2 [Mus musculus] [M.musculus]
1426	2242	AI012635	L, O, P, UU, KKK, General Alternate	flavin-containing monooxygenase 3	flavin-containing monooxygenase 3
1427	17132	AI012648	KKK		ESTs, Moderately similar to RIKEN cDNA 1110055L24 [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1433	1828	AI012942	D	cell division cycle 25B	cell division cycle 25B
1447	22709	AI013404	B	RAP1B, member of RAS oncogene family	RAP1B, member of RAS oncogene family
1456	16584	AI013765	VV	Arrestin, beta 2	Arrestin, beta 2
1459	21950	AI013861	G, General Alternate	3-hydroxyisobutyrate dehydrogenase	3-hydroxyisobutyrate dehydrogenase
1462	7316	AI013883	Y		ESTs, Highly similar to MKR1_MOUSE Makorin 1 [M.musculus]
1496	16840	AI029733	Q, R		ESTs, Highly similar to RIKEN cDNA 2010100O12 [Mus musculus] [M.musculus]
1523	16169	AI030932	C		ESTs, Moderately similar to ADFP_MOUSE ADIPOPHILIN (ADIPOSE DIFFERENTIATION-RELATED PROTEIN) (ADRP) [M.musculus]
1524	3167	AI031012	F, S, RRR		ESTs, Moderately similar to CLPP_MOUSE Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial precursor (Endopeptidase Clp) [M.musculus]
1529	18002	AI043655	O, P, YY	spp-24 precursor	spp-24 precursor
1540	7913	AI043849	DD, EE, WW		ESTs, Weakly similar to ELL_MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) [M.musculus]
1550	976	AI044259	Z, AA	putative cell surface antigen	putative cell surface antigen
1552	5451	AI044322	DD, EE		ESTs, Highly similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 [Mus musculus] [M.musculus]
1561	3428	AI044653	C		ESTs, Weakly similar to serine/threonine kinase 25 (yeast); Ste20-like kinase; serine/threonine kinase 25 (Ste20, yeast homolog); Yeast Sps1/Ste20-related kinase 1 [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1564	5634	AI044883	FFF		ESTs, Moderately similar to RIKEN cDNA 2810430M08 [Mus musculus] [M.musculus]
1565	6941	AI044892	DDD, LLL		ESTs, Highly similar to S04328 protein-tyrosine kinase (EC 2.7.1.112) flk - rat (fragment) [R.norvegicus]
1578	5697	AI045119	WW	HMm: dihydrolipoamide dehydrogenase	ESTs, Weakly similar to A Chain A, Mammalian Thioredoxin Reductase [R.norvegicus]
1582	5712	AI045154	XX, YY		ESTs, Moderately similar to ORC5_MOUSE Origin recognition complex subunit 5 [M.musculus]
1584	5723	AI045191	PPP, QQQ		ESTs, Weakly similar to FSPO_RAT F-spondin precursor [R.norvegicus]
1628	5573	AI059063	D		ESTs, Weakly similar to FIBG_RAT Fibrinogen gamma chain precursor [R.norvegicus]
1631	10169	AI059204	KKK		ESTs, Weakly similar to CNE6_MOUSE Copine VI (Neuronal-copine) (N-copine) [M.musculus]
1637	6906	AI059403	DDD		ESTs, Highly similar to YY1 associated factor 2 [Mus musculus] [M.musculus]
1649	900	AI059963	T	vacuolar protein sorting homolog r-vps33b	vacuolar protein sorting homolog r-vps33b
1669	12243	AI070133	RR		ESTs, Highly similar to histone acetyltransferase [Mus musculus] [M.musculus]
1684	2838	AI070511	G, H	HMm: valyl-tRNA synthetase 2	ESTs, Highly similar to SYV2_MOUSE Valyl-tRNA synthetase 2 (Valine--tRNA ligase 2) (VALRS 2) [M.musculus]
1694	1831	AI071137	T	cell division cycle 25B	cell division cycle 25B
1700	9604	AI071230	JJ, KK		ESTs, Weakly similar to I48842 testin - mouse [M.musculus]
1718	9795	AI071989	D, E		ESTs, Weakly similar to NPA1_MOUSE Neuronal PAS domain protein 1 (Neuronal PAS1) [M.musculus]
1731	8856	AI072402	FF		ESTs, Weakly similar to S42077 finger protein 30 - mouse [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1747	9399	AI072812	General Core Tox Markers		ESTs, Highly similar to glioma-amplified sequence-41 [Mus musculus] [M.musculus]
1769	15192	AI101099	T		ESTs, Highly similar to SMRT2 metallothionein II - rat [R.norvegicus]
1782	3537	AI101690	SS	dishevelled 1	dishevelled 1
1791	15080	AI102045	MM, PPP, QQQ, TTT		ESTs, Moderately similar to NIF1_MOUSE Nuclear LIM interactor-interacting factor 1 (NLI-interacting factor 1) (NIF-like protein) [M.musculus]
1792	7051	AI102055	ZZ, AAA		Rattus norvegicus clone ZG52 mRNA sequence
1801	15218	AI102495	PPP, QQQ		ESTs, Moderately similar to PNPH_MOUSE Purine nucleoside phosphorylase (Inosine phosphorylase) (PNP) [M.musculus]
1802	11953	AI102505	LL	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
1802	11954	AI102505	F, LL, RRR, UUU	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
1807	22487	AI102578	A		ESTs, Highly similar to I49523 tumor necrosis factor alpha-induced protein 2 - mouse [M.musculus]
1828	17400	AI103097	KKK	HMm:ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2	ESTs, Highly similar to ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform 2; hypothetical protein, clone:2-31 [Mus musculus] [M.musculus]
1833	13305	AI103332	E		ESTs, Highly similar to CA1B_MOUSE Collagen alpha 1(XI) chain precursor [M.musculus]
1843	23874	AI103556	L, General Core Tox Markers, General Alternate	HMm:CDC28 protein kinase 1	ESTs, Highly similar to CDC28 protein kinase 1; cyclin-dependent kinase regulatory subunit 1 [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1845	2297	AI103602	GGG		ESTs, Highly similar to SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [M.musculus]
1847	13317	AI103637	VV		ESTs, Moderately similar to RIKEN cDNA 2810411G23 [Mus musculus] [M.musculus]
1857	20833	AI104035	SS		ESTs, Highly similar to COXG_MOUSE Cytochrome c oxidase polypeptide VIb (AED) [M.musculus]
1873	21832	AI104521	LL	Protein-L-isoaspartate (D-aspartate) O-methyltransferase	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
1879	3504	AI104659	BB, CC, PP, QQ	B-cell CLL/lymphoma 10	B-cell CLL/lymphoma 10
1886	18742	AI105131	U, FF, LL, XX, BBB, RRR, SSS, UUU		ESTs, Highly similar to lung alpha/beta hydrolase 1; alpha/beta hydrolase-1 [Mus musculus] [M.musculus]
1905	24211	AI111853	E		ESTs, Highly similar to H33_HUMAN Histone H3.3 (H3.A) (H3.B) (H3.3Q) [M.musculus]
1917	9575	AI112250	SS	protein tyrosine phosphatase type IVA, member 2	protein tyrosine phosphatase type IVA, member 2
1918	2501	AI112343	Q, R	ubiquitin fusion degradation 1-like	ubiquitin fusion degradation 1-like
1925	2296	AI112979	GGG		ESTs, Highly similar to SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [M.musculus]
1929	7317	AI136123	T		ESTs, Highly similar to MKR1_MOUSE Makorin 1 [M.musculus]
1930	11165	AI136372	PPP, QQQ		ESTs, Weakly similar to plexin B3; plexin 6 [Mus musculus] [M.musculus]
1936	24212	AI136747	PPP, QQQ		ESTs, Highly similar to H33_HUMAN Histone H3.3 (H3.A) (H3.B) (H3.3Q) [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	Genbank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1942	13090	AI136977	JJ, KK, KKK		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
1942	13091	AI136977	T, W, JJ, KK		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
1943	10754	AI137038	FF		ESTs, Weakly similar to TO1B_MOUSE Torsin B precursor [M.musculus]
1947	21520	AI137332	T		ESTs, Highly similar to Ras and a-factor-converting enzyme 1 homolog (S. cerevisiae) [Mus musculus] [M.musculus]
1950	9166	AI137406	BB, CC		ESTs, Moderately similar to A55945 endothelial cell protein C receptor precursor - mouse [M.musculus]
1954	18943	AI137495	F, II		ESTs, Highly similar to H2A1_RAT Histone H2A.1 [R.norvegicus]
1960	11321	AI137752	S		ESTs, Weakly similar to RL7_RAT 60S RIBOSOMAL PROTEIN L7 [R.norvegicus]
1966	13157	AI138020	M		ESTs, Weakly similar to S43429 diamine N-acetyltransferase (EC 2.3.1.57) - mouse [M.musculus]
1988	11363	AI145997	S, LL		ESTs, Moderately similar to 2206377B MHR23B gene [Mus musculus] [M.musculus]
1991	11693	AI168953	X, III, JJJ, General Core Tox Markers	sulfotransferase family, cytosolic, 1C, member 2	sulfotransferase family, cytosolic, 1C, member 2
2003	14962	AI169171	GGG		ESTs, Highly similar to ERH_HUMAN Enhancer of rudimentary homolog [M.musculus]
2009	24213	AI169289	LL		ESTs, Highly similar to H33_HUMAN Histone H3.3 (H3.A) (H3.B) (H3.3Q) [M.musculus]
2013	23427	AI169321	U, BBB, CCC		ESTs, Weakly similar to B30605 acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, short-chain-specific - rat [R.norvegicus]
2016	15286	AI169361	UUU		ESTs, Highly similar to RU1C_MOUSE U1 small nuclear ribonucleoprotein C (U1-C) [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2030	21660	AI169751	BB, EEE, MMM		Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
2031	20503	AI169779	B, PPP, General Core Tox Markers	solute carrier family (organic anion transporter) member 10	solute carrier family (organic anion transporter) member 10
2034	3909	AI169903	O, P		ESTs, Moderately similar to lymphocyte antigen 96 [Mus musculus] [M.musculus]
2037	8794	AI170002	CC	discs, large (Drosophila) homolog 2 (chapsyn-110)	discs, large (Drosophila) homolog 2 (chapsyn-110)
2042	3429	AI170124	C, HH		ESTs, Weakly similar to serine/threonine kinase 25 (yeast); Ste20-like kinase; serine/threonine kinase 25 (Ste20, yeast homolog); Yeast Sps1/Ste20-related kinase 1 [Mus musculus] [M.musculus]
2045	3579	AI170314	PPP, QQQ	complement component factor h	complement component factor h
2046	2248	AI170332	BB, CC		ESTs, Highly similar to A3B1_MOUSE Adapter-related protein complex 3 beta 1 subunit (Beta-adaptin 3A) (AP-3 complex beta-3A subunit) (Beta-3A-adaptin) [M.musculus]
2056	3013	AI170532	D		ESTs, Highly similar to T14265 golgin-245 - mouse [M.musculus]
2078	16170	AI170894	VV		ESTs, Moderately similar to ADFP_MOUSE ADIPOPHILIN (ADIPOSE DIFFERENTIATION-RELATED PROTEIN) (ADRP) [M.musculus]
2084	22340	AI171276	HH, KKK		ESTs, Weakly similar to S11661 talin - mouse [M.musculus]
2094	17529	AI171460	WW		ESTs, Weakly similar to HCD2_RAT 3-hydroxyacyl-CoA dehydrogenase type II (Type II HADH) (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) [R.norvegicus]

TABLE 1					
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Seq ID	GLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2096	15684	AI171535	KK, FFF, HHH, General Core Tox Markers, General Alternate		ESTs, Weakly similar to PAB1_MOUSE Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) (PABP1) [M.musculus]
2098	16102	AI171586	G, H		ESTs, Highly similar to ZPR1_MOUSE Zinc-finger protein ZPR1 (Zinc finger protein 259) [M.musculus]
2105	6582	AI171726	Z, OOO		ESTs, Weakly similar to I67424 hERR-2 homolog - rat (fragment) [R.norvegicus]
2118	20783	AI171966	O, P, V, NN, OO		R.norvegicus mRNA for RT1.Mb
2122	2218	AI172011	RR		ESTs, Moderately similar to S12207 hypothetical protein (B2 element) - mouse [M.musculus]
2124	7642	AI172045	C, MM, TTT	HMM:histone deacetylase 5	ESTs, Highly similar to HDA5_MOUSE Histone deacetylase 5 (HD5) (Histone deacetylase mHDA1) [M.musculus]
2129	7733	AI172086	O, P		ESTs, Highly similar to SH3 domain binding glutamic acid-rich protein-like 3 [Mus musculus] [M.musculus]
2132	1957	AI172143	KKK	phytanoyl-CoA hydroxylase (Refsum disease)	phytanoyl-CoA hydroxylase (Refsum disease)
2137	2140	AI172272	XX, General Alternate		ESTs, Weakly similar to A53004 transcription elongation factor S-II - rat [R.norvegicus]
2138	4193	AI172274	PPP		ESTs, Weakly similar to A Chain A, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 [R.norvegicus]
2147	11623	AI172471	N, XX, YY, PPP, QQQ		ESTs, Highly similar to small EDRK-rich factor 2; 4F5rel (4F5 related); modifier of spinal muscular atrophy candidate 1-like [Mus musculus] [M.musculus]
2154	15557	AI175019	R		ESTs, Moderately similar to RIKEN cDNA 2410001H17 [Mus musculus] [M.musculus]
2162	22105	AI175221	RR		ESTs, Highly similar to RIKEN cDNA 2310039D06 [Mus musculus] [M.musculus]

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2170	18507	AI175551	H, General Core Tox Markers, General Alternate		ESTs, Highly similar to EF1B_MOUSE Elongation factor 1-beta (EF-1-beta) [M.musculus]
2177	19004	AI175875	NN, OO		Rattus norvegicus Sprague-Dawley lipid-binding protein mRNA, complete cds
2180	6549	AI176002	JJ		ESTs, Highly similar to 2206297A folypoly-gamma-Glu synthetase [Mus musculus] [M.musculus]
2185	7022	AI176041	LLL, SSS, UUU		ESTs, Highly similar to PIR_MOUSE Pirin [M.musculus]
2187	5876	AI176117	UU	HMm:pyruvate dehydrogenase (lipoamide) beta	ESTs, ESTs, Highly similar to S15892 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - rat [R.norvegicus]
2206	15191	AI176456	C, E, L, T, W, DD, SS, WW, III, JJJ, KKK, NNN		ESTs, Highly similar to SMRT2 metallothionein II - rat [R.norvegicus]
2211	22823	AI176491	WW, BBB, CCC		ESTs, Moderately similar to RIKEN cDNA 2310016K22; RIKEN cDNA 2310016K22 gene [Mus musculus] [M.musculus]
2241	10310	AI176961	A, B, H	ribosomal protein, mitochondrial, L12	ribosomal protein, mitochondrial, L12
2242	16124	AI176963	UUU	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
2246	2359	AI177029	DD	tec protein tyrosine kinase	tec protein tyrosine kinase
2260	14083	AI177181	General Core Tox Markers		ESTs, Weakly similar to FYV1_MOUSE FYVE finger-containing phosphoinositide kinase (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) (p235) [M.musculus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2265	15251	AI177363	Z	HMm:c-src tyrosine kinase	ESTs, Highly similar to 1709363A protein Tyr kinase CSK [Rattus norvegicus] [R.norvegicus]
2275	21603	AI177742	PPP, QQQ		ESTs, Highly similar to FKB8_MOUSE 38 kDa FK-506 binding protein homolog (FKBPR38) (FK506-binding protein 8) (muFKBP38) [M.musculus]
2284	19184	AI178025	Q, W		ESTs, Highly similar to TGIF_MOUSE 5'-TG-3' INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF) [M.musculus]
2287	13389	AI178104	KKK		ESTs, Highly similar to RIKEN cDNA 2400009B11 [Mus musculus] [M.musculus]
2300	6502	AI178283	XX	HMm:phenylalanine-tRNA synthetase-like	ESTs, Highly similar to SYFB_MOUSE Phenylalanyl-tRNA synthetase beta chain (Phenylalanine--tRNA ligase beta chain) (PheRS) [M.musculus]
2307	15252	AI178605	GG, HH	HMm:c-src tyrosine kinase	ESTs, Highly similar to 1709363A protein Tyr kinase CSK [Rattus norvegicus] [R.norvegicus]
2313	2825	AI178752	WW		ESTs, Highly similar to CLN3_MOUSE CLN3 PROTEIN (BATTENIN) [M.musculus]
2319	6628	AI178793	GG		ESTs, Highly similar to M2A1_RAT Alpha-mannosidase II (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A member 1) [R.norvegicus]
2324	3076	AI179075	RR	Chorionic somatomammotropin hormone 1 variant; Placental lactogen-1	Chorionic somatomammotropin hormone 1 variant; Placental lactogen-1
2325	5887	AI179099	U, XX, BBB		ESTs, Moderately similar to VNN1_MOUSE Pantetheinase precursor (Pantetheine hydrolase) (Vascular non-inflammatory molecule 1) (Vanin 1) [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2338	16703	AI179300	K, U, FF, LL, TT, UU, HHH, LLL, SSS, UUU, General Core Tox Markers		ESTs, Highly similar to RIKEN cDNA 1300002A08 [Mus musculus] [M.musculus]
2364	17224	AI179883	PP, QQ		ESTs, Highly similar to testis expressed gene 189 [Mus musculus] [M.musculus]
2374	2099	AI180015	R	ribosomal protein L14	ribosomal protein L14
2380	9821	AI180114	O, P, PP, QQ		ESTs, Highly similar to NIP2_MOUSE BCL2/ADENOVIRUS E1B 19-KDA PROTEIN-INTERACTING PROTEIN 2 [M.musculus]
2389	24368	AI180392	G, H, ZZ		ESTs, Highly similar to NUB2_MOUSE Nucleotide binding protein 2 (NBP 2) [M.musculus]
2409	11782	AI228004	Z, AA		ESTs, Highly similar to ATPase, class 1, member h; ATPase 11A, p type; ATPase 11A, class VI [Mus musculus] [M.musculus]
2413	16913	AI228236	QQQ		ESTs, Highly similar to neuronal protein 15.6 [Mus musculus] [M.musculus]
2419	22915	AI228299	L		ESTs, Highly similar to craniofacial development protein 1 [Mus musculus] [M.musculus]
2473	16093	AI229849	T		ESTs, Highly similar to WDR1_MOUSE WD-repeat protein 1 (Actin interacting protein 1) [M.musculus]
2479	17672	AI230074	N, PPP, QQQ	HMm:NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	ESTs, Highly similar to NIMM_MOUSE NADH-ubiquinone oxidoreductase MWFE subunit (Complex I-MWFE) (CI-MWFE) [M.musculus]
2486	1480	AI230260	RR	casein kinase II beta subunit	casein kinase II beta subunit
2488	23628	AI230278	GG		ESTs, Highly similar to mitochondrial ribosomal protein S16 [Mus musculus] [M.musculus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2492	14662	AI230413	Z, AA		ESTs, Highly similar to ZW10_MOUSE Centromere/kinetochore protein zw10 homolog [M.musculus]
2505	15551	AI230759	A, B, Z, AA, RR		ESTs, Moderately similar to ornithine decarboxylase antizyme 2; ornithine decarboxylase antizyme; antizyme 2 [Mus musculus] [M.musculus]
2509	17720	AI230778	I, J		ESTs, Highly similar to protein-tyrosine sulfotransferase 2 [Mus musculus] [M.musculus]
2518	2299	AI231094	GGG		ESTs, Highly similar to SAP3_MOUSE Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein 3) (SAP-3) [M.musculus]
2526	22791	AI231230	SS		ESTs, Weakly similar to dual-specificity phosphatase [Mus musculus] [M.musculus]
2534	22379	AI231448	X, Y, Z, RR, XX		ESTs, Highly similar to G6PI_MOUSE Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) [M.musculus]
2539	13092	AI231547	T, W, DD, EE, JJ, UU, KKK		ESTs, Highly similar to S14538 transition protein - mouse [M.musculus]
2542	4703	AI231606	C, KKK		ESTs, Moderately similar to RIKEN cDNA 6330579B17 [Mus musculus] [M.musculus]
2544	17297	AI231785	S		ESTs, Moderately similar to Niemann Pick type C2 [Mus musculus] [M.musculus]
2545	15171	AI231792	Q, AA		ESTs, Highly similar to BAG3_MOUSE BAG-family molecular chaperone regulator-3 (BCL-2 binding athanogene-3) (BAG-3) (Bcl-2-binding protein Bis) [M.musculus]
2551	17144	AI231921	YY	Protein-L-isoaspartate (D-aspartate) O-methyltransferase	Protein-L-isoaspartate (D-aspartate) O-methyltransferase

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2554	19094	AI232021	C		ESTs, Highly similar to SUI1_MOUSE Protein translation factor SUI1 homolog [M.musculus]
2561	19274	AI232135	DDD, General Alternate		ESTs, Highly similar to COG2_MOUSE Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) [M.musculus]
2567	409	AI232268	GG	low density lipoprotein receptor-related protein associated protein 1	low density lipoprotein receptor-related protein associated protein 1
2574	15582	AI232320	U, FF, PP, QQ		Rat mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase mRNA, complete cds
2587	8709	AI232534	ZZ		ESTs, Weakly similar to DnaJ (Hsp40) homolog, subfamily B, member 3; heat shock protein, DNAJ-like 3 [Mus musculus] [M.musculus]
2592	3860	AI232703	U, LL, BBB, CCC, LLL, RRR, SSS, UUU	malonyl-CoA decarboxylase	malonyl-CoA decarboxylase
2593	12463	AI232706	L, PP	translin-associated factor X	translin-associated factor X
2611	14103	AI233172	GGG, LLL, RRR, SSS, UUU, General Core Tox Markers		ESTs, Weakly similar to A Chain A, Crystal Structure Of The Epsin N-Terminal Homology (Enth) Domain At 1.56 Angstrom Resolution [R.norvegicus]
2618	19470	AI233266	GGG, HHH		ESTs, Weakly similar to PROD_MOUSE PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR (PROLINE DEHYDROGENASE) [M.musculus]
2619	10378	AI233300	K		ESTs, Moderately similar to CO5_MOUSE Complement C5 precursor (Hemolytic complement) [Contains: C5A anaphylatoxin] [M.musculus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2651	12736	AI233972	JJJ	Gap junction membrane channel, protein alpha 4 (connexin 37)	Gap junction membrane channel, protein alpha 4 (connexin 37)
2667	16781	AI234527	M, GG, TT	HMm:glutathione S-transferase, alpha 4	ESTs, Highly similar to S23433 glutathione transferase (EC 2.5.1.18) 8 - rat [R.norvegicus]
2680	19057	AI235094	E	cortactin isoform B	cortactin isoform B
2681	22380	AI235217	Z, AA, NNN		ESTs, Highly similar to G6PI_MOUSE Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) [M.musculus]
2684	15004	AI235224	SS, EEE, III, JJJ, MMM	tissue inhibitor of metalloproteinase 1	tissue inhibitor of metalloproteinase 1
2687	11644	AI235282	FFF, GGG, General Alternate	HMm:low density lipoprotein receptor-related protein 1	ESTs, Highly similar to S25111 alpha-2-macroglobulin receptor precursor - mouse [M.musculus]
2698	1462	AI235585	K	cathepsin D	cathepsin D
2712	3617	AI236021	DD		ESTs, Highly similar to JC4857 hepatocarcinogenesis-related transcription factor - rat [R.norvegicus]
2716	11465	AI236084	JJ		ESTs, Moderately similar to TNR9_MOUSE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen) [M.musculus]
2717	16943	AI236097	PPP, QQQ		ESTs, Highly similar to ITMB_MOUSE Integral membrane protein 2B (E25B protein) [M.musculus]
2728	5052	AI236302	ZZ, UUU		ESTs, Weakly similar to TTHY_RAT Transthyretin precursor (Prealbumin) (TBPA) [R.norvegicus]
2740	7691	AI236611	Y	isopentenyl-diphosphate delta isomerase	isopentenyl-diphosphate delta isomerase
2753	15850	AI236795	F, J, S, RR		ESTs; ESTs, Highly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2757	22176	AI236907	RR, SS		ESTs, Moderately similar to MBNL_MOUSE Muscleblind-like protein (Triplet-expansion RNA-binding protein) [M.musculus]
2761	11404	AI237002	H, Z, KK, FFF, GGG, General Core Tox Markers	spermidine synthase	spermidine synthase
2780	18854	AI237636	OOO		ESTs, Weakly similar to CNE6_MOUSE Copine VI (Neuronal-copine) (N-copine) [M.musculus]
2792	11692	AI638982	M	sulfotransferase family, cytosolic, 1C, member 2	sulfotransferase family, cytosolic, 1C, member 2
2794	17108	AI639017	C		ESTs, Weakly similar to T17453 ERG-associated protein ESET - mouse [M.musculus]
2828	20082	AI639488	F, II, VV	HMM:transformed mouse 3T3 cell double minute 2	ESTs, Highly similar to A42772 mdm2 protein - rat (fragments) [R.norvegicus]
2833	23220	AJ000347	V, X, Y, HH, JJ, SS, ZZ, AAA, HHH	3'(2'),5'-bisphosphate nucleotidase	3'(2'),5'-bisphosphate nucleotidase
2835	14332	AJ001044	II	tumor-associated calcium signal transducer 1	tumor-associated calcium signal transducer 1
2838	14882	D00362	O, P, NN, OO, XX, YY, BBB, DDD	Esterase 2	Esterase 2
2841	3292	D00753	E, BB, III, JJJ, KKK, NNN	Serine protease inhibitor	Serine protease inhibitor
2842	1515	D10233	O, P	renin-binding protein	renin-binding protein
2846	19053	D12770	ZZ, AAA	solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4	solute carrier family 25 (mitochondrial adenine nucleotide translocator) member 4

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2850	1728	D16479	U, FF, XX, YY, BBB, RRR, SSS	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
2853	179	D17809	GG, WW	beta-4N-acetylgalactosaminyltransferase	beta-4N-acetylgalactosaminyltransferase
2862	1354	D38065	E, I, J, K, X, Y, TT, RRR, SSS, UUU	dynein, cytoplasmic, intermediate polypeptide 2	dynein, cytoplasmic, intermediate polypeptide 2
2865	1350	D38560	DD, EE, NNN	cyclin G-associated kinase	cyclin G-associated kinase
2868	2578	D50694	S, BBB, CCC, GGG	Proteasome (prosome, macropain) 26S subunit, ATPase	Proteasome (prosome, macropain) 26S subunit, ATPase
2869	1884	D50695	G, H, X, Y, General Alternate	proteasome (prosome, macropain) 26S subunit, ATPase, 4	proteasome (prosome, macropain) 26S subunit, ATPase, 4
2870	727	D50696	Y, CCC, PPP, QQQ	protease (prosome, macropain) 26S subunit, ATPase 1	protease (prosome, macropain) 26S subunit, ATPase 1
2873	826	D82928	Z, AA, EE	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
2877	134	D87839	A, B, III, JJJ, OOO, General Core Tox Markers	4-aminobutyrate aminotransferase	4-aminobutyrate aminotransferase
2877	135	D87839	B, J, OO, RRR	4-aminobutyrate aminotransferase	4-aminobutyrate aminotransferase
2879	1218	D89340	OOO, General Alternate	dipeptidylpeptidase III	dipeptidylpeptidase III

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2888	1888	E13573	F, X, Y, LLL	BH3 interacting (with BCL2 family) domain, apoptosis agonist	BH3 interacting (with BCL2 family) domain, apoptosis agonist
2915	14266	H33842	JJ		ESTs, Weakly similar to A45988 dentin matrix acidic phosphoprotein AG1 - rat [R.norvegicus]
2920	16130	J01435	F, DD, EE, HH, NNN	unknown Glu-Pro dipeptide repeat protein	unknown Glu-Pro dipeptide repeat protein
2924	1514	J02780	O, P, VV	Tropomyosin 4	Tropomyosin 4
2933	293	J05499	GG, VV, GGG	liver mitochondrial glutaminase	liver mitochondrial glutaminase
2934	1549	J05519	MM, TTT	C1-tetrahydrofolate synthase	C1-tetrahydrofolate synthase
2938	23486	K02816	FF	pR-ET2 encoded oncodevelopmental protein	pR-ET2 encoded oncodevelopmental protein
2945	1894	L03201	DDD	cathepsin S	cathepsin S
2950	4144	L12380	PP, QQ, TT	ADP-ribosylation factor 1	ADP-ribosylation factor 1
2957	1481	L15619	N, V, ZZ, AAA, PPP, QQQ	casein kinase II beta subunit	casein kinase II beta subunit
2964	1795	L24207	K, L, N, O, P, X, NN, OO, PP, TT, LLL, UUU	Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
2964	1796	L24207	K, L, M, N, X, TT	Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
2967	13499	L26267	O, P, Q, R, W, NN, OO, PP, QQ	nuclear factor kappa B p105 subunit	nuclear factor kappa B p105 subunit
2970	31	L27651	XX, YY, General Alternate	solute carrier family 22 (organic anion transporter), member 7	solute carrier family 22 (organic anion transporter), member 7

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2970	32	L27651	M, U, GGG, OOO, PPP, QQQ, General Core Tox Markers, General Alternate	solute carrier family 22 (organic anion transporter), member 7	solute carrier family 22 (organic anion transporter), member 7
2976	695	L41254	F	corticosteroid-induced protein	corticosteroid-induced protein
2978	11955	L48209	F	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
2989	24860	M13506	E, K, M, X, TT, BBB, DDD, EEE, MMM		Rat liver UDP-glucuronosyltransferase, phenobarbital-inducible form mRNA, complete cds
2994	19255	M15562	X, OO		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
2994	19256	M15562	M, X, OO		Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
3000	14881	M20629	O, P, NN, OO, XX, YY, CCC	Esterase 2	Esterase 2
3008	11956	M28255	LL	cytochrome c oxidase, subunit VIIIa	cytochrome c oxidase, subunit VIIIa
3009	1580	M29293	ZZ, AAA	small nuclear ribonucleoparticle-associated protein (snRNP) mRNA, clone Sm51	small nuclear ribonucleoparticle-associated protein (snRNP) mRNA, clone Sm51
3010	17123	M29295	C, KK, FFF, GGG, HHH, General Alternate	small nuclear ribonucleoprotein polypeptides B and B1	small nuclear ribonucleoprotein polypeptides B and B1
3014	15579	M33648	Y, FF, RRR, SSS		Rat mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase mRNA, complete cds
3014	15580	M33648	U, FF		Rat mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase mRNA, complete cds

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3015	16807	M33936	FF		Rat Cyp4a locus, encoding cytochrome P450 (IVA3) mRNA, complete cds
3021	9223	M36151	X, Y, NN, OO, PP		Rat mRNA for MHC class II antigen RT1.B-1 beta-chain, Rattus norvegicus MHC class II antigen RT1.B beta chain mRNA, partial cds
3023	17145	M38566	VV	Serine protease inhibitor	Serine protease inhibitor
3024	1246	M57507	A, B, M, FFF, HHH, KKK, NNN, OOO, General Core Tox Markers	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)
3034	20207	M64378	RR		Rat olfactory protein mRNA, complete cds
3038	1138	M76740	RR, SS	Mucin3	Mucin3
3038	25446	M76740	D, SS	Mucin3	Mucin3
3042	1529	M81687	S, FFF, GGG, OOO, UUU, General Core Tox Markers	Ryudocan/syndecan 2	Ryudocan/syndecan 2
3044	4198	M83143	F, S, U, BB, CC, TT, III, JJJ, LLL, OOO, SSS, UUU, General Alternate		Rat beta-galactoside-alpha 2,6-sialyltransferase mRNA
3044	4199	M83143	E, F, G, U, LL, CCC, LLL, RRR, SSS, UUU		Rat beta-galactoside-alpha 2,6-sialyltransferase mRNA
3045	1991	M83196	UU	Microtubule-associated protein 1a	Microtubule-associated protein 1a

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3050	25467	M93297	A, B, II, WW	ornithine aminotransferase	ornithine aminotransferase
3051	3424	M94557	A, B	Single-stranded DNA-binding protein	ESTs, Highly similar to SSB_RAT SINGLE-STRANDED DNA-BINDING PROTEIN, MITOCHONDRIAL PRECURSOR (MT-SSB) (MTSSB) (P16) [R.norvegicus]
3052	729	M95762	FFF	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
3053	1624	M95768	Z, AA	di-N-acetylchitobiase	di-N-acetylchitobiase
3056	1508	M97662	M	ureidopropionase, beta	ureidopropionase, beta
3086	17292	NM_012584	K, GGG	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase (Hsd3b), mRNA. 1/2002 Length = 1947	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase
3092	382	NM_012599	FF, RRR	Mannose binding protein A, serum (MbpA), mRNA. 11/2000 Length = 717	Mannose binding protein A, serum
3106	17147	NM_012657	L, TT	Serine protease inhibitor (Spin2b), mRNA. 11/2002 Length = 1664	Serine protease inhibitor
3106	17148	NM_012657	HH, TT	Serine protease inhibitor (Spin2b), mRNA. 11/2002 Length = 1664	Serine protease inhibitor
3128	18730	NM_012730	N, TT	Cytochrome P450, subfamily IID2 (Cyp2d2), mRNA. 11/2000 Length = 1698	Cytochrome P450, subfamily IID2
3135	13731	NM_012755	P	Fyn proto-oncogene (Fyn), mRNA. 9/2002 Length = 1844	Fyn proto-oncogene
3136	18068	NM_012762	P, VV	caspase 1 (Casp1), mRNA. 11/2002 Length = 1209	Interleukin 1beta converting enzyme

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3137	17257	NM_012766	NN, OO, PP, QQ, ZZ	Cyclin D3 (Ccnd3), mRNA. 11/2002 Length = 1843	Cyclin D3
3137	17258	NM_012766	NN, ZZ, AAA	Cyclin D3 (Ccnd3), mRNA. 11/2002 Length = 1843	Cyclin D3
3174	16581	NM_012911	VV	Arrestin, beta 2 (Arrb2), mRNA. 11/2002 Length = 1758	Arrestin, beta 2
3180	18695	NM_012931	T, III, JJJ, KKK, General Alternate	v-crk-associated tyrosine kinase substrate (Crkas), mRNA. 11/2002 Length = 3335	v-crk-associated tyrosine kinase substrate
3187	20943	NM_012985	MM, TTT	NADH ubiquinone oxidoreductase subunit B13 (Ndufa5), mRNA. 11/2000 Length = 553	NADH ubiquinone oxidoreductase subunit B13
3190	9917	NM_012993	JJ, KK, HHH	N-arginine dibasic convertase 1 (Nrd1), mRNA. 11/2000 Length = 3581	N-arginine dibasic convertase 1
3190	9918	NM_012993	JJ, KK	N-arginine dibasic convertase 1 (Nrd1), mRNA. 11/2000 Length = 3581	N-arginine dibasic convertase 1
3194	24718	NM_013003	EE, JJ, KK	phosphatidylethanolamine N-methyltransferase (Pemt), mRNA. 11/2002 Length = 893	Phosphatidylethanolamine N-methyltransferase
3200	17174	NM_013030	JJ, KK, HHH	Solute carrier family 34 (sodium phosphate), member 1 (Slc34a1), mRNA. 11/2002 Length = 2440	R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22

TABLE 1					
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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3202	17401	NM_013043	B, L, X, Y, HH, GGG, LLL, OOO, SSS, UUU, General Core Tox Markers	Transforming growth factor beta stimulated clone 22 (Tgfb1i4), mRNA. 11/2000 Length = 1666	Transforming growth factor beta stimulated clone 22
3206	14423	NM_013053	O, P	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (Ywhaq), mRNA. 11/2002 Length = 2099	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
3211	19335	NM_013067	FF	Ribophorin I (Rpn1), mRNA. 11/2002 Length = 2214	Ribophorin I
3213	17181	NM_013073	ZZ, AAA	Protein-L-isoaspartate (D-aspartate) O-methyltransferase (Pcmt1), mRNA. 11/2002 Length = 1658	Protein-L-isoaspartate (D-aspartate) O-methyltransferase
3216	1521	NM_013091	C, E, Q, R, General Alternate	Tumor necrosis factor receptor (Tnfr1), mRNA. 11/2002 Length = 2130	Tumor necrosis factor receptor superfamily, member 1a
3221	1793	NM_013105	K, L, M, N, FF, TT, DDD, UUU	Cytochrome P450, subfamily IIIA, polypeptide 3 (Cyp3a3), mRNA. 11/2000 Length = 2026	Cytochrome P450, subfamily IIIA, polypeptide 3
3221	1794	NM_013105	K, L, M, N, TT, DDD, LLL, UUU	Cytochrome P450, subfamily IIIA, polypeptide 3 (Cyp3a3), mRNA. 11/2000 Length = 2026	Cytochrome P450, subfamily IIIA, polypeptide 3

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3221	1797	NM_013105	K, L, TT, DDD	Cytochrome P450, subfamily IIIA, polypeptide 3 (Cyp3a3), mRNA. 11/2000 Length = 2026	Cytochrome P450, subfamily IIIA, polypeptide 3, Rattus norvegicus Sprague Dawley testosterone 6-beta-hydroxylase, cytochrome P450/6-beta-A, (CYP3A2) mRNA, complete cds
3223	23709	NM_013113	I, M, MM, TT, TTT	ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2000 Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
3223	23710	NM_013113	I, M, MM, TTT	ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2000 Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
3223	23711	NM_013113	I, M, MM, WW, TTT	ATPase Na+/K+ transporting beta 1 polypeptide (Atp1b1), mRNA. 11/2000 Length = 2528	ATPase Na+/K+ transporting beta 1 polypeptide
3224	22582	NM_013120	A, B, G, S, GGG, OOO, General Core Tox Markers	Glucokinase regulatory protein (Gckr), mRNA. 11/2002 Length = 2156	Glucokinase regulatory protein
3225	16650	NM_013132	O, VV	Annexin V (Anx5), mRNA. 11/2002 Length = 1417	Annexin V
3227	16982	NM_013144	I, J, W, MM, OOO, TTT, General Core Tox Markers	insulin-like growth factor binding protein 1 (Igfbp1), mRNA. 11/2002 Length = 1500	Insulin-like growth factor binding protein 1
3231	1258	NM_013185	VV	Hemopoietic cell tyrosine kinase (Hck), mRNA. 11/2000 Length = 1911	Hemopoietic cell tyrosine kinase
3233	21396	NM_013198	OO, OOO, General Core Tox Markers	Monoamine oxidase B (Maob), mRNA. 11/2002 Length = 2389	Monoamine oxidase B

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3239	20826	NM_013218	C, HH	adenylate kinase 3 (Ak3), mRNA. 11/2002 Length = 1061	adenylate kinase 3
3269	18452	NM_017074	L, OO, UU	CTL target antigen (Cth), mRNA. 11/2000 Length = 1743	CTL target antigen
3269	18453	NM_017074	L, NN, OO, III, JJJ, OOO	CTL target antigen (Cth), mRNA. 11/2000 Length = 1743	CTL target antigen
3294	2967	NM_017158	HH	cytochrome P450, 2c39 (Cyp2c39), mRNA. 11/2002 Length = 1731	cytochrome P450, 2c39
3294	2968	NM_017158	MM, TTT	cytochrome P450, 2c39 (Cyp2c39), mRNA. 11/2002 Length = 1731	cytochrome P450, 2c39
3294	2969	NM_017158	N, TT	cytochrome P450, 2c39 (Cyp2c39), mRNA. 11/2002 Length = 1731	cytochrome P450, 2c39
3294	2970	NM_017158	N, HH, SS	cytochrome P450, 2c39 (Cyp2c39), mRNA. 11/2002 Length = 1731	cytochrome P450, 2c39
3297	20702	NM_017166	ZZ, AAA	stathmin 1 (Stmn1), mRNA. 11/2002 Length = 1054	Leukemia-associated cytosolic phosphoprotein stathmin
3310	18445	NM_017220	F, L	6-pyruvoyl-tetrahydropterin synthase (Pts), mRNA. 11/2002 Length = 1176	growth and transformation-dependent protein
3340	17516	NM_017321	T, LL, YY, RRR, SSS	iron-responsive element-binding protein (Ratireb), mRNA. 11/2000 Length = 3564	iron-responsive element-binding protein
3341	24766	NM_017322	EE	stress activated protein kinase alpha II (SAPK), mRNA. 11/2000 Length = 2622	stress activated protein kinase alpha II

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Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3341	24767	NM_017322	A, B, L	stress activated protein kinase alpha II (SAPK), mRNA. 11/2000 Length = 2622	stress activated protein kinase alpha II
3343	24247	NM_017332	V	fatty acid synthase (Fasn), mRNA. 11/2002 Length = 9136	fatty acid synthase
3346	16382	NM_017343	V	myosin regulatory light chain (MRLCB), mRNA. 6/2001 Length = 1139	myosin regulatory light chain
3348	20146	NM_017362	I, J	muscarinic acetylcholine receptor M5 (Chrm5), mRNA. 11/2002 Length = 2733	muscarinic acetylcholine receptor M5
3349	20778	NM_019124	E, K, L, KKK, NNN, OOO, General Alternate	rabaptin 5 (LOC54190), mRNA. 11/2002 Length = 3465	rabaptin 5
3350	24392	NM_019129	D, Z, AA	Insulin (Ins1), mRNA. 11/2000 Length = 333	Insulin
3358	17304	NM_019144	GG	Acid phosphatase 5, tartrate resistant (Acp5), mRNA. 11/2002 Length = 1381	Acid phosphatase 5, tartrate resistant
3387	10015	NM_019289	B, I, J, O, P, NN, OO, VV	Actin-related protein complex 1b (Arpc1b), mRNA. 11/2000 Length = 1430	Actin-related protein complex 1b
3387	10016	NM_019289	A, O, NN, OO, VV	Actin-related protein complex 1b (Arpc1b), mRNA. 11/2000 Length = 1430	Actin-related protein complex 1b
3391	17507	NM_019299	A, B, TT	clathrin, heavy polypeptide (Hc) (Cltc), mRNA. 11/2002 Length = 6071	clathrin, heavy polypeptide (Hc)

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3394	24757	NM_019317	D, Z, AA	Mucosal vascular addressin cell adhesion molecule 1 (Madcam1), mRNA. 11/2000 Length = 1279	Mucosal vascular addressin cell adhesion molecule 1
3399	3775	NM_019354	M, VV	Uncoupling protein 2, mitochondrial (Ucp2), mRNA. 11/2000 Length = 1575	Uncoupling protein 2, mitochondrial
3400	4592	NM_019356	D, PPP, General Alternate	eukaryotic translation initiation factor 2, subunit 1 (alpha) (Eif2s1), mRNA. 11/2000 Length = 1377	eukaryotic translation initiation factor 2, subunit 1 (alpha)
3404	20057	NM_019370	F, XX, YY	alkaline phosphodiesterase (LOC54410), mRNA. 11/2000 Length = 2777	alkaline phosphodiesterase
3405	15066	NM_019373	PPP, QQQ	apolipoprotein M (Apom), mRNA. 11/2002 Length = 757	apolipoprotein M
3410	24066	NM_019384	UU	CTD-binding SR-like (rA1), mRNA. 11/2000 Length = 3851	CTD-binding SR-like rA1
3411	20716	NM_019623	N, EEE, HHH, MMM, PPP, QQQ, General Alternate	cytochrome P450, subfamily IVF, polypeptide 14 (leukotriene B4 omega hydroxylase) (Cyp4f14), mRNA. 11/2002 Length = 1977	cytochrome P450 4F1
3416	18702	NM_020080	T, MM, TTT	nuclear protein E3-3 orf1 (LOC56769), mRNA. 11/2000 Length = 721	nuclear protein E3-3 orf1
3419	13486	NM_020306	O, P	a disintegrin and metalloproteinase domain 17 (Adam17), mRNA. 11/2002 Length = 4128	a disintegrin and metalloproteinase domain 17

TABLE 1					
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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3424	18727	NM_021577	A, B, I, J, L, MM, WW, BBB, KKK, OOO, TTT, General Alternate	argininosuccinate lyase (Asl), mRNA. 11/2002 Length = 1574	argininosuccinate lyase
3426	17324	NM_021593	L, GG, EEE, GGG, KKK, LLL, MMM, UUU, General Core Tox Markers	kynurenine 3-hydroxylase (Kmo), mRNA. 11/2002 Length = 1733	kynurenine 3-hydroxylase
3432	19710	NM_021744	II, KKK	CD14 antigen (Cd14), mRNA. 11/2002 Length = 1591	CD14 antigen
3432	19711	NM_021744	N, GG	CD14 antigen (Cd14), mRNA. 11/2002 Length = 1591	CD14 antigen
3434	19824	NM_021750	A, B, JJ, HHH, General Alternate	cysteine-sulfinate decarboxylase (Csad), mRNA. 11/2000 Length = 2413	cysteine-sulfinate decarboxylase
3434	19825	NM_021750	B, I, J, JJ, HHH, General Alternate	cysteine-sulfinate decarboxylase (Csad), mRNA. 11/2000 Length = 2413	cysteine-sulfinate decarboxylase
3436	17885	NM_021765	X, Y, SS	beta prime COP (Copb), mRNA. 11/2000 Length = 3025	beta prime COP
3439	20161	NM_021836	CC, DD, EE, II, NNN	jun B proto-oncogene (Junb), mRNA. 11/2002 Length = 1035	jun B proto-oncogene
3445	17100	NM_022179	F	Hexokinase 3 (Hk3), mRNA. 12/2000 Length = 3692	Hexokinase 3

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3445	17101	NM_022179	JJ, KK, FFF, HHH	Hexokinase 3 (Hk3), mRNA. 12/2000 Length = 3692	Hexokinase 3
3448	20266	NM_022212	D, SS	insulin receptor-related receptor (Insrr), mRNA. 11/2002 Length = 1410	insulin receptor-related receptor
3449	20276	NM_022216	SS	G protein-coupled receptor 5-1 (Gpcr5-1), mRNA. 12/2000 Length = 1062	G protein-coupled receptor 5-1
3450	20299	NM_022220	A, B, Y, FFF, GGG, HHH, LLL, PPP, QQQ, General Core Tox Markers	L-gulono-gamma-lactone oxidase (Gulo), mRNA. 12/2000 Length = 1323	L-gulono-gamma-lactone oxidase
3451	20385	NM_022229	G, H, S, T, U	heat shock protein 60 (liver) (Hsp60), mRNA. 12/2000 Length = 2175	heat shock protein 60 (liver)
3454	760	NM_022245	LL	cytochrome b5 (Cyb5), mRNA. 12/2000 Length = 751	cytochrome b5
3454	762	NM_022245	K, GG, PP, QQ, TT	cytochrome b5 (Cyb5), mRNA. 12/2000 Length = 751	cytochrome b5
3455	6263	NM_022251	EEE, III, JJJ, MMM, OOO, General Core Tox Markers, General Alternate	aminopeptidase A (Enpep), mRNA. 12/2000 Length = 4075	aminopeptidase A
3456	6585	NM_022266	A	connective tissue growth factor (Ctgf), mRNA. 11/2002 Length = 2345	connective tissue growth factor

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3461	17158	NM_022298	O, P	alpha-tubulin (Tuba1), mRNA. 12/2000 Length = 1617	alpha-tubulin
3461	17161	NM_022298	V, XX, YY	alpha-tubulin (Tuba1), mRNA. 12/2000 Length = 1617	alpha-tubulin
3465	12082	NM_022389	KKK, NNN, General Alternate	7-dehydrocholesterol reductase (Dhcr7), mRNA. 11/2002 Length = 2427	7-dehydrocholesterol reductase
3465	12083	NM_022389	KKK, NNN, General Alternate	7-dehydrocholesterol reductase (Dhcr7), mRNA. 11/2002 Length = 2427	7-dehydrocholesterol reductase
3466	13479	NM_022390	III, JJJ, KKK	quinoid dihydropteridine reductase (Qdpr), mRNA. 11/2002 Length = 1307	quinoid dihydropteridine reductase
3466	13480	NM_022390	E, XX, YY, III, JJJ, General Alternate	quinoid dihydropteridine reductase (Qdpr), mRNA. 11/2002 Length = 1307	quinoid dihydropteridine reductase
3475	2384	NM_022513	X, Y	dopa/tyrosine sulfotransferase (LOC64305), mRNA. 11/2002 Length = 1279	dopa/tyrosine sulfotransferase
3480	7505	NM_022534	N	transcobalamin II precursor (Tcn2p), mRNA. 11/2002 Length = 1808	transcobalamin II precursor
3484	9240	NM_022540	E, BBB, CCC	peroxiredoxin 3 (Prdx3), mRNA. 11/2002 Length = 1433	peroxiredoxin 3
3484	9241	NM_022540	KK	peroxiredoxin 3 (Prdx3), mRNA. 11/2002 Length = 1433	peroxiredoxin 3
3487	11039	NM_022543	G, General Alternate	steroid sensitive gene 1 (Ssg1), mRNA. 11/2002 Length = 3719	steroid sensitive gene-1 protein

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3494	20802	NM_022592	J, Y, FF	transketolase (Tkt), mRNA. 11/2002 Length = 2098	transketolase
3494	20803	NM_022592	J, X, BB, CC, HH	transketolase (Tkt), mRNA. 11/2002 Length = 2098	transketolase
3494	20804	NM_022592	X	transketolase (Tkt), mRNA. 11/2002 Length = 2098	transketolase
3497	20944	NM_022597	W, EEE, MMM	cathepsin B (Ctsb), mRNA. 11/2002 Length = 1904	cathepsin B
3498	20959	NM_022598	D	cellular nucleic acid binding protein (Cnbp), mRNA. 11/2002 Length = 1640	cellular nucleic acid binding protein
3498	20960	NM_022598	D	cellular nucleic acid binding protein (Cnbp), mRNA. 11/2002 Length = 1640	cellular nucleic acid binding protein
3499	21115	NM_022602	JJ, KK	serine threonine kinase pim3 (Pim3), mRNA. 1/2001 Length = 2133	serine threonine kinase pim3
3504	6121	NM_022686	GG	germinal histone H4 gene (Hist4), mRNA. 1/2001 Length = 377	ESTs, Highly similar to I48404 histone H4 (55AA) (1 is 3rd base in codon) - mouse (fragment) [M.musculus]
3505	20507	NM_022687	F	transcription factor HES-3 (Hes3), mRNA. 1/2001 Length = 964	transcription factor HES-3
3506	20509	NM_022689	VV	synaptosomal-associated protein, 23 kD (Snap23), mRNA. 1/2001 Length = 633	synaptosomal-associated protein, 23 kD
3507	20303	NM_022692	Q, R	small GTP-binding protein rab5 (Rab5a), mRNA. 1/2001 Length = 649	small GTP-binding protein rab5
3508	17586	NM_022694	KK	p105 coactivator (U83883), mRNA. 8/2001 Length = 3166	p105 coactivator

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3510	17757	NM_022698	YY	bcl-2 associated death agonist (Bad), mRNA. 1/2001 Length = 1015	bcl-2 associated death agonist
3511	17809	NM_022699	O, P, XX, YY	ribosomal protein L30 (Rpl30), mRNA. 11/2002 Length = 392	ribosomal protein L30
3517	24283	NM_022869	SS	nucleolar phosphoprotein p130 (Nopp140), mRNA. 1/2001 Length = 3609	nucleolar phosphoprotein p130
3517	24284	NM_022869	C, AAA, General Core Tox Markers	nucleolar phosphoprotein p130 (Nopp140), mRNA. 1/2001 Length = 3609	nucleolar phosphoprotein p130
3522	15697	NM_022939	PP, QQ, UU	syntaxin 12 (Stx12), mRNA. 11/2002 Length = 819	syntaxin 12
3524	18107	NM_022949	General Alternate	ribosomal protein L14 (Rpl14), mRNA. 11/2002 Length = 715	ribosomal protein L14
3525	21491	NM_022951	ZZ, AAA	putative protein phosphatase 1 nuclear targeting subunit (Ppp1r10), mRNA. 1/2001 Length = 4131	putative protein phosphatase 1 nuclear targeting subunit
3527	15743	NM_022958	HH	phosphatidylinositol 3-kinase (Pik3c3), mRNA. 1/2001 Length = 2752	phosphatidylinositol 3-kinase
3529	1053	NM_022962	E	CL1BA protein (CL1BA), mRNA. 1/2001 Length = 5579	CL1BA protein
3531	8266	NM_023103	N, SS, TT	alpha(1)-inhibitor 3, variant I (Mug1), mRNA. 2/2001 Length = 4620	alpha(1)-inhibitor 3, variant I
3531	8267	NM_023103	General Alternate	alpha(1)-inhibitor 3, variant I (Mug1), mRNA. 2/2001 Length = 4620	alpha(1)-inhibitor 3, variant I

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3531	8269	NM_023103	RR, WW	alpha(1)-inhibitor 3, variant I (Mug1), mRNA. 2/2001 Length = 4620	alpha(1)-inhibitor 3, variant I
3539	17517	NM_024151	LL, UU	ADP-ribosylation factor 4 (Arf4), mRNA. 11/2002 Length = 1608	ADP-ribosylation factor 4
3541	1161	NM_024153	D	adrenodoxin reductase (Fdxr), mRNA. 2/2001 Length = 1786	adrenodoxin reductase
3544	4504	NM_024159	PP	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (Dab2), mRNA. 5/2002 Length = 3170	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
3545	20770	NM_024160	VV	cytochrome b558 alpha-subunit (Cyba), mRNA. 2/2001 Length = 709	cytochrome b558 alpha-subunit
3546	15779	NM_024163	RR	brain-enriched guanylate kinase-associated (BEGAIN), mRNA. 2/2001 Length = 2640	brain-enriched guanylate kinase-associated
3552	15623	NM_024369	K, Y	folliculin-related protein (Frp), mRNA. 11/2002 Length = 1370	folliculin-related protein precursor
3553	23489	NM_024375	RR	prepro bone inducing protein (Gdf10), mRNA. 3/2001 Length = 2411	prepro bone inducing protein
3555	9929	NM_024392	U, EE, XX, YY, RRR, SSS	peroxisomal multifunctional enzyme type II (Hsd17b4), mRNA. 3/2001 Length = 2535	peroxisomal multifunctional enzyme type II
3555	9931	NM_024392	U, RRR, SSS	peroxisomal multifunctional enzyme type II (Hsd17b4), mRNA. 3/2001 Length = 2535	peroxisomal multifunctional enzyme type II

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3555	25070	NM_024392	U, FF, LL, CCC, RRR, SSS	peroxisomal multifunctional enzyme type II (Hsd17b4), mRNA. 3/2001 Length = 2535	peroxisomal multifunctional enzyme type II
3558	13633	NM_024403	W	activating transcription factor ATF-4 (Atf4), mRNA. 3/2001 Length = 1173	activating transcription factor ATF-4
3558	13634	NM_024403	M	activating transcription factor ATF-4 (Atf4), mRNA. 3/2001 Length = 1173	activating transcription factor ATF-4
3566	10306	NM_030835	BB, CC	ribosome associated membrane protein 4 (RAMP4), mRNA. 4/2001 Length = 2335	ribosome associated membrane protein 4
3566	10308	NM_030835	LL	ribosome associated membrane protein 4 (RAMP4), mRNA. 4/2001 Length = 2335	ribosome associated membrane protein 4
3567	1221	NM_030845	A, E, BB, CC, DD, EE, NN, OO, PP, EEE, III, KKK, MMM, NNN	gro (Gro1), mRNA. 4/2001 Length = 929	gro
3568	18023	NM_030846	S	growth factor receptor bound protein 2 (Grb2), mRNA. 11/2002 Length = 2099	growth factor receptor bound protein 2
3568	18728	NM_030846	N, MM, PPP, QQQ, TTT	growth factor receptor bound protein 2 (Grb2), mRNA. 11/2002 Length = 2099	growth factor receptor bound protein 2
3569	21509	NM_030847	O, P	epithelial membrane protein 3 (Emp3), mRNA. 11/2002 Length = 737	epithelial membrane protein 3

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3570	1035	NM_030851	I, J	Bradykinin receptor B1 (Bdkrb1), mRNA. 5/2002 Length = 1312	Bradykinin receptor B1
3571	9594	NM_030855	RR	DNA ligase I (Lig1), mRNA. 11/2002 Length = 3112	DNA ligase I
3578	8815	NM_030991	W	synaptosomal-associated protein (Snap25), mRNA. 11/2002 Length = 2100	ESTs, Highly similar to LAS1_MOUSE LIM AND SH3 DOMAIN PROTEIN 1 (LASP-1) (MLN 50) [M.musculus]
3580	23109	NM_031000	G, H	aldo-keto reductase family 1, member A1 (Akr1a1), mRNA. 11/2002 Length = 1124	aldo-keto reductase family 1, member A1 (aldehyde reductase)
3584	6911	NM_031027	H, II, VV, EEE, FFF, LLL, MMM, UUU, General Alternate	dihydropyrimidine dehydrogenase (Dpyd), mRNA. 11/2002 Length = 4358	dihydropyrimidine dehydrogenase
3584	6912	NM_031027	X, Y, II, VV, XX, YY	dihydropyrimidine dehydrogenase (Dpyd), mRNA. 11/2002 Length = 4358	dihydropyrimidine dehydrogenase
3586	15886	NM_031035	ZZ, AAA	GTP-binding protein (G-alpha-i2) (Gnai2), mRNA. 4/2001 Length = 1748	GTP-binding protein (G-alpha-i2)
3587	21094	NM_031039	HH, XX, General Alternate	glutamic-pyruvate transaminase (alanine aminotransferase) (Gpt), mRNA. 11/2002 Length = 1744	glutamic-pyruvate transaminase (alanine aminotransferase)
3587	21096	NM_031039	M	glutamic-pyruvate transaminase (alanine aminotransferase) (Gpt), mRNA. 11/2002 Length = 1744	glutamic-pyruvate transaminase (alanine aminotransferase)

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3588	20899	NM_031041	TT, ZZ, AAA	general transcription factor IIB (Gtf2b), mRNA. 11/2002 Length = 1227	general transcription factor IIB
3589	17727	NM_031043	O, P, VV	glycogenin (Gyg), mRNA. 11/2002 Length = 1624	glycogenin
3595	24508	NM_031073	UU, KKK	neurotrophin-3 (HDNF/NT-3) (Ntf3), mRNA. 4/2001 Length = 1020	neurotrophin-3 (HDNF/NT-3)
3597	4683	NM_031083	N, Z, AA	phosphatidylinositol 4-kinase (Pik4cb), mRNA. 11/2002 Length = 3205	phosphatidylinositol 4-kinase
3599	15201	NM_031093	F	#NAME? (Rala), mRNA. 11/2002 Length = 952	#NAME?
3599	15202	NM_031093	V, LL, WW	#NAME? (Rala), mRNA. 11/2002 Length = 952	#NAME?
3600	12638	NM_031099	T	ribosomal protein L5 (Rpl5), mRNA. 11/2002 Length = 1069	ribosomal protein L5
3600	12639	NM_031099	H, S, II, FFF, General Alternate	ribosomal protein L5 (Rpl5), mRNA. 11/2002 Length = 1069	ribosomal protein L5
3606	16929	NM_031108	H	ribosomal protein S9 (Rps9), mRNA. 11/2002 Length = 688	mRNA for ribosomal protein S9
3607	16847	NM_031109	U, RR, FFF	ribosomal protein S10 (Rps10), mRNA. 11/2002 Length = 610	ribosomal protein S10
3613	14970	NM_031127	G, I, J, OOO, PPP, QQQ, General Core Tox Markers, General Alternate	sulfite oxidase (Suox), mRNA. 11/2002 Length = 1777	sulfite oxidase

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3614	6525	NM_031129	F	transcription elongation factor B (SIII) polypeptide 2 (18kD, elongin B) (TCEB2), mRNA. 4/2001 Length = 357	transcription elongation factor B (SIII) polypeptide 2 (18kD, elongin B)
3615	15052	NM_031136	BBB, CCC	thymosin beta-4 (Tmsb4x), mRNA. 4/2001 Length = 686	thymosin beta-4
3618	15185	NM_031140	O, P, Z, AA, NN, OO, VV, EEE, MMM	vimentin (Vim), mRNA. 11/2002 Length = 1796	vimentin
3620	20862	NM_031154	A, B, GGG, HHH, General Alternate	glutathione S-transferase, mu type 3 (Yb3) (Gstm3), mRNA. 4/2001 Length = 1208	glutathione S-transferase, mu type 3 (Yb3)
3625	18597	NM_031325	E, S, WW, DDD	UDP-glucose dehydrogenase (Ugdh), mRNA. 4/2001 Length = 2318	UDP-glucose dehydrogenase
3627	18375	NM_031331	G, H, S	proteasome (prosome, macropain) 26S subunit, non-ATPase,4 (Psm4), mRNA. 4/2001 Length = 1334	proteasome (prosome, macropain) 26S subunit, non-ATPase,4
3627	18376	NM_031331	SS	proteasome (prosome, macropain) 26S subunit, non-ATPase,4 (Psm4), mRNA. 4/2001 Length = 1334	proteasome (prosome, macropain) 26S subunit, non-ATPase,4
3628	12682	NM_031332	M	organic anion transporter (LOC83500), mRNA. 4/2001 Length = 2157	organic anion transporter
3629	6672	NM_031333	L, LLL, SSS	cadherin 2 (Cdh2), mRNA. 11/2002 Length = 4350	cadherin 2, type 1, N-cadherin (neuronal)
3629	6673	NM_031333	GGG, LLL	cadherin 2 (Cdh2), mRNA. 11/2002 Length = 4350	cadherin 2, type 1, N-cadherin (neuronal)

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935823.1	
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3632	18539	NM_031353	KK	voltage-dependent anion channel 1 (Vdac1), mRNA. 11/2002 Length = 1818	voltage-dependent anion channel 1
3640	14633	NM_031533	K	Androsterone UDP-glucuronosyltransferase (Ugt2b2), mRNA. 5/2001 Length = 1593	Androsterone UDP-glucuronosyltransferase
3641	445	NM_031535	I, J	B cell lymphoma 2 like (Bcl2l), mRNA. 5/2001 Length = 1748	B cell lymphoma 2 like, ESTs, Moderately similar to ilvB (bacterial acetolactate synthase)-like; acetolactate synthase homolog [Homo sapiens] [H.sapiens]
3650	15024	NM_031572	GG	Cytochrom P450 15-beta gene (Cyp2c12), mRNA. 11/2002 Length = 1714	Cytochrom P450 15-beta gene
3662	20765	NM_031643	LL	mitogen activated protein kinase kinase 1 (Map2k1), mRNA. 11/2002 Length = 2136	mitogen-activated protein kinase kinase 1
3662	20767	NM_031643	P	mitogen activated protein kinase kinase 1 (Map2k1), mRNA. 11/2002 Length = 2136	mitogen-activated protein kinase kinase 1
3664	20502	NM_031650	A, N	solute carrier family 21, member 10 (Slc21a10), mRNA. 11/2002 Length = 3212	solute carrier family (organic anion transporter) member 10
3674	16918	NM_031709	F	ribosomal protein S12 (Rps12), mRNA. 11/2002 Length = 499	ribosomal protein S12
3682	20724	NM_031753	XX, YY, ZZ, AAA, LLL, RRR, SSS	activated leukocyte cell adhesion molecule (Alcam), mRNA. 11/2002 Length = 2866	activated leukocyte cell adhesion molecule

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3685	4314	NM_031760	G, L, BB, II, VV, DDD	ATP-binding cassette, sub-family B (MDR/TAP), member 11 (Abcb11), mRNA. 11/2002 Length = 5036	ATP-binding cassette, sub-family B (MDR/TAP), member 11
3687	14184	NM_031776	V, UU	guanine deaminase (Gda), mRNA. 11/2002 Length = 1568	guanine deaminase
3687	14185	NM_031776	V, NN	guanine deaminase (Gda), mRNA. 11/2002 Length = 1568	guanine deaminase
3692	16039	NM_031811	J, FF	transaldolase 1 (Taldo1), mRNA. 11/2002 Length = 1057	transaldolase 1
3701	11170	NM_031833	O, P, General Alternate	nucleoside diphosphate kinase (Nme2), mRNA. 5/2001 Length = 631	ESTs, nucleoside diphosphate kinase
3704	10176	NM_031837	WW, KKK	E-septin (LOC83788), mRNA. 5/2001 Length = 3061	E-septin
3713	1475	NM_031971	A, B, Q	Heat shock protein 70-1 (Hspa1a), mRNA. 5/2001 Length = 2455	ESTs, Highly similar to S10A_RAT S-100 protein, alpha chain [R.norvegicus], Heat shock protein 70-1
3714	24644	NM_031972	GG	Aldehyde dehydrogenase family 3, subfamily A1 (Aldh3a1), mRNA. 11/2002 Length = 1725	Aldehyde dehydrogenase class 3
3715	16257	NM_031975	N, General Alternate	parathymosin (Ptms), mRNA. 11/2002 Length = 936	parathymosin
3715	17556	NM_031975	N, S, V	parathymosin (Ptms), mRNA. 11/2002 Length = 936	parathymosin
3718	17805	NM_031980	PP, QQ, TT	UDP-glucuronosyltransferase (Ugt2b12), mRNA. 5/2001 Length = 1846	UDP-glucuronosyltransferase

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3718	17806	NM_031980	RRR	UDP-glucuronosyltransferase (Ugt2b12), mRNA. 5/2001 Length = 1846	UDP-glucuronosyltransferase
3719	15265	NM_031981	Q, R	p47 protein (p47), mRNA. 11/2002 Length = 1451	p47 protein
3719	15266	NM_031981	Q, R	p47 protein (p47), mRNA. 11/2002 Length = 1451	p47 protein
3719	15267	NM_031981	WW	p47 protein (p47), mRNA. 11/2002 Length = 1451	p47 protein
3720	18899	NM_031985	LL, TT	S6 kinase (Rps6kb1), mRNA. 5/2001 Length = 2287	S6 kinase
3724	20793	NM_032058	UU	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (Eif2b2), mRNA. 5/2001 Length = 1474	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)
3725	9106	NM_032066	BBB, CCC	smooth muscle-specific 17 beta-hydroxysteroid dehydrogenase type 3 (LOC84013), mRNA. 5/2001 Length = 1830	smooth muscle-specific 17 beta-hydroxysteroid dehydrogenase type 3
3729	8817	NM_032613	L, W, AA, CC	LIM and SH3 protein 1 (Lasp1), mRNA. 11/2002 Length = 792	ESTs, ESTs, Highly similar to LAS1_MOUSE LIM AND SH3 DOMAIN PROTEIN 1 (LASP-1) (MLN 50) [M.musculus]
3733	25529	NM_033096	WW	Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform (Ppm1b), mRNA. 7/2001 Length = 3257	Protein phosphatase type 1B (formely 2C), Mg-dependent, beta isoform
3735	2577	NM_033236	R, VV	Proteasome (prosome, macropain) 26S subunit, ATPase (Psmc2), mRNA. 8/2001 Length = 1403	Proteasome (prosome, macropain) 26S subunit, ATPase

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3742	16364	NM_053019	A, B, H, I, GG, OOO, General Core Tox Markers	arginine vasopressin receptor 1A (Avpr1a), mRNA. 10/2002 Length = 1606	Vasopressin receptor V1a
3752	15791	NM_053341	D	regulator of G-protein signaling 19 interacting protein 1 (Rgs19ip1), mRNA. 11/2002 Length = 1607	regulator of G-protein signaling 19
3755	11319	NM_053357	HH	beta-catenin (Catnb), mRNA. 11/2002 Length = 2650	beta-catenin
3759	16018	NM_053401	GG, ZZ, AAA	nerve growth factor receptor (TNFRSF16) associated protein 1 (Ngfrap1), mRNA. 11/2002 Length = 519	brain expressed X-linked 3
3761	6962	NM_053404	LL	dynactin 4 (Dctn4), mRNA. 11/2002 Length = 2573	ESTs, Moderately similar to C54354 calnexin precursor - rat [R.norvegicus]
3763	6774	NM_053410	CC	acyl-CoA: dihydroxyacetonephosphate acyltransferase (Gnpat), mRNA. 11/2001 Length = 2065	acyl-CoA: dihydroxyacetonephosphate acyltransferase
3765	5561	NM_053438	AA	zinc finger protein 103 (Zfp103), mRNA. 11/2002 Length = 3258	zinc finger protein 103
3767	4621	NM_053463	JJ, KK	nucleobindin (Nucb), mRNA. 11/2002 Length = 2303	nucleobindin
3767	4622	NM_053463	JJ, KK	nucleobindin (Nucb), mRNA. 11/2002 Length = 2303	nucleobindin
3768	11403	NM_053464	H, FFF, General Core Tox Markers	spermidine synthase (Srm), mRNA. 11/2002 Length = 1268	spermidine synthase

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3769	23274	NM_053467	O, P, FF	integral membrane protein Tmp21-l (p23) (Tmp21), mRNA. 11/2001 Length = 1314	integral membrane protein Tmp21-l (p23)
3769	23276	NM_053467	V	integral membrane protein Tmp21-l (p23) (Tmp21), mRNA. 11/2001 Length = 1314	integral membrane protein Tmp21-l (p23)
3772	9573	NM_053475	ZZ, AAA	protein tyrosine phosphatase type IVA, member 2 (Ptp4a2), mRNA. 11/2002 Length = 1095	protein tyrosine phosphatase type IVA, member 2
3774	4290	NM_053487	BBB	peroxisomal membrane protein Pmp26p (Peroxin-11) (Pex11a), mRNA. 11/2001 Length = 1194	peroxisomal membrane protein Pmp26p (Peroxin-11)
3775	9307	NM_053491	N, XX, YY	plasminogen (Plg), mRNA. 11/2002 Length = 2737	plasminogen
3775	25443	NM_053491	GGG, HHH, PPP, QQQ, UUU, General Alternate	plasminogen (Plg), mRNA. 11/2002 Length = 2737	plasminogen
3776	23558	NM_053507	OO, III, JJJ, KKK, General Core Tox Markers	expressed in non-metastatic cells 3, protein (nucleoside diphosphate kinase) (Nme3), mRNA. 11/2001 Length = 645	expressed in non-metastatic cells 3, protein (nucleoside diphosphate kinase)
3777	7219	NM_053512	F	peroxiredoxin 4 (Prdx4), mRNA. 11/2002 Length = 965	peroxiredoxin 4
3778	16125	NM_053514	PP, WW, DDD, General Alternate	lin-7-Ba (Veli1), mRNA. 11/2001 Length = 660	lin-7-Ba

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3779	16134	NM_053516	III, JJJ	unknown Glu-Pro dipeptide repeat protein (LOC85383), mRNA. 11/2001 Length = 1876	unknown Glu-Pro dipeptide repeat protein
3779	16135	NM_053516	L, S, DD, EE, HH	unknown Glu-Pro dipeptide repeat protein (LOC85383), mRNA. 11/2001 Length = 1876	unknown Glu-Pro dipeptide repeat protein
3780	19205	NM_053522	Q, R	ras-like protein (Tc10), mRNA. 11/2002 Length = 3873	ras-like protein
3783	14199	NM_053538	O, P	lysosomal-associated protein transmembrane 5 (Laptm5), mRNA. 11/2001 Length = 1309	lysosomal-associated protein transmembrane 5
3784	8358	NM_053540	X, Y	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast) (Cox17), mRNA. 11/2001 Length = 229	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)
3785	12496	NM_053541	XX, YY, RRR	low density lipoprotein receptor-related protein 3 (Lrp3), mRNA. 11/2001 Length = 3891	low density lipoprotein receptor-related protein 3
3787	15829	NM_053551	ZZ, AAA	pyruvate dehydrogenate kinase 4 (Pdk4), mRNA. 11/2002 Length = 1435	pyruvate dehydrogenase kinase, isoenzyme 4
3788	11843	NM_053555	ZZ, AAA	vesicle-associated membrane protein 5 (Vamp5), mRNA. 11/2001 Length = 309	vesicle-associated membrane protein 5
3790	4327	NM_053563	R	nuclear RNA helicase, DECD variant of DEAD box family (Ddx1), mRNA. 11/2001 Length = 1511	nuclear RNA helicase, DECD variant of DEAD box family

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3792	21940	NM_053568	KKK, NNN	phosphate cytidyltransferase 2, ethanolamine (Pcyt2), mRNA. 11/2001 Length = 1846	phosphate cytidyltransferase 2, ethanolamine
3792	21941	NM_053568	T, XX, KKK	phosphate cytidyltransferase 2, ethanolamine (Pcyt2), mRNA. 11/2001 Length = 1846	phosphate cytidyltransferase 2, ethanolamine
3795	21424	NM_053586	XX, YY	cytochrome c oxidase subunit Vb (Cox5b), mRNA. 11/2001 Length = 485	cytochrome c oxidase subunit Vb
3797	20842	NM_053590	X, Y, RR, UUU	proteasome (prosome, macropain) subunit, beta type 1 (Psm1), mRNA. 11/2001 Length = 799	proteasome (prosome, macropain) subunit, beta type 1
3798	20896	NM_053592	U, NNN	Deoxyuridinetriphosphatase (dUTPase) (Dut), mRNA. 5/2002 Length = 952	Deoxyuridinetriphosphatase (dUTPase)
3800	21708	NM_053596	PP, QQ, UU, WW	Endothelin-converting enzyme 1 (Ece1), mRNA. 5/2002 Length = 4469	Endothelin-converting enzyme 1
3800	21709	NM_053596	MM, PP, UU, III, JJ, TTT, UUU	Endothelin-converting enzyme 1 (Ece1), mRNA. 5/2002 Length = 4469	Endothelin-converting enzyme 1
3801	11830	NM_053598	M, DD, SS, TT, FFF, General Core Tox Markers, General Alternate	diphosphoinositol polyphosphate phosphohydrolase type II (Nudt4), mRNA. 11/2001 Length = 2954	diphosphoinositol polyphosphate phosphohydrolase type II

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3801	18795	NM_053598	E, DD, JJ, KK, MM, UU, FFF, KKK, NNN, TTT, General Alternate	diphosphoinositol polyphosphate phosphohydrolase type II (Nudt4), mRNA. 11/2001 Length = 2954	diphosphoinositol polyphosphate phosphohydrolase type II
3801	23192	NM_053598	N, GG, JJ, KK, General Alternate	diphosphoinositol polyphosphate phosphohydrolase type II (Nudt4), mRNA. 11/2001 Length = 2954	diphosphoinositol polyphosphate phosphohydrolase type II
3807	1127	NM_053626	III, JJJ	D-amino acid oxidase (Dao1), mRNA. 11/2001 Length = 1646	D-amino acid oxidase
3808	9055	NM_053631	X, Y, UUU	Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor (Bcrp1), mRNA. 11/2001 Length = 733	Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor
3811	3454	NM_053662	Q, R, W	cyclin L (Ccnl), mRNA. 11/2001 Length = 2092	cyclin L
3811	3455	NM_053662	Q, R	cyclin L (Ccnl), mRNA. 11/2001 Length = 2092	cyclin L
3812	24204	NM_053670	C, UU	calcitonin gene-related peptide-receptor component protein (Crcp), mRNA. 11/2002 Length = 1408	calcitonin gene-related peptide-receptor component protein
3813	16123	NM_053698	F, DD, EE	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2), mRNA. 11/2001 Length = 1155	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3814	14795	NM_053699	JJ, KK	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4 (Cited4), mRNA. 11/2001 Length = 897	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
3815	5798	NM_053719	T	embigin (Emb), mRNA. 11/2001 Length = 1458	embigin
3816	15269	NM_053739	PP, QQ, DDD, HHH	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein) (Becn1), mRNA. 11/2001 Length = 1908	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
3827	25625	NM_053783	PP, QQ	interferon gamma receptor (Ifngr), mRNA. 11/2001 Length = 1860	interferon gamma receptor
3828	25594	NM_053799	M	aspartyl-tRNA synthetase (Dars), mRNA. 11/2001 Length = 2143	aspartyl-tRNA synthetase
3829	15615	NM_053800	DDD	thioredoxin (Txn), mRNA. 11/2002 Length = 330	thioredoxin
3831	4361	NM_053812	O, P	BCL2-antagonist/killer 1 (Bak1), mRNA. 11/2001 Length = 1923	BCL2-antagonist/killer 1
3834	15002	NM_053819	UU, EEE, III, JJJ, MMM	tissue inhibitor of metalloproteinase 1 (Timp1), mRNA. 11/2001 Length = 740	tissue inhibitor of metalloproteinase 1
3836	17154	NM_053835	K, Q, R, BBB, CCC, LLL, RRR, SSS	clathrin, light polypeptide (Lcb) (Cltb), mRNA. 11/2002 Length = 982	clathrin, light polypeptide (Lcb)
3836	17155	NM_053835	H, LLL, UUU, General Alternate	clathrin, light polypeptide (Lcb) (Cltb), mRNA. 11/2002 Length = 982	clathrin, light polypeptide (Lcb)

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3837	17299	NM_053842	PPP, QQQ	mitogen activated protein kinase 1 (Mapk1), mRNA. 11/2002 Length = 1467	mitogen activated protein kinase 1
3839	19018	NM_053849	C, FF	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) (Erp70), mRNA. 11/2001 Length = 2398	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)
3840	16362	NM_053853	C, W	N-acetyltransferase 1 (arylamine N-acetyltransferase) (Nat1), mRNA. 11/2002 Length = 2533	N-acetyltransferase 1 (arylamine N-acetyltransferase)
3848	15934	NM_053904	W	5-oxoprolinase (ATP-hydrolysing) (Oplah), mRNA. 11/2001 Length = 4003	5-oxoprolinase (ATP-hydrolysing)
3850	15718	NM_053907	HH, General Alternate	deoxyribonuclease I-like 3 (Dnase1l3), mRNA. 11/2001 Length = 1417	deoxyribonuclease I-like 3
3851	8152	NM_053908	O	protein tyrosine phosphatase, non-receptor type 6 (Ptph6), mRNA. 11/2001 Length = 2176	protein tyrosine phosphatase, non-receptor type 6
3855	14591	NM_053961	DD, EE, NNN	endoplasmic reticulum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	ESTs, Moderately similar to N-acetyl galactosaminidase, alpha [Mus musculus] [M.musculus]
3855	16553	NM_053961	I, J	endoplasmic reticulum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	endoplasmic reticulum protein 29
3856	24778	NM_053962	C, MM, FFF, TTT	Serine dehydratase (Sdh), mRNA. 11/2002 Length = 1444	serine dehydratase

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3856	24779	NM_053962	C, MM, TTT	Serine dehydratase (Sdh), mRNA. 11/2002 Length = 1444	serine dehydratase
3856	25321	NM_053962	MM, FFF, TTT	Serine dehydratase (Sdh), mRNA. 11/2002 Length = 1444	serine dehydratase
3859	15135	NM_053971	G, H, FFF	ribosomal protein L6 (Rpl6), mRNA. 11/2001 Length = 963	ribosomal protein L6
3859	15136	NM_053971	M, X, Y, KK, HHH, General Core Tox Markers	ribosomal protein L6 (Rpl6), mRNA. 11/2001 Length = 963	ribosomal protein L6
3860	18798	NM_053978	HHH	RAB28, member RAS oncogene family (Rab28), mRNA. 11/2001 Length = 1483	RAB28, member RAS oncogene family
3863	15642	NM_053985	C, I, J, N, W, II, MM, WW, OOO, TTT	H3 histone, family 3B (H3f3b), mRNA. 11/2001 Length = 1107	H3 histone, family 3B
3863	15643	NM_053985	W	H3 histone, family 3B (H3f3b), mRNA. 11/2001 Length = 1107	H3 histone, family 3B
3863	15645	NM_053985	W	H3 histone, family 3B (H3f3b), mRNA. 11/2001 Length = 1107	H3 histone, family 3B
3865	18025	NM_053989	ZZ, AAA	progesterin induced protein (dd5), mRNA. 11/2001 Length = 3180	progesterin induced protein

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3866	16809	NM_053990	B, W, BB, CC, DD, EE, JJ, NN, OO, PP, HHH, III, KKK, NNN, General Core Tox Markers, General Alternate	protein tyrosine phosphatase, non-receptor type 2 (Ptpn2), mRNA. 11/2002 Length = 1494	protein tyrosine phosphatase, non-receptor type 2
3868	24430	NM_053996	Z, AA	proline transporter (Prot), mRNA. 11/2001 Length = 2722	proline transporter
3870	16964	NM_053999	Q, R	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (Ppp2r2a), mRNA. 11/2001 Length = 2142	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
3870	16965	NM_053999	Q, R	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform (Ppp2r2a), mRNA. 11/2001 Length = 2142	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
3871	21066	NM_054001	B, OO, General Alternate	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (Cd36l2), mRNA. 11/2001 Length = 1938	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2
3872	17431	NM_054006	LL	unr protein (unr), mRNA. 11/2001 Length = 3755	unr protein
3872	17433	NM_054006	N, UU	unr protein (unr), mRNA. 11/2001 Length = 3755	unr protein
3880	15391	NM_057114	U, LLL	peroxiredoxin 1 (Prdx1), mRNA. 11/2001 Length = 882	peroxiredoxin 1

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3883	15151	NM_057131	E	phosphoribosyl pyrophosphate synthetase-associated protein 2 (Prpsap2), mRNA. 11/2001 Length = 1612	phosphoribosyl pyrophosphate synthetase-associated protein 2
3885	8592	NM_057137	G, WW, General Alternate	phenylalkylamine Ca ²⁺ antagonist (emopamil) binding protein (Ebp), mRNA. 11/2001 Length = 1071	phenylalkylamine Ca ²⁺ antagonist (emopamil) binding protein
3888	12331	NM_057155	A, B, General Core Tox Markers	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound (Xpnpep2), mRNA. 11/2001 Length = 2828	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound
3888	12332	NM_057155	General Core Tox Markers	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound (Xpnpep2), mRNA. 11/2001 Length = 2828	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound
3893	14125	NM_057208	VV	tropomyosin 3, gamma (Tpm3), mRNA. 11/2001 Length = 1101	R.norvegicus mRNA for tropomyosin isoform 6, Rattus norvegicus nonmuscle tropomyosin 5 (Tpm5) isoforms NM 5 and NM 6 mRNA, partial cds
3894	24459	NM_057209	UU	myosin light chain kinase 2, skeletal muscle (Mylk2), mRNA. 11/2001 Length = 2799	myosin light chain kinase 2, skeletal muscle
3899	15764	NM_080480	K	phosphatidylinositol-4 phosphate 5-kinase, type II, gamma (Pip5k2c), mRNA. 12/2001 Length = 2669	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma
3903	18004	NM_080688	EE, NNN	phospholipase C, delta 4 (Plcd4), mRNA. 11/2002 Length = 2696	phospholipase C, delta 4

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Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3904	17662	NM_080697	GG	dynein light chain-2 (Dlc2), mRNA. 1/2002 Length = 510	dynein light chain-2
3905	23550	NM_080698	D	fibromodulin (Fmod), mRNA. 11/2002 Length = 2960	fibromodulin
3910	18902	NM_080887	A, B	thioredoxin-like (32kD) (Txnl), mRNA. 1/2002 Length = 1061	ESTs, thioredoxin-like (32kD)
3911	13799	NM_080888	L, Z	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like (Bnip3l), mRNA. 1/2002 Length = 3219	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like
3911	19605	NM_080888	I, J, L, Z	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like (Bnip3l), mRNA. 1/2002 Length = 3219	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like
3911	23033	NM_080888	L	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like (Bnip3l), mRNA. 1/2002 Length = 3219	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like
3912	6143	NM_080892	K, GG, HH, NN, OO	selenium binding protein 2 (Selenbp2), mRNA. 1/2002 Length = 1685	selenium binding protein 2
3913	16267	NM_080896	P, Q, R	heterogeneous nuclear ribonucleoprotein H1 (Hnrnp1), mRNA. 11/2002 Length = 1967	heterogeneous nuclear ribonucleoprotein H1
3915	17413	NM_080909	T	reticulon 3 (Rtn3), mRNA. 11/2002 Length = 2773	Rattus norvegicus CaM-kinase II inhibitor alpha mRNA, complete cds, reticulon 3
3916	11421	NM_130405	K	src associated in mitosis, 68 kDa (Sam68), mRNA. 1/2002 Length = 2655	src associated in mitosis, 68 kDa

TABLE 1					
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Seq. ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3916	12035	NM_130405	O, P	src associated in mitosis, 68 kDa (Sam68), mRNA. 1/2002 Length = 2655	src associated in mitosis, 68 kDa
3919	19316	NM_130411	VV	coronin, actin binding protein 1A (Coro1a), mRNA. 1/2002 Length = 1386	coronin, actin binding protein 1A
3923	18293	NM_130433	K, U, FF, LL	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (Acaa2), mRNA. 1/2002 Length = 1619	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)
3925	15961	NM_130744	E, III, JJJ	stellate cell activation associated protein (Staap), mRNA. 11/2002 Length = 2028	stellate cell activation associated protein
3926	18846	NM_130755	F	citrate synthase (Cs), mRNA. 2/2002 Length = 1498	citrate synthase
3929	16767	NM_130826	I, J, U, FF, XX, YY, RRR	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hioase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (Hadha), mRNA. 2/2002 Length = 2775	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hioase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
3929	16768	NM_130826	U, Z, AA, XX, BBB, CCC, RRR, SSS	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hioase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (Hadha), mRNA. 2/2002 Length = 2775	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hioase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3929	16769	NM_130826	WW, BBB, CCC	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hioase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (Hadha), mRNA. 2/2002 Length = 2775	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A hioase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
3931	20707	NM_131906	K, M, N, X, BB, CC, GG, TT, FFF, GGG, UUU, General Core Tox Markers	solute carrier family 21 (organic anion transporter), member 5 (Slc21a5), mRNA. 2/2002 Length = 3622	solute carrier family 21 (organic anion transporter), member 5
3941	17634	NM_133418	PP, QQ	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (Slc25a10), mRNA. 3/2002 Length = 1946	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10
3941	17635	NM_133418	GG	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (Slc25a10), mRNA. 3/2002 Length = 1946	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10
3946	19613	NM_133544	Q, R, XX	dapit (LOC171069), mRNA. 3/2002 Length = 322	dapit
3951	1827	NM_133572	NN, OO	cell division cycle 25B (Cdc25b), mRNA. 3/2002 Length = 2804	cell division cycle 25B
3955	24352	NM_133589	L	protein phosphatase V (LOC171121), mRNA. 3/2002 Length = 1270	protein phosphatase V

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3956	1546	NM_133595	KKK, PPP, QQQ, General Alternate	GTP cyclohydrolase I feedback regulatory protein (Gchfr), mRNA. 3/2002 Length = 676	GTP cyclohydrolase I feedback regulatory protein
3957	15637	NM_133599	XX	lectin, galactoside-binding, soluble, 2 (galectin 2) (Lgals2), mRNA. 3/2002 Length = 624	lectin, galactoside-binding, soluble, 2 (galectin 2)
3958	17758	NM_133606	G, U, FF, LL, XX, YY, BBB, CCC, FFF, RRR, SSS, UUU, General Alternate	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (Ehhadh), mRNA. 11/2002 Length = 3097	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
3960	19706	NM_134329	M, U	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (Adh7), mRNA. 3/2002 Length = 2048	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
3961	16456	NM_134346	P	RAP1B, member of RAS oncogene family (Rap1b), mRNA. 3/2002 Length = 1874	RAP1B, member of RAS oncogene family
3961	16457	NM_134346	A, B, O, P, VV	RAP1B, member of RAS oncogene family (Rap1b), mRNA. 3/2002 Length = 1874	RAP1B, member of RAS oncogene family
3966	2643	NM_134408	Z, AA, RR	calcium-independent alpha-latrotoxin receptor homolog 2 (Cirl2), mRNA. 3/2002 Length = 5602	calcium-independent alpha-latrotoxin receptor homolog 2
3969	2802	NM_134449	A	PKC-delta binding protein (SRBC), mRNA. 3/2002 Length = 1049	PKC-delta binding protein

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3975	24672	NM_138517	SS	granzyme B (Gzmb), mRNA. 4/2002 Length = 925	Rat natural killer (NK) cell protease 1 (RNKP-1) mRNA, complete cds
3979	20999	NM_138548	I, J	expressed in non-metastatic cells 1 (Nme1), mRNA. 11/2002 Length = 737	expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase)
3984	23166	NM_138839	B, WW, General Alternate	vacuole Membrane Protein 1 (Vmp1), mRNA. 11/2002 Length = 1830	Vacuole Membrane Protein 1
3986	17530	NM_138877	R, BB, CC, JJ, KK, General Alternate	Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002 Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
3986	17531	NM_138877	General Alternate	Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002 Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
3986	17532	NM_138877	FFF, General Alternate	Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002 Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
3986	17533	NM_138877	I, J, FFF, General Alternate	Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002 Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
3986	25039	NM_138877	KK, General Alternate	Diaphorase (NADH) (cytochrome b-5 reductase) (Dia1), mRNA. 4/2002 Length = 1893	Diaphorase (NADH) (cytochrome b-5 reductase)
3987	4593	NM_138881	W	Best5 protein (Best5), mRNA. 4/2002 Length = 3628	Best5 protein
3987	4594	NM_138881	W	Best5 protein (Best5), mRNA. 4/2002 Length = 3628	Best5 protein

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3988	7394	NM_138883	DDD	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (Atp5o), mRNA. 4/2002 Length = 707	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
3989	14964	NM_138884	EEE, MMM	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (Akr1d1), mRNA. 4/2002 Length = 3189	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)
3989	14965	NM_138884	RR	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) (Akr1d1), mRNA. 4/2002 Length = 3189	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)
3993	18867	NM_138900	I, J, U, X, Y, Z, AA, GG, HH, LL, FFF, GGG, LLL, RRR, SSS, UUU	complement component 1, s subcomponent (C1s), mRNA. 11/2002 Length = 2908	complement component 1, s subcomponent
4000	809	NM_139089	W	small inducible cytokine B subfamily (Cys-X-Cys), member 10 (Cxcl10), mRNA. 11/2002 Length = 1133	small inducible cytokine B subfamily (Cys-X-Cys), member 10
4004	17684	NM_139102	F, G, NN, OO, General Alternate	dimethylglycine dehydrogenase precursor (Dmgdh), mRNA. 5/2002 Length = 2574	dimethylglycine dehydrogenase precursor

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4006	18450	NM_139106	LL, CCC, RRR	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (Atp5d), mRNA. 5/2002 Length = 811	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit
4010	1301	NM_139192	S, XX	stearoyl-Coenzyme A desaturase 1 (Scd1), mRNA. 5/2002 Length = 4689	stearoyl-Coenzyme A desaturase 1
4014	8719	NM_139333	GG	neuronal differentiation-related gene (LOC246216), mRNA. 11/2002 Length = 1853	neuronal differentiation-related gene
4019	23682	NM_144746	HH, SS	protein phosphatase 2A B regulatory subunit delta isoform (LOC246255), mRNA. 11/2002 Length = 2034	Rattus norvegicus protein phosphatase 2A B regulatory subunit delta isoform mRNA, complete cds
4027	24657	NM_145774	L, OOO, General Alternate	Rab38, member of RAS oncogene family (Rab38), mRNA. 11/2002 Length = 1405	Rattus norvegicus rab-related GTP-binding protein mRNA, complete cds
4028	16278	NM_145782	X	cytochrome P450, 3a18 (Cyp3a18), mRNA. 11/2002 Length = 2005	R.norvegicus CYP3 mRNA
4029	1448	NM_145783	U	cytochrome c oxidase, subunit Va (Cox5a), mRNA. 10/2002 Length = 600	Rat CoxVa mRNA for mitochondrial cytochrome c oxidase subunit Va
4035	6439	NM_147209	U	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (Ppm1g), mRNA. 11/2002 Length = 1629	ESTs, Weakly similar to JC2524 phosphoprotein phosphatase (EC 3.1.3.16) 1A-beta - rat [R.norvegicus]
4036	16963	NM_147214	F, SS, NNN	alpha-2u globulin PGCL1 (LOC259246), mRNA. 11/2002 Length = 878	Caldesmon 1, protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform

TABLE 1					
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Seq. ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4037	16969	NM_147215	O, P	alpha-2u globulin PGCL4 (LOC259247), mRNA. 11/2002 Length = 1003	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform
4041	10544	NM_152935	C, H, JJ, KK, PP, QQ, ZZ, AAA, HHH, PPP, QQQ, General Core Tox Markers	outer mitochondrial membrane receptor rTOM20 (LOC266601), mRNA. 11/2002 Length = 976	Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
4041	10545	NM_152935	C, FFF, GGG, HHH, PPP, QQQ, General Core Tox Markers	outer mitochondrial membrane receptor rTOM20 (LOC266601), mRNA. 11/2002 Length = 976	Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
4042	12700	NM_152936	F	pancreatic secretory trypsin inhibitor type II (PSTI-II) (LOC266602), mRNA. 11/2002 Length = 379	Rat pancreatic secretory trypsin inhibitor type II (PSTI-II) mRNA, complete cds
4043	9176	NM_153303	HH	dystonia 1, torsion (autosomal dominant; torsin A) (Dyt1), mRNA. 10/2002 Length = 1254	ESTs, Highly similar to TO1A_MOUSE Torsin A precursor [M.musculus]
4046	1130	NM_153313	T	cytochrome P450 2D1 (CYP2D1), mRNA. 10/2002 Length = 1630	Rat cytochrome P450CMF1b mRNA, complete cds
4047	14346	NM_153314	N	UDP- glucuronosyltransfera se 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length = 1716	Rat UDP-glucuronosyltransferase mRNA, complete cds

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Seq. ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4047	14347	NM_153314	K, QQ, UU	UDP-glucuronosyltransferase 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length = 1716	Rat UDP-glucuronosyltransferase mRNA, complete cds
4047	14632	NM_153314	MM, TTT	UDP-glucuronosyltransferase 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length = 1716	Androsterone UDP-glucuronosyltransferase
4048	1753	NM_153318	II, III, JJJ, KKK, General Core Tox Markers	cytochrome P450 4F6 (CYP4F6), mRNA. 10/2002 Length = 1782	Rattus norvegicus cytochrome P450 4F6 (CYP4F6) mRNA, complete cds
4074	21981	S75019	VV		ESTs, Highly similar to B54676 antiqutin - rat (fragment) [R.norvegicus]
4077	24469	S77858	J, Q, R, GG, II, EEE, FFF, HHH, MMM		ESTs, Highly similar to MLES_RAT Myosin light chain alkali, smooth-muscle isoform (MLC3SM) [R.norvegicus]
4080	16131	S79304	LL, YY	unknown Glu-Pro dipeptide repeat protein	unknown Glu-Pro dipeptide repeat protein
4082	14121	S82383	O, P, VV		R.norvegicus mRNA for tropomyosin isoform 6
4084	13520	S87522	KK, PP, QQ	HMM:leukotriene A4 hydrolase	ESTs, Highly similar to S20444 leukotriene-A4 hydrolase (EC 3.3.2.6) - rat [R.norvegicus]
4102	53	U16253	K	corticotropin-releasing factor receptor subtype 2	corticotropin-releasing factor receptor subtype 2
4104	17999	U19485	BBB, CCC	spp-24 precursor	spp-24 precursor
4104	18000	U19485	CCC	spp-24 precursor	spp-24 precursor
4105	1948	U19614	L		Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4107	228	U20194	H, K, DD, EE, UUU, General Alternate		Rattus norvegicus complement C8 beta (C8b) mRNA, partial cds
4107	229	U20194	S, Z, AA, BBB, CCC, PPP, QQQ, RRR		Rattus norvegicus complement C8 beta (C8b) mRNA, partial cds
4119	21488	U32575	GG, PP, QQ		ESTs, Weakly similar to I49523 tumor necrosis factor alpha-induced protein 2 - mouse [M.musculus]
4126	255	U39206	F, FFF, General Alternate		Rattus norvegicus cytochrome P450 4F4 (CYP4F4) mRNA, complete cds
4139	358	U52948	BB, CC	complement component 9	complement component 9
4144	699	U55765	D, E, BB, GG, NN, III, JJJ, RRR	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10
4147	1337	U57715	C	FGF receptor activating protein 1	FGF receptor activating protein 1
4148	1731	U58858	D, KKK	unction plakoglobin	unction plakoglobin
4150	990	U60096	RR	Integrin, beta 4	Integrin, beta 4
4151	1283	U61729	Z, AA, LL		Rattus norvegicus proline rich protein mRNA, complete cds
4153	1547	U66471	MM, TTT	cell growth regulatory with ring finger domain	cell growth regulatory with ring finger domain
4154	870	U66478	PP, QQ	MAD (mothers against decapentaplegic, Drosophila) homolog 1	MAD (mothers against decapentaplegic, Drosophila) homolog 1
4157	953	U67915	D	mast cell protease 1	mast cell protease 1
4160	20386	U68562	Q, R, S, T, BBB, CCC	heat shock protein 60 (liver)	heat shock protein 60 (liver)
4165	16398	U75392	UU, BBB, CCC	B-cell receptor-associated protein 37	B-cell receptor-associated protein 37
4170	1602	U76379	C, T, TT, EEE, MMM	Organic cation transporter	Organic cation transporter

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4187	428	X03468	T	Apolipoprotein A-II	Apolipoprotein A-II
4195	672	X13722	JJ		Rat mRNA for LDL-receptor
4198	15653	X14210	CC, II	NADH ubiquinone oxidoreductase subunit B13	NADH ubiquinone oxidoreductase subunit B13
4200	18541	X14671	BB, CC, RR		ESTs, Highly similar to RL26_RAT 60S RIBOSOMAL PROTEIN L26 [R.norvegicus]
4202	19244	X15013	G, H, JJJ		ESTs, Highly similar to RL7A_HUMAN 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide) [R.norvegicus]
4213	517	X52713	RR	Myxovirus (influenza) resistance, homolog of murine Mx (also interferon-inducible protein IFI78), myxovirus (influenza virus) resistance 3	myxovirus (influenza virus) resistance 3
4216	18606	X53504	G, H, CC, DDD, GGG, HHH, General Core Tox Markers		ESTs, Highly similar to RL12_RAT 60S RIBOSOMAL PROTEIN L12 [R.norvegicus]
4217	1899	X53565	WW	trans-golgi network protein 1	trans-golgi network protein 1
4220	24577	X55153	C, F, K, DDD		ESTs, Highly similar to R6RTP2 acidic ribosomal protein P2, cytosolic [validated] - rat [R.norvegicus]
4227	17175	X58389	II, JJ, KK, FFF, GGG, HHH		R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22
4233	17176	X60212	LL, SS		R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22
4235	21657	X61381	BB, CC, GG, HH, NN, OO, PP, QQ, LLL		Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
4242	16780	X62660	X, GG, II, XX, YY	HMm:glutathione S-transferase, alpha 4	ESTs, Highly similar to S23433 glutathione transferase (EC 2.5.1.18) 8 - rat [R.norvegicus]
4249	1391	X66366	C, XX, YY	Gephyrin	Gephyrin
4250	602	X68101	ZZ, AAA		R.norvegicus trg mRNA
4252	588	X69834	H, O, P, GG, PPP, QQQ		R.norvegicus mRNA for serine protease inhibitor 2.4
4255	16300	X70706	DDD	plastin 3 (T-isoform)	plastin 3 (T-isoform)
4258	16725	X73371	V, X, Y, LL, ZZ, AAA, LLL		R.norvegicus mRNA for Fc gamma receptor
4259	768	X74549	General Alternate	leuserpin-2	leuserpin-2
4264	1603	X78855	TT	Organic cation transporter	Organic cation transporter
4271	1764	X83399	R	eukaryotic translation initiation factor 4E	eukaryotic translation initiation factor 4E
4272	463	X83579	S, PPP, QQQ	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)
4280	853	X95189	M, XX, YY		R.norvegicus mRNA for Trihydroxycoprostanoyl-CoA Oxidase
4282	17146	Y07534	J	Serine protease inhibitor	Serine protease inhibitor
1846	2069	AI103616	VV	HHs:ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	ESTs, Weakly similar to ras-like protein [Rattus norvegicus] [R.norvegicus]
2362	23120	AI179857	S	HHs:huntingtin interacting protein 2	ESTs, Weakly similar to ubiquitin-conjugating enzyme E2D 2 [Rattus norvegicus] [R.norvegicus]
2616	5778	AI233246	G, H	HHs:polymerase (RNA) II (DNA directed) polypeptide B (140kD)	ESTs, Weakly similar to RNA polymerase I (127 kDa subunit) [Rattus norvegicus] [R.norvegicus]
3	2417	AA684857	VV	heterogeneous nuclear ribonucleoprotein K	heterogeneous nuclear ribonucleoprotein K
408	18578	AA859980	L, FF	T-complex 1	T-complex 1
412	17110	AA860062	Z, AA	Albumin	Albumin

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
412	17111	AA860062	S, SS	Albumin	Albumin
445	18897	AA875207	C, T, Z, AA	Hemoglobin, beta	Hemoglobin, beta
535	4259	AA892123	JJ, KK, FFF, GGG	ribosomal protein L36	ribosomal protein L36
588	12118	AA892775	OO, VV, XX, YY	Lysozyme	Lysozyme
593	17080	AA892814	M	calpain, small subunit 1	calpain, small subunit 1
628	20985	AA893242	H, BBB, CCC, RRR, General Alternate	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
628	20986	AA893242	A, B, BBB, CCC, FFF, General Alternate	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
673	6377	AA894273	UU	dimethylarginine dimethylaminohydrolase 1	dimethylarginine dimethylaminohydrolase 1
699	23778	AA899854	U	topoisomerase (DNA) II alpha	topoisomerase (DNA) II alpha
785	22843	AA925473	VV	cell division cycle 42	cell division cycle 42
845	1682	AA943555	SS	linker of T-cell receptor pathways	linker of T-cell receptor pathways
854	19425	AA943842	N	dimethylarginine dimethylaminohydrolase 1	ESTs, dimethylarginine dimethylaminohydrolase 1
855	2655	AA943886	F, DD, PP	serum-inducible kinase	serum-inducible kinase
889	22504	AA944827	Q, R	bone morphogenetic protein 2	bone morphogenetic protein 2
902	19421	AA945152	S, NNN	dimethylarginine dimethylaminohydrolase 1	dimethylarginine dimethylaminohydrolase 1
1008	16722	AA956311	CCC	Acyl-CoA dehydrogenase, Very long chain	Acyl-CoA dehydrogenase, Very long chain
1023	23919	AA956992	D	secretory carrier membrane protein 3	secretory carrier membrane protein 3
1064	2329	AA964157	SS	SMC (segregation of mitotic chromosomes 1)-like 1 (yeast)	SMC (segregation of mitotic chromosomes 1)-like 1 (yeast)
1083	1322	AA964628	W	Glucose-6-phosphatase	Glucose-6-phosphatase

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1153	1437	AA997844	V	Cd63 antigen	Cd63 antigen
1205	3512	AB006607	BBB, CCC, RRR	choline kinase-like	choline kinase-like
1205	3513	AB006607	BBB, RRR, SSS	choline kinase-like	choline kinase-like
1209	17962	AB012230	General Alternate	nuclear factor I/B	nuclear factor I/B
1210	17963	AB012231	FFF, General Core Tox Markers, General Alternate	nuclear factor I/B	nuclear factor I/B
1211	24414	AB012234	D, SS	Nuclear factor I/X (CCAAT-binding transcription factor)	Nuclear factor I/X (CCAAT-binding transcription factor)
1215	954	AF000114	D	contactin associated protein 1	contactin associated protein 1
1244	25211	AF087839	SSS, UUU	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
1359	16521	AI010470	FF	Ceruloplasmin (ferroxidase)	Ceruloplasmin (ferroxidase)
1442	12300	AI013333	N	aldehyde dehydrogenase 2, mitochondrial	aldehyde dehydrogenase 2, mitochondrial
1480	2866	AI029058	Z, AA	Cyclin D1	Cyclin D1
1515	7665	AI030668	General Core Tox Markers, General Alternate	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
1558	1431	AI044610	I, J, CC, II, General Alternate	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	Dopa decarboxylase (aromatic L-amino acid decarboxylase)
1566	20983	AI044900	A, FF, JJ, KK, LL, FFF, HHH, SSS, General Core Tox Markers, General Alternate	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
1583	169	AI045171	E	calsequestrin 2	calsequestrin 2

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1870	18277	AI104399	T, HHH	Triosephosphate isomerase 1	Triosephosphate isomerase 1
1887	17171	AI105137	M, V, JJ, KK	Somatostatin	ESTs, Highly similar to GTK1_RAT Glutathione S-transferase, mitochondrial (GST 13-13) (Glutathione S-transferase subunit 13) (GST class-kappa) [R.norvegicus], Somatostatin
1928	1841	AI113289	O, P, Q, R, V, DD, NN, OO, PP, QQ, III, JJJ, General Alternate	protein tyrosine phosphatase, non-receptor type 1	protein tyrosine phosphatase, non-receptor type 1
1939	20920	AI136891	W	zinc finger protein 36, C3H type-like 1	zinc finger protein 36, C3H type-like 1
1958	16510	AI137583	L, T	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
1990	5232	AI168942	WW	branched chain keto acid dehydrogenase E1, beta polypeptide	branched chain keto acid dehydrogenase E1, beta polypeptide
2033	8213	AI169883	F, PP, QQ, XX, YY, LLL, UUU	ferritin light chain 1	ferritin light chain 1
2104	8215	AI171692	CC, GG, HH, EEE, III, JJJ, MMM, General Core Tox Markers, General Alternate	ferritin light chain 1	ESTs, Highly similar to S66270 kynurenine--oxoglutarate transaminase (EC 2.6.1.7) / glutamine--phenylpyruvate transaminase (EC 2.6.1.64) mitochondrial precursor [validated] - rat [R.norvegicus], ferritin light chain 1
2163	12614	AI175294	T	ribosomal protein L21	ribosomal protein L21
2209	24763	AI176488	Y, LLL, General Core Tox Markers, General Alternate	nuclear factor I/B	nuclear factor I/B
2296	5459	AI178246	RR	ALG-2 interacting protein 1	ALG-2 interacting protein 1
2323	18907	AI178971	T	Hemoglobin, alpha 1	Hemoglobin, alpha 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2349	19427	AI179510	EE, PP, QQ, YY	dimethylarginine dimethylaminohydrolase 1	dimethylarginine dimethylaminohydrolase 1
2370	1687	AI179971	T	Hemoglobin, alpha 1	Hemoglobin, alpha 1
2403	22845	AI227887	K	cell division cycle 42	cell division cycle 42
2429	18612	AI228624	JJ, XX, YY, HHH	ribosomal protein L29	ribosomal protein L29
2512	1688	AI230970	T	Hemoglobin, alpha 1	Hemoglobin, alpha 1
2638	22866	AI233754	E, HH	prolactin regulatory element binding	prolactin regulatory element binding
2699	8440	AI235611	T	ZAP 36/annexin IV	ZAP 36/annexin IV
2731	1689	AI236360	T, XX, YY	Hemoglobin, alpha 1	Hemoglobin, alpha 1
2766	2416	AI237051	LL	heterogeneous nuclear ribonucleoprotein K	heterogeneous nuclear ribonucleoprotein K
2845	1375	D12573	Z, AA	hippocalcin	hippocalcin
2849	25041	D14014	E, HH	Cyclin D1	Cyclin D1
2860	9029	D30804	A, B, RR, WW, SSS	proteasome (prosome, macropain) subunit, alpha type 7	ESTs, Highly similar to S60038 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha chain RC6-I - rat [R.norvegicus]
2861	1351	D31874	RRR	LIM motif-containing protein kinase 2	LIM motif-containing protein kinase 2
2867	9135	D45247	N, RRR	proteasome beta type subunit 5	ESTs, Highly similar to PSB5_RAT Proteasome subunit beta type 5 precursor (Proteasome epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6) [R.norvegicus]
2881	20984	D90109	U, FF, FFF, HHH, General Alternate	fatty acid Coenzyme A ligase, long chain 2	fatty acid Coenzyme A ligase, long chain 2
2917	26368	H34047	E	T-complex 1	T-complex 1
2968	19	L26268	N, BB, CC, DD, HH, III, JJJ, KKK, NNN, General Alternate	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2968	20	L26268	BB, CC, DD, LL, UU, III, JJJ, KKK, NNN, General Alternate	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
2979	427	M00001	CCC	Apolipoprotein A-I	Apolipoprotein A-I
2980	17472	M10934	HH, SS	Retinol binding protein 4	ESTs, Highly similar to RETB_RAT Plasma retinol-binding protein precursor (PRBP) (RBP) [R.norvegicus]
2990	1466	M14050	LL	Heat shock 70kD protein 5	ESTs, Heat shock 70kD protein 5
3001	16427	M21354	M, II	procollagen, type III, alpha 1	procollagen, type III, alpha 1
3012	1312	M31788	I, J, LLL	phosphoglycerate kinase 1	ESTs, Highly similar to A33792 phosphoglycerate kinase (EC 2.7.2.3) - rat [R.norvegicus], phosphoglycerate kinase 1
3016	1843	M33962	DD, ZZ, AAA, III, JJJ, KKK	protein tyrosine phosphatase, non-receptor type 1	protein tyrosine phosphatase, non-receptor type 1
3016	1844	M33962	E, DD, ZZ, AAA, III, JJJ	protein tyrosine phosphatase, non-receptor type 1	ESTs, protein tyrosine phosphatase, non-receptor type 1
3029	1973	M60103	I, J, Y, FF, KKK, LLL, OOO, RRR, SSS, General Core Tox Markers, General Alternate	protein tyrosine phosphatase, receptor-type, F	protein tyrosine phosphatase, receptor-type, F
3033	13547	M63983	EE	hypoxanthine guanine phosphoribosyl transferase	ESTs, Moderately similar to ICA2_MOUSE Intercellular adhesion molecule-2 precursor (ICAM-2) (CD102) (Lymphocyte function-associated AG-1 counter-receptor) [M.musculus], hypoxanthine guanine phosphoribosyl transferase
3036	17344	M75168	C	HLA-B associated transcript 1A	HLA-B associated transcript 1A
3039	997	M80550	RR	adenylyl cyclase 2	adenylyl cyclase 2

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1985828.1	
Seq. ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3040	21670	M80601	R	programmed cell death 2	programmed cell death 2
3046	1430	M84648	TT, DDD, General Core Tox Markers, General Alternate	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	Dopa decarboxylase (aromatic L-amino acid decarboxylase)
3057	22512	NM_012488	BB, NN, EEE, MMM	alpha-2-macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3057	22513	NM_012488	A, E, W, BB, UU, EEE, MMM	alpha-2-macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3057	22514	NM_012488	BB, NN, UU	alpha-2-macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3057	22515	NM_012488	E, W, BB, NN, OO, EEE, III, JJJ, KKK, MMM	alpha-2-macroglobulin (A2m), mRNA. 11/2002 Length = 4595	Alpha-2-macroglobulin
3059	23942	NM_012493	General Alternate	Alpha-fetoprotein (Afp), mRNA. 11/2000 Length = 1990	Alpha-fetoprotein
3065	563	NM_012516	BB, JJ, KK	Complement component 4 binding protein, alpha (C4bpa), mRNA. 11/2000 Length = 1882	Complement component 4 binding protein, alpha
3068	16214	NM_012523	O, P	CD53 antigen (Cd53), mRNA. 11/2002 Length = 1699	Leukocyte antigen (Ox-44)
3072	16519	NM_012532	BB, CC, NN, SSS, UUU	Ceruloplasmin (ferroxidase) (Cp), mRNA. 11/2002 Length = 3700	Ceruloplasmin (ferroxidase)

TABLE 1					
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Seq. ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3072	16520	NM_012532	BB, CC	Ceruloplasmin (ferroxidase) (Cp), mRNA. 11/2002 Length = 3700	Ceruloplasmin (ferroxidase)
3076	19407	NM_012554	G, H, VV	Enolase 1, alpha (Eno1), mRNA. 11/2000 Length = 1725	Enolase 1, alpha
3077	21836	NM_012555	O, P, PP, QQ	Ets avian erythroblastosis virus E2 oncogene homolog 1 (tumor progression locus 1) (Ets1), mRNA. 11/2000 Length = 4991	Ets avian erythroblastosis virus E2 oncogene homolog 1 (tumor progression locus 1)
3089	20126	NM_012591	T, W	Interferon regulatory factor 1 (Irf1), mRNA. 11/2002 Length = 2078	Interferon regulatory factor 1, sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)
3091	18385	NM_012598	O, P, EEE, MMM	Lipoprotein lipase (Lpl), mRNA. 11/2002 Length = 3617	Lipoprotein lipase
3095	1299	NM_012610	V	Nerve growth factor receptor, fast (Ngfr), mRNA. 11/2000 Length = 3259	Nerve growth factor receptor, fast
3107	21087	NM_012661	FFF	steroid sulfatase (Sts), mRNA. 11/2002 Length = 2472	Steroid sulfatase
3129	10260	NM_012732	T, GG, HH, LL	lipase A, lysosomal acid (Lipa), mRNA. 10/2002 Length = 3144	Cholesterol esterase (pancreatic)
3129	25563	NM_012732	DD, EE	lipase A, lysosomal acid (Lipa), mRNA. 10/2002 Length = 3144	Cholesterol esterase (pancreatic)
3140	7784	NM_012789	BB, CC, II, OO	Dipeptidyl peptidase 4 (Dpp4), mRNA. 11/2000 Length = 4835	Dipeptidyl peptidase 4

TABLE 1					
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Seq ID	GLCC ID No.	Genbank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3141	23445	NM_012792	A, GG, II, TT, III, JJJ, LLL, SSS, UUU, General Core Tox Markers	Flavin-containing monooxygenase 1 (Fmo1), mRNA. 11/2000 Length = 2042	Flavin-containing monooxygenase 1
3145	21729	NM_012804	WW, RRR, SSS	ATP-binding cassette, sub-family D (ALD), member 3 (Abcd3), mRNA. 10/2002 Length = 3324	ATP-binding cassette, sub-family D (ALD), member 3
3145	21730	NM_012804	K, U, FF	ATP-binding cassette, sub-family D (ALD), member 3 (Abcd3), mRNA. 10/2002 Length = 3324	ATP-binding cassette, sub-family D (ALD), member 3
3146	17992	NM_012811	XX, YY	O-acetyltransferase Milk fat globule membrane protein (Mfge8), mRNA. 11/2000 Length = 1969	O-acetyltransferase Milk fat globule membrane protein
3147	20605	NM_012812	BB, CC	Cytochrome c oxidase subunit VIa polypeptide 2 (heart) (Cox6a2), mRNA. 11/2000 Length = 395	Cytochrome c oxidase subunit VIa polypeptide 2 (heart)
3160	18770	NM_012857	EE	Lysosomal associated membrane protein 1 (120 kDa) (Lamp1), mRNA. 11/2000 Length = 2006	Lysosomal associated membrane protein 1 (120 kDa)
3168	16721	NM_012891	U, XX, YY, BBB, CCC, RRR, SSS	Acyl-CoA dehydrogenase, Very long chain (Acadvl), mRNA. 10/2002 Length = 2117	Acyl-CoA dehydrogenase, Very long chain
3175	24431	NM_012912	W, II	Activating transcription factor 3 (Atf3), mRNA. 11/2002 Length = 1893	Activating transcription factor 3

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3178	20755	NM_012923	F, R, II, VV, General Alternate	Cyclin G1 (Ccng1), mRNA. 11/2002 Length = 3169	Cyclin G1
3178	20757	NM_012923	F, II, FFF, General Core Tox Markers	Cyclin G1 (Ccng1), mRNA. 11/2002 Length = 3169	Cyclin G1
3192	24263	NM_012999	BB, CC	Subtilisin - like endoprotease (Pace4), mRNA. 10/2001 Length = 4153	Subtilisin - like endoprotease
3192	24264	NM_012999	MM, TTT	Subtilisin - like endoprotease (Pace4), mRNA. 10/2001 Length = 4153	Subtilisin - like endoprotease
3196	20926	NM_013013	PP, QQ	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Psap), mRNA. 11/2000 Length = 2175	Peroxisomal enoyl hydratase-like protein, Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator)
3200	18078	NM_013030	RR	Solute carrier family 34 (sodium phosphate), member 1 (Slc34a1), mRNA. 11/2002 Length = 2440	Rattus norvegicus mRNA for NaPi-2 alpha, complete cds, Solute carrier family 17 (sodium/hydrogen exchanger), member 2
3201	730	NM_013040	E, Z, AA, RR	ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (Abcc9), mRNA. 4/2002 Length = 6628	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
3204	20535	NM_013049	I, J	tumor necrosis factor superfamily, member 4 (Tnfrsf4), mRNA. 11/2002 Length = 1017	tumor necrosis factor receptor superfamily, member 4
3217	1684	NM_013096	T	Hemoglobin, alpha 1 (Hba1), mRNA. 11/2000 Length = 556	Hemoglobin, alpha 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3218	1321	NM_013098	L	Glucose-6-phosphatase (G6pc), mRNA. 11/2000 Length = 2237	Glucose-6-phosphatase
3230	17628	NM_013177	General Alternate	Glutamate oxaloacetate transaminase 2, mitochondrial (aspartate aminotransferase 2) (Got2), mRNA. 11/2000 Length = 2325	Glutamate oxaloacetate transaminase 2, mitochondrial (aspartate aminotransferase 2)
3242	24649	NM_016988	GG, HH	acid phosphatase 2 (Acp2), mRNA. 11/2002 Length = 2009	Acid phosphatase 2, lysozymal
3246	1958	NM_016994	L, S, HH	Complement component 3 (C3), mRNA. 11/2002 Length = 5066	Complement component 3
3247	1698	NM_017000	K, S, GG, HH, GGG	Diaphorase (NADH/NADPH) (Dia4), mRNA. 11/2000 Length = 1396	Diaphorase (NADH/NADPH)
3250	18989	NM_017013	F, K, M, N, GG, HH, TT, DDD, EEE, LLL, MMM, UUU	glutathione-S-transferase, alpha type2 (Gsta2), mRNA. 11/2002 Length = 831	Glutathione-S-transferase, alpha type (Yc?)
3256	24861	NM_017033	T	Phosphoglucomutase 1 (Pgm1), mRNA. 11/2002 Length = 1842	Phosphoglucomutase 1
3256	24862	NM_017033	HH, UU	Phosphoglucomutase 1 (Pgm1), mRNA. 11/2002 Length = 1842	Phosphoglucomutase 1
3263	14533	NM_017055	S, V, NNN	Transferrin (Tf), mRNA. 11/2002 Length = 2275	Transferrin
3263	14534	NM_017055	S, TT, NNN	Transferrin (Tf), mRNA. 11/2002 Length = 2275	Transferrin

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3271	1262	NM_017077	R, MM, NN, OO, TTT	Hepatocyte nuclear factor 3 gamma (Hnf3g), mRNA. 11/2000 Length = 1497	Hepatocyte nuclear factor 3 gamma
3272	23660	NM_017080	T, U, RRR, SSS	Hydroxysteroid dehydrogenase, 11 beta type 1 (Hsd11b1), mRNA. 11/2000 Length = 1265	Hydroxysteroid dehydrogenase, 11 beta type 1
3278	4391	NM_017101	II	Peptidylprolyl isomerase A (cyclophilin A) (Ppia), mRNA. 11/2002 Length = 743	Peptidylprolyl isomerase A (cyclophilin A)
3278	4392	NM_017101	XX, YY	Peptidylprolyl isomerase A (cyclophilin A) (Ppia), mRNA. 11/2002 Length = 743	Peptidylprolyl isomerase A (cyclophilin A)
3287	10503	NM_017143	VV, FFF, GGG, General Alternate	coagulation factor 10 (F10), mRNA. 11/2002 Length = 1497	coagulation factor X
3287	10504	NM_017143	S, GG, VV, PPP, QQQ	coagulation factor 10 (F10), mRNA. 11/2002 Length = 1497	coagulation factor X
3291	5351	NM_017150	KK, FFF, HHH	ribosomal protein L29 (Rpl29), mRNA. 11/2002 Length = 630	ribosomal protein L29
3296	17686	NM_017165	I, J, LL	glutathione peroxidase 4 (Gpx4), mRNA. 11/2002 Length = 872	glutathione peroxidase 4
3299	8182	NM_017170	GG, LL, MM, CCC, GGG, RRR, TTT	serum amyloid P-component (Sap), mRNA. 11/2002 Length = 931	serum amyloid P-component
3300	20919	NM_017172	L	zinc finger protein 36, C3H type-like 1 (Zfp36l1), mRNA. 5/2002 Length = 2741	zinc finger protein 36, C3H type-like 1

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3302	23961	NM_017181	PPP, QQQ	fumarylacetoacetate hydrolase (Fah), mRNA. 11/2002 Length = 1386	fumarylacetoacetate hydrolase
3304	24437	NM_017190	D	Myelin-associated glycoprotein (Mag), mRNA. 11/2002 Length = 2475	Myelin-associated glycoprotein
3306	9124	NM_017199	NN, OO, XX, YY	signal sequence receptor 4 (Ssr4), mRNA. 11/2002 Length = 757	signal sequence receptor, delta
3306	9125	NM_017199	U, NN, OO, XX, YY	signal sequence receptor 4 (Ssr4), mRNA. 11/2002 Length = 757	signal sequence receptor, delta
3306	9126	NM_017199	Z, AA	signal sequence receptor 4 (Ssr4), mRNA. 11/2002 Length = 757	signal sequence receptor, delta
3309	20529	NM_017208	A, D, E, V, W, BB, NN, EEE, III, JJJ, MMM	lipopolysaccharide binding protein (Lbp), mRNA. 11/2002 Length = 2622	lipopolysaccharide binding protein
3312	16263	NM_017223	Z, AA	solute carrier family 20, member 2 (Slc20a2), mRNA. 11/2002 Length = 2287	solute carrier family 20, member 2
3313	24598	NM_017231	T	phosphatidylinositol transfer protein (Pitpn), mRNA. 11/2002 Length = 1638	phosphatidylinositol transfer protein
3316	17561	NM_017245	N, RR	eukaryotic translation elongation factor 2 (Eef2), mRNA. 11/2002 Length = 2626	eukaryotic translation elongation factor 2
3316	17562	NM_017245	VV	eukaryotic translation elongation factor 2 (Eef2), mRNA. 11/2002 Length = 2626	eukaryotic translation elongation factor 2, mitogen activated protein kinase kinase 2

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3316	17563	NM_017245	E	eukaryotic translation elongation factor 2 (Eef2), mRNA. 11/2002 Length = 2626	eukaryotic translation elongation factor 2
3317	15012	NM_017248	VV	heterogeneous nuclear ribonucleoprotein A1 (Hnrpa1), mRNA. 11/2002 Length = 1696	ESTs, Highly similar to DDRT helix-destabilizing protein - rat [R.norvegicus], heterogeneous nuclear ribonucleoprotein A1
3317	17502	NM_017248	O, P, JJ, KK, VV, HHH	heterogeneous nuclear ribonucleoprotein A1 (Hnrpa1), mRNA. 11/2002 Length = 1696	heterogeneous nuclear ribonucleoprotein A1
3328	15535	NM_017283	S, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 6 (Psm6), mRNA. 11/2002 Length = 932	proteasome (prosome, macropain) subunit, alpha type 6
3328	15538	NM_017283	NNN	proteasome (prosome, macropain) subunit, alpha type 6 (Psm6), mRNA. 11/2002 Length = 932	proteasome (prosome, macropain) subunit, alpha type 6
3330	12523	NM_017285	G, H, PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 3 (Psm3), mRNA. 11/2002 Length = 828	proteasome (prosome, macropain) subunit, beta type, 3
3330	12524	NM_017285	G, H, S, X, Y, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 3 (Psm3), mRNA. 11/2002 Length = 828	proteasome (prosome, macropain) subunit, beta type, 3

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3336	23130	NM_017307	V, FF	solute carrier family 25, member 1 (Slc25a1), nuclear gene encoding mitochondrial protein, mRNA. 11/2002 Length = 1575	solute carrier family 25 (mitochondrial carrier; citrate transporter) member 1
3353	15977	NM_019132	S	Guanine nucleotide-binding protein G-s, alpha subunit, Genbank no U51565 (Gnas), mRNA. 11/2002 Length = 1738	Guanine nucleotide-binding protein G-s, alpha subunit
3354	24785	NM_019133	SS	synapsin 1 (Syn1), mRNA. 11/2002 Length = 2400	Synapsin I
3372	2632	NM_019213	S	jumping translocation breakpoint (Jtb), mRNA. 11/2002 Length = 897	jumping translocation breakpoint
3374	15347	NM_019222	P, T	coronin, actin-binding protein, 1B (Coro1b), mRNA. 11/2002 Length = 1800	coronin, actin binding protein 1B
3374	15348	NM_019222	X, Y	coronin, actin-binding protein, 1B (Coro1b), mRNA. 11/2002 Length = 1800	coronin, actin binding protein 1B
3377	15503	NM_019237	NN, EEE, MMM	procollagen C-proteinase enhancer protein (Pcolce), mRNA. 11/2002 Length = 1547	procollagen C-proteinase enhancer protein
3377	15504	NM_019237	NN	procollagen C-proteinase enhancer protein (Pcolce), mRNA. 11/2002 Length = 1547	procollagen C-proteinase enhancer protein
3379	17908	NM_019242	Q, W, MM, QQ, TTT	interferon-related developmental regulator 1 (Ifrd1), mRNA. 5/2002 Length = 1736	interferon-related developmental regulator 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3388	15057	NM_019291	JJ	carbonic anhydrase 2 (Ca2), mRNA. 11/2002 Length = 1459	carbonic anhydrase 2
3412	574	NM_019905	O, VV, EEE, MMM	calpactin I heavy chain (Anxa2), mRNA. 11/2002 Length = 1395	calpactin I heavy chain, hydroxyacid oxidase 3 (medium-chain), unknown Glu-Pro dipeptide repeat protein
3417	12087	NM_020082	B, LLL, SSS, UUU	ribonuclease, RNase A family 4 (Rnase4), mRNA. 11/2002 Length = 546	ribonuclease 4
3428	19679	NM_021653	S, U, RR, CCC, LLL, RRR, SSS, UUU	deiodinase, iodothyronine, type 1 (Dio1), mRNA. 11/2002 Length = 2106	Thyroxine deiodinase, type I
3446	23782	NM_022183	WW	topoisomerase (DNA) 2 alpha (Top2a), mRNA. 11/2002 Length = 6052	topoisomerase (DNA) II alpha
3473	8211	NM_022500	N, MM, DDD, TTT	ferritin light chain 1 (Ftl1), mRNA. 11/2002 Length = 552	ferritin light chain 1
3473	8212	NM_022500	F, N, T, HH, QQ, TT, YY, DDD, LLL, UUU	ferritin light chain 1 (Ftl1), mRNA. 11/2002 Length = 552	ferritin light chain 1
3493	20762	NM_022588	YY	metastasis associated 1 (Mta1), mRNA. 1/2001 Length = 2741	metastasis associated 1
3495	20925	NM_022594	U, FF, LL, CCC, RRR, SSS	enoyl coenzyme A hydratase 1 (Ech1), mRNA. 11/2002 Length = 1097	Peroxisomal enoyl hydratase-like protein
3521	16184	NM_022935	Z, AA	Amiloride binding protein 1 (Abp1), mRNA. 11/2002 Length = 2668	amiloride binding protein 1
3542	8439	NM_024155	O, P	ZAP 36/annexin IV (Anxa4), mRNA. 2/2001 Length = 960	ZAP 36/annexin IV

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3564	1853	NM_030826	MM, TT, TTT	Glutathione peroxidase 1 (Gpx1), mRNA. 11/2002 Length = 1539	ESTs, Glutathione peroxidase 1
3577	20410	NM_030990	SS	Proteolipid protein (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated) (Plp), mRNA. 11/2002 Length = 3019	Proteolipid protein (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)
3585	690	NM_031034	RR	guanine nucleotide binding protein, alpha 12 (Gna12), mRNA. 11/2002 Length = 1423	guanine nucleotide binding protein (G protein) alpha 12
3601	23854	NM_031101	G, II, FFF, GGG, General Alternate	ribosomal protein L13 (Rpl13), mRNA. 11/2002 Length = 722	ribosomal protein L13
3603	16938	NM_031103	F, H, II	ribosomal protein L19 (Rpl19), mRNA. 11/2002 Length = 703	ribosomal protein L19
3605	17300	NM_031107	KKK	S6 protein kinase (Rsk-1) (Rps6ka1), mRNA. 4/2001 Length = 3131	S6 protein kinase (Rsk-1)
3610	20839	NM_031113	F, II, FFF, General Alternate	ribosomal protein S27a (Rps27a), mRNA. 4/2001 Length = 552	ribosomal protein S27a
3611	19040	NM_031114	O, VV	S-100 related protein, clone 42C (S100A10), mRNA. 2/2002 Length = 573	S-100 related protein, clone 42C
3634	18990	NM_031509	G, K, TT, SSS	Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	Glutathione-S-transferase, alpha type (Yc?)
3635	17427	NM_031510	Q, R, GG, PPP, QQQ, General Alternate	Isocitrate dehydrogenase 1, soluble (Idh1), mRNA. 5/2001 Length = 1719	Isocitrate dehydrogenase 1, soluble

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3639	20448	NM_031530	W, II, EEE, MMM	small inducible cytokine A2 (Scya2), mRNA. 11/2002 Length = 780	Small inducible gene JE
3639	20449	NM_031530	W, II, QQ	small inducible cytokine A2 (Scya2), mRNA. 11/2002 Length = 780	Small inducible gene JE
3649	9620	NM_031570	KK, FFF, HHH, General Alternate	ribosomal protein S7 (Rps7), mRNA. 11/2002 Length = 650	ribosomal protein S7
3649	9621	NM_031570	B, JJ, OO, HHH	ribosomal protein S7 (Rps7), mRNA. 11/2002 Length = 650	ribosomal protein S7
3655	14295	NM_031599	ZZ, AAA, PPP, QQQ	eukaryotic translation initiation factor 2 alpha kinase 3 (Eif2ak3), mRNA. 11/2002 Length = 4510	eukaryotic translation initiation factor 2 alpha kinase 3
3658	21586	NM_031620	G	3-phosphoglycerate dehydrogenase (Phgdh), mRNA. 11/2002 Length = 1803	3-phosphoglycerate dehydrogenase
3659	14956	NM_031622	C	mitogen-activated protein kinase 6 (Mapk6), mRNA. 11/2002 Length = 3662	mitogen-activated protein kinase 6
3659	14957	NM_031622	C, TT	mitogen-activated protein kinase 6 (Mapk6), mRNA. 11/2002 Length = 3662	mitogen-activated protein kinase 6
3668	20743	NM_031684	I, J, KKK, General Alternate	solute carrier family 29, member 1 (Slc29a1), mRNA. 11/2002 Length = 1766	solute carrier family 29 (nucleoside transporters), member 1
3669	19727	NM_031687	N	ubiquitin A-52 residue ribosomal protein fusion product 1 (Uba52), mRNA. 11/2002 Length = 467	ubiquitin A-52 residue ribosomal protein fusion product 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3671	13706	NM_031699	QQ	claudin 1 (Cldn1), mRNA. 11/2002 Length = 893	claudin 1
3677	12052	NM_031722	CC, WW	coated vesicle membrane protein (Rnp24), mRNA. 11/2002 Length = 716	coated vesicle membrane protein
3680	17554	NM_031736	U, FF, GG	solute carrier family 27 (fatty acid transporter), member 32 (Slc27a2), mRNA. 11/2002 Length = 2963	solute carrier family 27 (fatty acid transporter), member 2
3702	4748	NM_031834	GGG, SSS	sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1), mRNA. 1/2002 Length = 1227	sulfotransferase family 1A, phenol-preferring, member 1
3702	4749	NM_031834	Y	sulfotransferase family 1A, phenol-preferring, member 1 (Sult1a1), mRNA. 1/2002 Length = 1227	Aryl sulfotransferase cytosolic, 1A, phenol-preferring, member 3, sulfotransferase family 1A, phenol-preferring, member 1
3707	15069	NM_031840	I, J, N, T, General Alternate	farnesyl diphosphate synthase (Fdps), mRNA. 11/2002 Length = 1271	Farnesyl diphosphate synthase
3707	15070	NM_031840	I, T	farnesyl diphosphate synthase (Fdps), mRNA. 11/2002 Length = 1271	Farnesyl diphosphate synthase
3707	25460	NM_031840	I, J, T	farnesyl diphosphate synthase (Fdps), mRNA. 11/2002 Length = 1271	Farnesyl diphosphate synthase
3708	15601	NM_031851	U, LL, RR, SS, BBB, CCC, LLL, RRR, SSS	Prohibitin (Phb), mRNA. 11/2002 Length = 1688	Prohibitin

TABLE 1					
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Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3727	18492	NM_032079	HHH	DnaJ (Hsp40) homolog, subfamily A, member 2 (Dnaja2), mRNA. 11/2002 Length = 1518	DnaJ (Hsp40) homolog, subfamily A, member 2
3727	18494	NM_032079	PPP, QQQ	DnaJ (Hsp40) homolog, subfamily A, member 2 (Dnaja2), mRNA. 11/2002 Length = 1518	DnaJ (Hsp40) homolog, subfamily A, member 2
3728	12299	NM_032416	N, YY	aldehyde dehydrogenase 2 (Aldh2), mRNA. 11/2002 Length = 1889	aldehyde dehydrogenase 2, mitochondrial
3734	17829	NM_033234	T, HH, NNN	Hemoglobin, beta (Hbb), mRNA. 12/2001 Length = 620	Hemoglobin, beta
3734	17832	NM_033234	T	Hemoglobin, beta (Hbb), mRNA. 12/2001 Length = 620	Hemoglobin, beta
3734	25468	NM_033234	K, T, HH, XX, YY	Hemoglobin, beta (Hbb), mRNA. 12/2001 Length = 620	Hemoglobin, beta
3738	24420	NM_033539	HH	eukaryotic translation elongation factor 1 alpha 2 (Eef1a2), mRNA. 11/2002 Length = 1404	eukaryotic translation elongation factor 1 alpha 1
3748	23597	NM_053323	Y	degenerative spermatocyte homolog (Drosophila) (Degs), mRNA. 11/2002 Length = 1390	degenerative spermatocyte homolog (Drosophila)
3750	14925	NM_053330	K, Z, AA, KK	ribosomal protein L21 (Rpl21), mRNA. 11/2002 Length = 554	ribosomal protein L21
3750	14926	NM_053330	V, Z, AA	ribosomal protein L21 (Rpl21), mRNA. 11/2002 Length = 554	ribosomal protein L21

TABLE 1					
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Seq. ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3750	14927	NM_053330	V	ribosomal protein L21 (Rpl21), mRNA. 11/2002 Length = 554	ribosomal protein L21
3750	14929	NM_053330	O, P, VV	ribosomal protein L21 (Rpl21), mRNA. 11/2002 Length = 554	ribosomal protein L21
3753	14042	NM_053348	N, YY	fetuin beta (Fetub), mRNA. 11/2002 Length = 1392	fetuin beta
3805	1178	NM_053620	PP, QQ	Cdc42-binding protein kinase beta (Cdc42bpb), mRNA. 11/2002 Length = 5333	Cdc42-binding protein kinase beta
3845	17728	NM_053867	FF	tumor protein, translationally-controlled 1 (Tpt1), mRNA. 11/2001 Length = 794	tumor protein, translationally-controlled 1
3864	17653	NM_053986	C, SS, WW, SSS, UUU	myosin Ib (Myo1b), mRNA. 11/2002 Length = 3607	myosin IB
3874	23250	NM_057097	ZZ, AAA	vesicle-associated membrane protein 3 (Vamp3), mRNA. 11/2002 Length = 1742	vesicle-associated membrane protein 3
3876	25290	NM_057100	E, BB, JJ	growth arrest specific 6 (Gas6), mRNA. 11/2002 Length = 2573	growth arrest specific 6
3895	8640	NM_057211	KKK	Kruppel-like factor 9 (Klf9), mRNA. 11/2002 Length = 2721	Kruppel-like factor 9
3895	8641	NM_057211	C, DD, EE, SS	Kruppel-like factor 9 (Klf9), mRNA. 11/2002 Length = 2721	Kruppel-like factor 9
3896	10498	NM_078617	F	ribosomal protein S23 (Rps23), mRNA. 11/2002 Length = 432	ribosomal protein S23
3937	656	NM_133380	Y	Interleukin 4 receptor (Il4r), mRNA. 3/2002 Length = 3576	Interleukin 4 receptor

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3959	17109	NM_134326	M, S, DD, EE, SS, TT	Albumin (Alb), mRNA. 3/2002 Length = 1956	Albumin
3959	17112	NM_134326	S, HH	Albumin (Alb), mRNA. 3/2002 Length = 1956	Albumin, Glutathione peroxidase 1
3970	25237	NM_134452	NNN	collagen, type V, alpha 1 (Col5a1), mRNA. 11/2002 Length = 5551	collagen, type V, alpha 1
3982	15189	NM_138826	C, E, L, T, W, BB, DD, KKK, NNN	Metallothionein (Mt1a), mRNA. 11/2002 Length = 389	Metallothionein
3982	15190	NM_138826	C, E, L, T, DD, SS, WW, KKK, NNN	Metallothionein (Mt1a), mRNA. 11/2002 Length = 389	Metallothionein
3994	1858	NM_138907	FF, LL	mitochondrial acyl-CoA thioesterase 1 (Mte1), mRNA. 4/2002 Length = 1711	acyl-CoA thioesterase 1, cytosolic, mitochondrial acyl-CoA thioesterase 1
4054	19428	R47028	HH	dimethylarginine dimethylaminohydrolase 1	dimethylarginine dimethylaminohydrolase 1
4063	8210	S61960	BB, CC, MM, UU, TTT, General Alternate	ferritin light chain 1	ferritin light chain 1
4079	9687	S79214	G, H	Collagen type X alpha 1	Collagen type X alpha 1
4096	1392	U10188	V	Polo-like kinase homolog	Polo-like kinase homolog
4099	1639	U11685	W, DD, EE, KKK, NNN, General Alternate	nuclear receptor subfamily 1, group H, member 3	nuclear receptor subfamily 1, group H, member 3
4117	14535	U31866	J, S	Transferrin	Rattus norvegicus Nclone10 mRNA, Transferrin
4141	17078	U53859	M	calpain, small subunit 1	calpain, small subunit 1
4141	17079	U53859	M	calpain, small subunit 1	calpain, small subunit 1
4143	25608	U53927	MM, SS, TTT	cationic amino acid transporter-2A	cationic amino acid transporter-2A

TABLE 1					
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Seq. ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4168	1279	U75916	A	tight junction protein 2	tight junction protein 2
4176	1084	U89514	UU	calpain 9 (nCL-4)	calpain 9 (nCL-4)
4208	10819	X51536	H	ribosomal protein S3	ESTs, Highly similar to RS3_MOUSE 40S ribosomal protein S3 [R.norvegicus]
4210	18250	X51706	F, V, EEE, MMM	ribosomal protein L9	ESTs, Highly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus]
4212	1959	X52477	S, HH, MM, SS, TTT	Complement component 3	Complement component 3
4223	1037	X57523	II	Transporter 1, ABC (ATP binding cassette)	Transporter 1, ABC (ATP binding cassette)
4226	18611	X58200	BB, CC, II, WW, EEE, MMM, General Alternate	ribosomal protein L29	ribosomal protein L29
4236	1435	X61654	O, P	Cd63 antigen	Cd63 antigen
4237	15875	X62145	F	ribosomal protein L8	ESTs, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus]
4243	20821	X62671	F, T	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	ESTs, Highly similar to UBIM_RAT UBIQUITIN-LIKE PROTEIN FUBI [R.norvegicus]
4246	556	X64336	V, NN, OO	Protein C	Protein C
4254	16426	X70369	M, II	procollagen, type III, alpha 1	procollagen, type III, alpha 1
4256	1548	X70900	V, General Alternate	hepsin	hepsin
4261	1955	X76453	M	Hras-revertant gene 107	Hras-revertant gene 107
4263	11260	X77934	WW	Amyloid protein precursor-like protein 2	Amyloid protein precursor-like protein 2
4285	1818	Y11283	D, E, S, CC, MM, TTT	inter-alpha-inhibitor H4 heavy chain	inter-alpha-inhibitor H4 heavy chain

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
23	17613	AA799511	B, JJ, WW, DDD, HHH, General Alternate		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
26	18981	AA799523	I, Z, AA, LL		ESTs, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus]
30	17599	AA799539	Q, R		ESTs, Weakly similar to KEAP_RAT Kelch-like ECH-associated protein 1 (Cytosolic inhibitor of Nrf2) (INrf2) [R.norvegicus]
39	18361	AA799591	U, V, GG		ESTs, Highly similar to TBB1_RAT TUBULIN BETA CHAIN (T BETA-15) [R.norvegicus]
42	17380	AA799612	MM, TTT	ubiquitin conjugating enzyme	ubiquitin conjugating enzyme
52	21679	AA799691	DD, EE, KKK, NNN, OOO		ESTs, Moderately similar to T31432 K-Cl cotransport protein 2, furosemide-sensitive - rat [R.norvegicus]
67	20998	AA799803	T, U, JJ, KK, WW, BBB, GGG, PPP, QQQ, RRR		ESTs, Weakly similar to JC6554 complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat [R.norvegicus]
70	21042	AA799814	MM, TTT	HMm:MAP kinase-activated protein kinase 2	ESTs, Weakly similar to A34366 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat [R.norvegicus]
71	1607	AA799879	C		ESTs, Moderately similar to SNG1_RAT SYNAPTOGYRIN 1 (P29) [R.norvegicus]
80	16653	AA799996	Z, AA		ESTs, Weakly similar to GBG5_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-5 subunit [R.norvegicus]
100	6892	AA800551	Q	DnaJ-like protein	DnaJ-like protein

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
128	5934	AA817695	A, I, J, FFF, OOO, General Core Tox Markers		ESTs, Highly similar to 2008147A protein RAKb [Rattus norvegicus] [R.norvegicus]
136	1822	AA817843	LLL, UUU	CCAAT binding transcription factor of CBF-B/NFY-B	CCAAT binding transcription factor of CBF-B/NFY-B
139	2109	AA817887	VV	profilin	profilin
143	2544	AA817968	LLL, SSS, UUU, General Alternate	ectonucleotide pyrophosphatase/phosphodiesterase 1	ectonucleotide pyrophosphatase/phosphodiesterase 1
152	3016	AA818069	EE	polyubiquitin	polyubiquitin
160	6016	AA818163	B, H, GG, HHH, PPP, General Core Tox Markers		ESTs, Weakly similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1) (Serum aryldiacylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus]
163	17771	AA818224	AA		Rat mRNA for beta-tubulin T beta15
178	6236	AA818627	K, L, UU		EST, Moderately similar to ISI1_RAT Insulin-induced protein 1 (Insulin-induced growth response protein CL-6) (Immediate-early protein CL-6) [R.norvegicus]
209	6237	AA819288	H, S		ESTs, Weakly similar to latexin [Rattus norvegicus] [R.norvegicus]
224	15668	AA819643	K	AMP-activated protein kinase	AMP-activated protein kinase
233	19433	AA819776	K, XX, YY		ESTs, Weakly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
240	17614	AA848306	SS		ESTs, Weakly similar to DDRT helix-destabilizing protein - rat [R.norvegicus]
278	21310	AA850055	E		ESTs, Weakly similar to solute carrier family 27 (fatty acid transporter), member 2 [Rattus norvegicus] [R.norvegicus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
284	14324	AA850402	E		ESTs, Moderately similar to S21348 probable pol polyprotein-related protein 4 - rat [R.norvegicus]
325	13772	AA851926	C, J		ESTs, Weakly similar to A57514 RNA helicase HEL117 - rat [R.norvegicus]
334	17461	AA858528	MM, TTT		ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus]
345	14987	AA858640	G, H, U	heat shock protein 60 (liver)	Rattus norvegicus CDK110 mRNA, heat shock protein 60 (liver)
367	6443	AA859150	OOO		ESTs, Highly similar to NFM_RAT Neurofilament triplet M protein (160 kDa neurofilament protein) (Neurofilament medium polypeptide) (NF-M) [R.norvegicus]
368	19105	AA859230	II		ESTs, Weakly similar to HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-17 [R.norvegicus]
370	21025	AA859241	III, JJJ, OOO, General Core Tox Markers	synaptojanin 2 binding protein	synaptojanin 2 binding protein
377	6342	AA859458	Z, AA		ESTs, Weakly similar to KPCG_MOUSE Protein kinase C, gamma type (PKC-gamma) [R.norvegicus]
390	16318	AA859648	Q		ESTs, Weakly similar to DJA1_MOUSE DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) [R.norvegicus]
407	23301	AA859975	BB, CC	2-oxoglutarate carrier	2-oxoglutarate carrier
414	4462	AA866264	General Alternate		ESTs, Weakly similar to PE2R_RAT 20-alpha-hydroxysteroid dehydrogenase (20-alpha-HSD) (HSD1) [R.norvegicus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
434	16327	AA875050	DD, EE, JJ, OO, III, JJJ, OOO, General Core Tox Markers		ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus]
435	20701	AA875097	E, V, W, Z, AA, BB, CC, OO, PP, SS, UU, EEE, III, KKK, LLL, MMM, UUU		EST, Highly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus]
448	15933	AA875253	PP, QQ	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
463	6079	AA891037	UU		ESTs, Moderately similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus]
472	9136	AA891226	G, H, X, Y, GGG, LLL		ESTs, Highly similar to PSB5_RAT Proteasome subunit beta type 5 precursor (Proteasome epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6) [R.norvegicus]
473	18397	AA891242	KKK		ESTs, Weakly similar to MLRV_RAT Myosin regulatory light chain 2, ventricular/cardiac muscle isoform (MLC-2) [R.norvegicus]
482	2753	AA891589	RR	sarcosine dehydrogenase	ESTs, sarcosine dehydrogenase
497	18269	AA891769	D, N		ESTs, Weakly similar to SC65 synaptonemal complex protein [Rattus norvegicus] [R.norvegicus]
513	3902	AA891901	JJ, KK	polypyrimidine tract binding protein	polypyrimidine tract binding protein
548	24295	AA892260	R		ESTs, Highly similar to JC5386 steroidogenic acute regulatory protein - rat [R.norvegicus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
556	13647	AA892367	B, XX, YY, HHH		ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus]
561	19226	AA892394	ZZ, AAA		ESTs, Weakly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus]
561	19227	AA892394	HH		ESTs, Weakly similar to ELV4_RAT ELAV-like protein 4 (Paraneoplastic encephalomyelitis antigen HuD) (Hu-antigen D) [R.norvegicus]
567	9254	AA892470	C, H, S, OOO		ESTs, Highly similar to S03644 histone H2A.Z - rat [R.norvegicus]
569	11992	AA892485	MM, TTT	dihydrolipoamide acetyltransferase	dihydrolipoamide acetyltransferase
570	24873	AA892498	N, O, P		ESTs, Weakly similar to CD63_RAT CD63 antigen (AD1 antigen) [R.norvegicus]
580	15876	AA892582	F, G, H		ESTs, Highly similar to RL8_HUMAN 60S ribosomal protein L8 [R.norvegicus]
592	22537	AA892799	S	HMm:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to 3-phosphoglycerate dehydrogenase [Rattus norvegicus] [R.norvegicus]
592	22538	AA892799	M	HMm:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to 3-phosphoglycerate dehydrogenase [Rattus norvegicus] [R.norvegicus]
598	7148	AA892842	L		ESTs, Weakly similar to CAZ3_RAT F-actin capping protein alpha-3 subunit (CAPZ alpha-3) [R.norvegicus]
609	3438	AA892921	K, V		ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus]
640	1562	AA893552	A, F, G, V, SSS, General Alternate		Rattus norvegicus kallistatin mRNA, complete cds
644	3465	AA893611	ZZ, AAA		ESTs, Moderately similar to MXI1_RAT MAX interacting protein 1 (MXI1 protein) [R.norvegicus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
662	7637	AA894089	XX, YY, ZZ, AAA	rotein carrying the RING-H2 sequence motif	rotein carrying the RING-H2 sequence motif
666	18419	AA894130	S		ESTs, Weakly similar to 2019243A amyloid precursor-like protein 2 [Rattus norvegicus] [R.norvegicus]
672	15274	AA894258	L, HH	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
704	15275	AA900187	D	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
706	4725	AA900290	Z, MM, TTT	HMm:carbon catabolite repression 4 homolog (S. cerevisiae)	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus]
710	17849	AA900460	GGG		ESTs, Weakly similar to JQ0866 T-complex protein 1 - rat [R.norvegicus]
711	6483	AA900461	RR		ESTs, Weakly similar to OBRG_RAT Leptin receptor gene-related protein (OB-R gene related protein) (OB-RGRP) [R.norvegicus]
716	3822	AA900863	OOO, General Core Tox Markers		ESTs, Weakly similar to HE47_RAT Probable ATP-dependent RNA helicase p47 [R.norvegicus]
753	5003	AA924691	UU		ESTs, Weakly similar to DnaJ-like protein [Rattus norvegicus] [R.norvegicus]
775	10666	AA925212	SS, ZZ, AAA	siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1	siah binding protein 1; FBP interacting repressor; pyrimidine tract binding splicing factor; Ro ribonucleoprotein-binding protein 1
777	21010	AA925306	D, U, FF, BBB, RRR, SSS	HMm:carnitine acetyltransferase	ESTs, Weakly similar to 1701410A choline acetyltransferase [Rattus norvegicus] [R.norvegicus]
836	22142	AA943066	KK		ESTs, Weakly similar to A57514 RNA helicase HEL117 - rat [R.norvegicus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
876	20795	AA944397	K	HMm:heat shock protein, 86 kDa 1	ESTs, Moderately similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
882	14763	AA944481	FF		ESTs, Weakly similar to FCN2_RAT Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin P35) (EBP-37) (Hucolin) [R.norvegicus]
884	12228	AA944536	ZZ, AAA		ESTs, Weakly similar to R6RT37 ribosomal protein L37, cytosolic [validated] - rat [R.norvegicus]
890	2893	AA944833	VV		ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) [R.norvegicus]
915	22606	AA945580	VV		ESTs, Weakly similar to ARG2_RAT Arginase II, mitochondrial precursor (Non-hepatic arginase) (Kidney-type arginase) [R.norvegicus]
915	22607	AA945580	VV		ESTs, Weakly similar to ARG2_RAT Arginase II, mitochondrial precursor (Non-hepatic arginase) (Kidney-type arginase) [R.norvegicus]
920	22612	AA945624	OOO		ESTs, Weakly similar to A34162 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) - rat [R.norvegicus]
922	20904	AA945683	ZZ, AAA		ESTs, Weakly similar to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 [Rattus norvegicus] [R.norvegicus]
966	23584	AA955071	J, GG, HH, General Core Tox Markers	retinoid X receptor gamma (retinoid X receptor gamma (
978	23542	AA955389	AA		ESTs, Weakly similar to GRB2_HUMAN Growth factor receptor-bound protein 2 (GRB2 adapter protein) (SH2/SH3 adapter GRB2) (ASH protein) [R.norvegicus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
993	12426	AA955760	YY		ESTs, Weakly similar to LIS1_MOUSE Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH alpha) (PAFAH alpha) (Lissencephaly-1 protein) (LIS-1) [R.norvegicus]
1005	11050	AA956164	HHH, General Alternate		ESTs, Weakly similar to JQ0866 T-complex protein 1 - rat [R.norvegicus]
1010	25112	AA956437	BB, CC		ESTs, Weakly similar to TERA_RAT TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) [CONTAINS: VALOSIN] [R.norvegicus]
1030	24040	AA957422	P, VV		ESTs, Highly similar to FCEG_RAT High affinity immunoglobulin epsilon receptor gamma-subunit precursor (FcERI) (IgE Fc receptor gamma-subunit) (Fc-epsilon RI-gamma) [R.norvegicus]
1031	23080	AA957423	General Alternate		ESTs, Weakly similar to JC5567 lamin B receptor - rat [R.norvegicus]
1042	23541	AA957999	WW		ESTs, Weakly similar to TXTP_RAT Tricarboxylate transport protein, mitochondrial precursor (Citrate transport protein) (CTP) (Tricarboxylate carrier protein) [R.norvegicus]
1049	16577	AA963286	V		ESTs, Moderately similar to A53770 growth factor-responsive protein, vascular smooth muscle - rat [R.norvegicus]
1058	18648	AA963782	SS		ESTs, Weakly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
1075	18830	AA964496	T, W		ESTs, Highly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) [R.norvegicus]
1145	13330	AA997716	X, Y	Kelch-like ECH-associated protein 1	Kelch-like ECH-associated protein 1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1174	3773	AA998356	A, B, E, CC, DD, EE, PP, QQ, III, JJJ, KKK, NNN		ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus]
1197	1962	AB000199	D	CCA2 protein	CCA2 protein
1222	19649	AF016387	XX, YY	retinoid X receptor gamma (retinoid X receptor gamma (
1223	1308	AF022774	HHH	rabphilin 3A-like (without C2 domains)	rabphilin 3A-like (without C2 domains)
1225	18072	AF026529	FF	stathmin-like-protein RB3	stathmin-like-protein RB3
1233	1995	AF038870	C, NN, OO, DDD	betaine-homocysteine methyltransferase	betaine-homocysteine methyltransferase
1241	20741	AF084186	A, Q, R, JJ, KK, WW, FFF, GGG, HHH, PPP, QQQ	alpha-fodrin	alpha-fodrin
1243	20133	AF087697	XX, YY	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
1248	2947	AF099093	D	ubiquitin-conjugating enzyme UBC7	ubiquitin-conjugating enzyme UBC7
1248	20511	AF099093	Y	ubiquitin-conjugating enzyme UBC7	ubiquitin-conjugating enzyme UBC7
1249	4014	AI007645	J, Z, AA		ESTs, Weakly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus]
1251	11251	AI007666	EE		ESTs, Weakly similar to JC4647 KW8 protein - rat [R.norvegicus]
1254	8368	AI007808	DD, EE		ESTs, Highly similar to A37056 AMP deaminase (EC 3.5.4.6), brain - rat (fragment) [R.norvegicus]
1262	22230	AI007920	EE		ESTs, Weakly similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus]
1279	4098	AI008642	VV		ESTs, Weakly similar to LANP_RAT Leucine-rich acidic nuclear protein [R.norvegicus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1280	949	AI008687	WW		ESTs, Highly similar to WASL_RAT Neural Wiskott-Aldrich syndrome protein (N-WASP) [R.norvegicus]
1286	344	AI008865	UU, III, JJJ	Signal transducer and activator of transcription 3	Signal transducer and activator of transcription 3
1300	21838	AI009131	C, General Alternate	laminin, gamma 1	laminin, gamma 1
1328	22545	AI009747	I, J, MM, TTT	transducer of ERBB2, 1	transducer of ERBB2, 1
1360	163	AI010480	X, Y	malate dehydrogenase mitochondrial	malate dehydrogenase mitochondrial
1360	164	AI010480	I	malate dehydrogenase mitochondrial	malate dehydrogenase mitochondrial
1382	16112	AI011706	C		ESTs, Weakly similar to SFR5_RAT Splicing factor, arginine/serine-rich 5 (Pre-mRNA splicing factor SRP40) (Insulin-induced growth response protein CL-4) (Delayed-early protein HRS) [R.norvegicus]
1404	21796	AI012221	II, OO, VV		ESTs, Weakly similar to intracellular chloride ion channel protein p64H1 [Rattus norvegicus] [R.norvegicus]
1408	3417	AI012337	General Alternate		ESTs, Highly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27) [R.norvegicus]
1414	7120	AI012393	T		ESTs, Weakly similar to JE0343 terf protein - rat [R.norvegicus]
1423	20817	AI012589	G	glutathione S-transferase, pi 2	glutathione S-transferase, pi 2
1441	1205	AI013107	D, V	kinesin family member 3C	kinesin family member 3C
1466	7299	AI013911	C, G, H, General Core Tox Markers		ESTs, Weakly similar to cold inducible RNA-binding protein [Rattus norvegicus] [R.norvegicus]
1469	15904	AI013971	QQ	neurofascin	neurofascin
1525	23949	AI031019	C, E	translation initiation factor eIF-2B alpha-subunit	translation initiation factor eIF-2B alpha-subunit

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1525	23950	AI031019	R, PPP, QQQ	translation initiation factor eIF-2B alpha-subunit	translation initiation factor eIF-2B alpha-subunit
1536	7891	AI043759	N		ESTs, Weakly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus]
1545	7961	AI044042	WW		ESTs, Weakly similar to TC17_RAT Zinc finger protein 354A (Transcription factor 17) (Renal transcription factor Kid-1) (Kidney, ischemia, and developmentally regulated protein-1) [R.norvegicus]
1563	18205	AI044836	EE, NNN		ESTs, Weakly similar to NUCL_RAT Nucleolin (Protein C23) [R.norvegicus]
1581	5711	AI045151	GGG, HHH, General Alternate		ESTs, Weakly similar to solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 [Rattus norvegicus] [R.norvegicus]
1594	7552	AI045802	G, General Alternate		Rattus norvegicus partial mRNA for glycosylphosphatidylinositol phospholipase D (gpld1 gene)
1605	10533	AI058430	BBB		ESTs, Highly similar to HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-17 [R.norvegicus]
1620	8584	AI058911	A, B, EEE, MMM		ESTs, Weakly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus]
1667	9067	AI070087	FFF, General Core Tox Markers, General Alternate		ESTs, Weakly similar to NUCL_RAT Nucleolin (Protein C23) [R.norvegicus]
1689	26184	AI070784	II		ESTs, Weakly similar to OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
1704	7775	AI071481	D	CCCTC-binding factor (zinc finger protein)	CCCTC-binding factor (zinc finger protein)
1721	3912	AI072035	Z, AA		ESTs, Weakly similar to JE0343 terf protein - rat [R.norvegicus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1723	9191	AI072107	A, B, OO, FFF, GGG, HHH, OOO, General Core Tox Markers		ESTs, Weakly similar to 2008147B protein RAKc [Rattus norvegicus] [R.norvegicus]
1727	5021	AI072308	RR		ESTs, Weakly similar to DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus] [R.norvegicus]
1737	1501	AI072634	A, I, W, PP, QQ, VV, FFF, GGG, General Core Tox Markers		Rattus norvegicus cytokeratin-18 mRNA, partial cds
1766	10573	AI101003	M		ESTs, Weakly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus]
1788	18642	AI102023	S		Rattus norvegicus mRNA for ribosomal protein L35
1803	5967	AI102520	EEE, MMM		ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus]
1803	5969	AI102520	EEE, MMM		ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus]
1813	23538	AI102727	A, B, Q, R	solute carrier family 20 (phosphate transporter), member 1	solute carrier family 20 (phosphate transporter), member 1
1815	17850	AI102750	GGG		ESTs, Weakly similar to JQ0866 T-complex protein 1 - rat [R.norvegicus]
1818	4898	AI102879	Q, R		ESTs, Weakly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus]
1819	11655	AI102881	T		ESTs, Weakly similar to I60486 gene trg protein - rat (fragment) [R.norvegicus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1830	3279	AI103224	U, LL, RRR, SSS, UUU		Rattus norvegicus mRNA for carbonyl reductase/NADP-retinol dehydrogenase, complete cds
1836	14981	AI103396	N, MM, TTT		Rattus norvegicus CDK110 mRNA
1837	3905	AI103403	JJ, KK	polypyrimidine tract binding protein	polypyrimidine tract binding protein
1839	2961	AI103415	DD, EE, PP, QQ		ESTs, Weakly similar to ZF94_RAT Zinc finger protein 94 (Zfp-94) (Zinc finger protein Y1) (RLZF-Y) [R.norvegicus]
1860	1440	AI104139	WW	SH2-B PH domain containing signaling mediator 1	SH2-B PH domain containing signaling mediator 1
1867	18831	AI104357	S, T, W		ESTs, Highly similar to ACTB_HUMAN Actin, cytoplasmic 1 (Beta-actin) [R.norvegicus]
1881	24323	AI104798	DDD, LLL		ESTs, Moderately similar to GTM1_RAT Glutathione S-transferase YB1 (Chain 3) (GST M1-1) (GST class-Mu 1) [R.norvegicus]
1893	17770	AI105294	LL		ESTs, Weakly similar to ARF6_HUMAN ADP-ribosylation factor 6 [R.norvegicus]
1901	16718	AI111537	XX, YY		Rat mRNA for RT1.D beta chain, Rattus norvegicus Class II MHC RT1.D(u) beta chain precursor (RT1.D(u)) mRNA, complete cds
1926	4969	AI113008	V, BB, EEE, III, JJJ, MMM		ESTs, Weakly similar to vitronectin [Rattus norvegicus] [R.norvegicus]
1940	5559	AI136892	L		Rattus norvegicus mRNA for a novel kinesin-related protein, KIF1D
1952	7122	AI137468	E, PP, JJJ		ESTs, Weakly similar to GPV_RAT Platelet glycoprotein V precursor (GPV) (CD42D) [R.norvegicus]
1977	14259	AI145037	PP, QQ		ESTs, Weakly similar to KEAP_RAT Kelch-like ECH-associated protein 1 (Cytosolic inhibitor of Nrf2) (INrf2) [R.norvegicus]
1981	2917	AI145614	S, UUU		ESTs, Weakly similar to S57449 fusca protein homolog - rat [R.norvegicus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1996	17812	AI169075	PPP, QQQ	HMm:glutathione transferase zeta 1 (maleylacetoacetate isomerase)	ESTs, Weakly similar to GTO1_RAT Glutathione transferase omega 1 (GSTO 1-1) (Glutathione-dependent dehydroascorbate reductase) [R.norvegicus]
1998	1335	AI169105	PPP, QQQ		ESTs, Weakly similar to PON1_RAT Serum paraoxonase/arylesterase 1 (PON 1) (Serum aryldiacylphosphatase 1) (A-esterase 1) (Aromatic esterase 1) [R.norvegicus]
2015	5716	AI169347	RR		ESTs, Weakly similar to S70642 ubiquitin ligase Nedd4 - rat (fragment) [R.norvegicus]
2043	18671	AI170270	FF		Rattus norvegicus transcription factor IIIA mRNA, partial cds
2054	11585	AI170502	PP, QQ, YY	HMm:glycogen synthase 3, brain	ESTs, Weakly similar to A35362 UDPglucose--glycogen glucosyltransferase (EC 2.4.1.11), hepatic - rat [R.norvegicus]
2055	13361	AI170516	E, NN, OO		ESTs, Weakly similar to 1917150A collagen:SUBUNIT=alpha1:ISOTYPE=VIII [Rattus norvegicus] [R.norvegicus]
2067	5968	AI170692	TT		ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus]
2097	18837	AI171583	G		ESTs, Weakly similar to I56246 lipopolysaccharide binding protein - rat [R.norvegicus]
2106	5339	AI171727	MM, III, JJJ, KKK, TTT		ESTs, Weakly similar to 1617160A phenylethanolamine N-methyltransferase [Rattus norvegicus] [R.norvegicus]
2141	21564	AI172301	E	HMm:ubiquitin-conjugating enzyme E2L 3	ESTs, Weakly similar to ubiquitin-conjugating enzyme E2D 2 [Rattus norvegicus] [R.norvegicus]
2144	23390	AI172328	G, GGG	RNA binding protein p45AUF1	RNA binding protein p45AUF1
2145	23325	AI172405	D		ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2148	23157	AI172489	Q, R		ESTs, Moderately similar to STRN_RAT Striatin [R.norvegicus]
2159	2895	AI175095	VV		ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) [R.norvegicus]
2166	4445	AI175466	N		ESTs, Weakly similar to RASH_RAT TRANSFORMING PROTEIN P21/H-RAS-1 (C-H-RAS) [R.norvegicus]
2167	3418	AI175475	MM, TTT, General Core Tox Markers		ESTs, Highly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27) [R.norvegicus]
2178	23519	AI175935	UU		R.norvegicus myr3 mRNA for myosin I heavy chain
2197	20823	AI176302	XX, YY		ESTs, Highly similar to UBIM_RAT UBIQUITIN-LIKE PROTEIN FUBI [R.norvegicus]
2214	16518	AI176546	H, T, II	HMm:heat shock protein, 86 kDa 1	ESTs, Moderately similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
2216	2532	AI176590	General Core Tox Markers		ESTs, Weakly similar to S68418 protein phosphatase 1M chain M110 isoform - rat (fragment) [R.norvegicus]
2251	14384	AI177096	JJ, KK, NN, OO, EEE, HHH, MMM	HMm:adenine phosphoribosyl transferase	ESTs, Highly similar to APT_RAT ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT) [R.norvegicus]
2258	1169	AI177161	GG, HH, II, FFF, KKK	NF-E2-related factor 2	NF-E2-related factor 2
2258	1170	AI177161	J, GG, HH, KKK	NF-E2-related factor 2	NF-E2-related factor 2
2285	6189	AI178027	G, CC, NN, OO, QQ, PPP, QQQ		ESTs, Weakly similar to GTP_RAT Glutathione S-transferase P (GST 7-7) (Chain 7) (GST class-pi) [R.norvegicus]
2290	18672	AI178189	H, General Alternate		Rattus norvegicus transcription factor IIIA mRNA, partial cds

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Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2295	19586	AI178239	LL		ESTs, Moderately similar to TVRTYP GTP-binding protein Rab1 - rat [R.norvegicus]
2315	3968	AI178764	RR, SS		ESTs, Weakly similar to ACDV_RAT Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial precursor (VLCAD) [R.norvegicus]
2320	1572	AI178828	D, V, NN, OO, PP, EEE, JJJ, MMM	eukaryotic translation initiation factor 4E binding protein 1	eukaryotic translation initiation factor 4E binding protein 1
2328	17890	AI179123	AA		ESTs, Weakly similar to NF-E2-related factor 2 [Rattus norvegicus] [R.norvegicus]
2332	14983	AI179150	F, S, HH, SS		Rattus norvegicus CDK110 mRNA
2355	16656	AI179634	YY		ESTs, Weakly similar to Gasz [Rattus norvegicus] [R.norvegicus]
2368	9032	AI179950	K, TT, LLL, SSS, UUU		ESTs, Highly similar to S60038 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha chain RC6-I - rat [R.norvegicus]
2372	6455	AI179984	XX, YY, PPP, QQQ		ESTs, Weakly similar to CPI3_RAT CONTRAPSIN-LIKE PROTEASE INHIBITOR 3 PRECURSOR (CPI-23) (SERINE PROTEASE INHIBITOR 1) (SPI-1) [R.norvegicus]
2373	17349	AI179987	AAA		ESTs, Highly similar to HG17_RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-17 [R.norvegicus]
2376	12568	AI180044	RR		ESTs, Moderately similar to S21348 probable pol polyprotein-related protein 4 - rat [R.norvegicus]
2377	19828	AI180087	F		ESTs, Weakly similar to OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
2386	22835	AI180367	MM, TTT	small zinc finger-like protein	small zinc finger-like protein
2387	1455	AI180373	W	mitogen activated protein kinase kinase 1	mitogen activated protein kinase kinase kinase 1
2404	16801	AI227894	TT		ESTs, Weakly similar to S53358 ubiquitin-conjugating enzyme E2.17kB - rat [R.norvegicus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2407	12413	AI227953	D		ESTs, Weakly similar to K6A1_RAT Ribosomal protein S6 kinase alpha 1 (S6K-alpha 1) (90 kDa ribosomal protein S6 kinase 1) (p90-RSK 1) (Ribosomal S6 kinase 1) (RSK-1) (pp90RSK1) [R.norvegicus]
2423	9038	AI228419	T		ESTs, Weakly similar to A Chain A, Crystal Structure Of S-Glutathiolated Carbonic Anhydrase Iii [R.norvegicus]
2449	7892	AI229172	N		ESTs, Weakly similar to FIBA_RAT Fibrinogen alpha/alpha-E chain precursor [R.norvegicus]
2451	6604	AI229192	General Core Tox Markers		ESTs, Weakly similar to 2209311A coagulation factor X [Rattus norvegicus] [R.norvegicus]
2461	23858	AI229450	K, L		ESTs, Weakly similar to A57514 RNA helicase HEL117 - rat [R.norvegicus]
2467	23573	AI229595	D		ESTs, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat [R.norvegicus]
2476	12587	AI229979	V, III, JJJ, General Core Tox Markers		ESTs, Weakly similar to MOT2_RAT Monocarboxylate transporter 2 (MCT 2) [R.norvegicus]
2481	7650	AI230142	O, P		ESTs, Weakly similar to KUCR_RAT Kupffer cell receptor [R.norvegicus]
2483	18425	AI230208	OOO		ESTs, Weakly similar to 2208374A cis-Golgi/intermediate compartment protein [Rattus norvegicus] [R.norvegicus]
2507	11553	AI230765	BB, CC		ESTs, Weakly similar to coated vesicle membrane protein [Rattus norvegicus] [R.norvegicus]
2520	20845	AI231140	X, Y, AA, TT		ESTs, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat [R.norvegicus]
2520	20846	AI231140	N, XX, YY		ESTs, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat [R.norvegicus]

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Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2523	21816	AI231217	L		ESTs, Highly similar to S611_HUMAN Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha-1) [R.norvegicus]
2557	22542	AI232066	QQ, XX, YY	HMm:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to 3-phosphoglycerate dehydrogenase [Rattus norvegicus] [R.norvegicus]
2572	17566	AI232301	M		ESTs, Weakly similar to GABA(A) receptor-associated protein like 2; ganglioside expression factor 2 [Rattus norvegicus] [R.norvegicus]
2589	5602	AI232611	K, U, FF, BBB, RRR		ESTs, Weakly similar to MTE1_RAT Acyl coenzyme A thioester hydrolase, mitochondrial precursor (Very-long-chain acyl-CoA thioesterase) (MTE-I) [R.norvegicus]
2591	14070	AI232649	FF		ESTs, Weakly similar to ribosomal protein S27a [Rattus norvegicus] [R.norvegicus]
2599	2896	AI232957	VV		ESTs, Weakly similar to ROD_RAT Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1) [R.norvegicus]
2602	12873	AI232984	II		ESTs, Weakly similar to OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
2606	13377	AI233056	SS		ESTs, Weakly similar to ZF37_RAT Zinc finger protein 37 (Zfp-37) [R.norvegicus]
2609	3823	AI233147	FFF, GGG, HHH, General Core Tox Markers		ESTs, Weakly similar to HE47_RAT Probable ATP-dependent RNA helicase p47 [R.norvegicus]
2620	23296	AI233316	X, Y, LLL, UUU		ESTs, Weakly similar to ribosomal protein S23 [Rattus norvegicus] [R.norvegicus]
2626	3073	AI233494	JJ, KKK, NNN	Mk1 protein	Mk1 protein
2626	3074	AI233494	JJ	Mk1 protein	Mk1 protein
2626	3075	AI233494	F, JJ	Mk1 protein	Mk1 protein

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2636	13023	AI233740	VV	HMM: fibroblast growth factor regulated protein	Rattus norvegicus mRNA for aldose reductase-like protein
2669	14676	AI234615	E	melastatin like 2 protein	melastatin like 2 protein
2675	22609	AI234828	X, Y		ESTs, Weakly similar to S25644 Ig mu chain C region - rat (fragment) [R.norvegicus]
2696	18252	AI235497	II		ESTs, Highly similar to RL9_RAT 60S RIBOSOMAL PROTEIN L9 [R.norvegicus]
2697	14740	AI235511	Z, AA		ESTs, Weakly similar to ZF94_RAT Zinc finger protein 94 (Zfp-94) (Zinc finger protein Y1) (RLZF-Y) [R.norvegicus]
2701	3650	AI235738	S		ESTs, Weakly similar to T42751 sulfonylurea receptor 2 - rat [R.norvegicus]
2708	7307	AI235935	X, Y, UUU		ESTs, Weakly similar to C1TC_RAT C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase ; Methenyltetrahydrofolate cyclohydrolase ; Formyltetrahydrofolate synthetase] [R.norvegicus]
2709	22717	AI235948	M		ESTs, Highly similar to NIDO_RAT NIDOGEN (ENTACTIN) [R.norvegicus]
2714	7604	AI236039	OO	reticulocalbin	reticulocalbin
2726	13911	AI236262	Q, R		Rattus norvegicus epidermal Langerhans cell protein LCP1 mRNA, complete cds
2730	19298	AI236338	UUU		ESTs, Weakly similar to NHPX_RAT NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27) [R.norvegicus]
2734	17571	AI236484	XX, YY		Rattus norvegicus mRNA for hnRNP protein, partial
2735	14777	AI236565	V		Rattus norvegicus transcription factor IIIA mRNA, partial cds

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2750	16978	AI236777	K		ESTs, Weakly similar to dimethylarginine dimethylaminohydrolase 1; NG,NG dimethylarginine dimethylaminohydrolase [Rattus norvegicus] [R.norvegicus]
2760	21091	AI236972	O, P		ESTs, Weakly similar to DH11_RAT Corticosteroid 11-beta-dehydrogenase, isozyme 1 (11-DH) (11-beta-hydroxysteroid dehydrogenase 1) (11-beta-HSD1) [R.norvegicus]
2768	13513	AI237091	JJJ		ESTs, Weakly similar to sialyltransferase 3; sialyltransferase (N-acetylglucosaminide alpha 2,3-sialyltransferase) [Rattus norvegicus] [R.norvegicus]
2773	14827	AI237404	QQ		ESTs, Moderately similar to PKL2_RAT PROTEIN KINASE C-LIKE 2 (PROTEIN-KINASE C-RELATED KINASE 2) (PROTEASE-ACTIVATED KINASE 2) (PAK-2) [R.norvegicus]
2786	21043	AI237813	MM, TTT	HMM:MAP kinase-activated protein kinase 2	ESTs, Weakly similar to A34366 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat [R.norvegicus]
2788	3467	AI237835	E		ESTs, Moderately similar to MX11_RAT MAX interacting protein 1 (MX11 protein) [R.norvegicus]
2832	8106	AI639534	M, LL		ESTs, Weakly similar to ATS4_RAT ADAMTS-4 precursor (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1) [R.norvegicus]
2837	6601	AJ131902	S, Z, AA	growth arrest specific 7	growth arrest specific 7
2844	5050	D10655	UU, WW	dihydrolipoamide acetyltransferase	dihydrolipoamide acetyltransferase
2864	959	D38072	DD, EE	protein tyrosine phosphatase, non-receptor type 12	protein tyrosine phosphatase, non-receptor type 12

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2878	2744	D87991	T, UU, DDD, EEE, MMM		ESTs, Highly similar to JC5026 UDP-galactose transporter related protein 1 - rat [R.norvegicus]
2885	238	E03859	VV	RAB11a, member RAS oncogene family	RAB11a, member RAS oncogene family
2886	62	E06822	A, B, P, General Core Tox Markers, General Alternate	20 alpha-hydroxysteroid dehydrogenase	20 alpha-hydroxysteroid dehydrogenase
2887	930	E12159	RR	130kDa-Ins(1,4,5)P3 binding protein	130kDa-Ins(1,4,5)P3 binding protein
2900	9745	H31847	Q, R		Rattus norvegicus dynein light intermediate chain 1 mRNA, complete cds
2903	3815	H31907	FFF, GGG	G protein pathway suppressor 1	G protein pathway suppressor 1
2952	107	L14001	XX, YY, JJJ		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
2953	108	L14002	L, MM, DDD, TTT		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
2955	109	L14004	M, N, V, SS, TT, DDD		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
2960	24518	L19927	GG	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1
2966	1373	L24907	L	calcium/calmodulin-dependent protein kinase I	calcium/calmodulin-dependent protein kinase I
2971	1791	L28801	RR, OOO	general transcription factor III C 1	general transcription factor III C 1
2972	1695	L35921	XX, YY, PPP, QQQ	G-protein gamma 8 subunit	G-protein gamma 8 subunit
2982	17883	M11851	PP, QQ, III, JJJ		Rat heart myosin light chain 2 (MLC2) mRNA, 3' end

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3005	1540	M25073	BB, CC, II, NNN, General Alternate	alanyl (membrane) aminopeptidase	alanyl (membrane) aminopeptidase
3017	17211	M34331	DDD		Rattus norvegicus mRNA for ribosomal protein L35
3017	26030	M34331	F, DDD		Rattus norvegicus mRNA for ribosomal protein L35
3028	24662	M59786	V	Ca channel, voltage-dependent, L type, alpha 1c subunit	Ca channel, voltage-dependent, L type, alpha 1c subunit
3035	239	M75153	D	RAB11a, member RAS oncogene family	RAB11a, member RAS oncogene family
3035	240	M75153	FF, LL	RAB11a, member RAS oncogene family	RAB11a, member RAS oncogene family
3054	1410	M96548	WW	zinc finger protein 354A	zinc finger protein 354A
3072	20305	NM_012532	N, V	Ceruloplasmin (ferroxidase) (Cp), mRNA. 11/2002 Length = 3700	R.norvegicus mRNA for bilitranslocase
3101	18726	NM_012645	F, M, DDD, LLL, RRR, UUU, General Alternate	RT1 class Ib gene (RT1Aw2), mRNA. 11/2002 Length = 1540	Rattus norvegicus MHC class Ib RT1.S3 (RT1.S3) mRNA, partial cds
3113	7101	NM_012679	II, TT	clusterin (Clu), mRNA. 10/2002 Length = 1638	Clusterin
3119	18718	NM_012695	X, Y	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA) -preferring, member 1
3134	8829	NM_012749	FFF, General Core Tox Markers	Nucleolin (Ncl), mRNA. 11/2002 Length = 2142	Nucleolin
3138	721	NM_012780	RR	Aryl hydrocarbon receptor nuclear translocator 1 (Arnt1), mRNA. 11/2000 Length = 2431	Aryl hydrocarbon receptor nuclear translocator 1

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3183	19108	NM_012963	V	high mobility group box 1 (Hmgb1), mRNA. 10/2002 Length = 1225	High mobility group 1
3183	19109	NM_012963	JJ, KK	high mobility group box 1 (Hmgb1), mRNA. 10/2002 Length = 1225	High mobility group 1
3183	19110	NM_012963	JJ, KK, PP, QQ, HHH	high mobility group box 1 (Hmgb1), mRNA. 10/2002 Length = 1225	High mobility group 1
3215	8898	NM_013087	G, H, J	CD81 antigen (target of antiproliferative antibody 1) (Cd81), mRNA. 11/2000 Length = 1303	CD81 antigen (target of antiproliferative antibody 1)
3215	8899	NM_013087	G, H, I, J, S, SSS, UUU	CD81 antigen (target of antiproliferative antibody 1) (Cd81), mRNA. 11/2000 Length = 1303	CD81 antigen (target of antiproliferative antibody 1)
3215	8900	NM_013087	PPP, QQQ	CD81 antigen (target of antiproliferative antibody 1) (Cd81), mRNA. 11/2000 Length = 1303	CD81 antigen (target of antiproliferative antibody 1)
3232	16448	NM_013197	M, T	Aminolevulinate synthase 2, delta (Alas2), mRNA. 11/2000 Length = 1899	Aminolevulinate synthase 2, delta
3236	20864	NM_013215	G, K, S, X, JJ, KK, NN, DDD, EEE, GGG, HHH, MMM	aflatoxin B1 aldehyde reductase (Afar), mRNA. 11/2002 Length = 1272	aflatoxin B1 aldehyde reductase
3289	18925	NM_017147	Z, AA, HH	cofilin 1 (Cfl1), mRNA. 11/2002 Length = 1039	Bone morphogenetic protein 6
3290	13392	NM_017148	T	cysteine rich protein 1 (Csrp1), mRNA. 1/2002 Length = 1403	cysteine rich protein 1
3337	16182	NM_017313	JJ, KK	rabin 3 (RABIN3), mRNA. 11/2000 Length = 1407	rabin 3

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3346	20848	NM_017343	A, B, P	myosin regulatory light chain (MRLCB), mRNA. 6/2001 Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
3346	20849	NM_017343	A, TT	myosin regulatory light chain (MRLCB), mRNA. 6/2001 Length = 1139	Rat mRNA for myosin regulatory light chain (RLC)
3390	24883	NM_019293	OO, General Core Tox Markers	carbonic anhydrase 5 (Ca5a), mRNA. 11/2002 Length = 1201	carbonic anhydrase 5
3393	1099	NM_019303	W, CC, General Core Tox Markers	Cytochrome P450, subfamily IIF, polypeptide 1 (Cyp2f1), mRNA. 11/2000 Length = 1768	Cytochrome P450, subfamily IIF, polypeptide 1
3395	16330	NM_019331	S	Proprotein convertase subtilisin/kexin type 3 (paired basic amino acid cleaving enzyme, furin, membrane associated receptor protein) (Pcsk3), mRNA. 10/2002 Length = 4259	Paired basic amino acid cleaving enzyme (furin)
3395	16331	NM_019331	S, W	Proprotein convertase subtilisin/kexin type 3 (paired basic amino acid cleaving enzyme, furin, membrane associated receptor protein) (Pcsk3), mRNA. 10/2002 Length = 4259	Paired basic amino acid cleaving enzyme (furin)
3396	5264	NM_019340	JJ, KK	regulator of G-protein signaling 3 (Rgs3), mRNA. 11/2002 Length = 3722	regulator of G-protein signaling 3
3402	23226	NM_019360	PP, QQ	cytochrome oxidase subunit VIc (Cox6c), mRNA. 11/2000 Length = 418	cytochrome oxidase subunit VIc

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3418	18705	NM_020103	D	Ly6-C antigen gene (Ly6c), mRNA. 11/2000 Length = 405	Ly6-C antigen gene
3425	18724	NM_021585	F	surface protein MCA-32 (Mca32), mRNA. 11/2002 Length = 1659	Rattus norvegicus MHC class Ib RT1.S3 (RT1.S3) mRNA, partial cds
3427	17340	NM_021594	E, BB, CC	ERM-binding phosphoprotein (LOC59114), mRNA. 11/2002 Length = 1492	ERM-binding phosphoprotein
3447	20248	NM_022205	III, JJJ	Chemokine receptor (LCR1) (Cxcr4), mRNA. 5/2002 Length = 1050	Chemokine receptor (LCR1)
3447	20249	NM_022205	SS, EEE, MMM	Chemokine receptor (LCR1) (Cxcr4), mRNA. 5/2002 Length = 1050	Chemokine receptor (LCR1)
3464	15931	NM_022385	T	ADP-ribosylation factor-like 1 (Arl1), mRNA. 11/2002 Length = 893	ADP-ribosylation factor-like 1
3467	22413	NM_022392	A, B	growth response protein (CL-6) (LOC64194), mRNA. 12/2000 Length = 2410	growth response protein (CL-6)
3468	23178	NM_022395	D, SS	mitochondrial processing peptidase beta (Pmpcb), mRNA. 12/2000 Length = 1570	mitochondrial processing peptidase beta
3469	23300	NM_022398	W, DD, EE, BBB, CCC	2-oxoglutarate carrier (LOC64201), mRNA. 12/2000 Length = 946	2-oxoglutarate carrier
3471	1069	NM_022402	V, CC, LL, DDD	acidic ribosomal protein P0 (Arbp), mRNA. 12/2000 Length = 1046	acidic ribosomal protein P0
3474	2236	NM_022512	BBB, CCC	short chain acyl-coenzyme A dehydrogenase (Acads), mRNA. 12/2000 Length = 1749	short chain acyl-coenzyme A dehydrogenase

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3476	162	NM_022516	VV	polypyrimidine tract binding protein (Ptb), mRNA. 11/2002 Length = 2723	malate dehydrogenase mitochondrial
3476	3900	NM_022516	VV	polypyrimidine tract binding protein (Ptb), mRNA. 11/2002 Length = 2723	polypyrimidine tract binding protein
3481	8097	NM_022536	BB, CC	cyclophilin B (Ppib), mRNA. 12/2000 Length = 840	cyclophilin B
3482	8597	NM_022538	BB, CC, NN, OO, QQ, ZZ, AAA	phosphatidate phosphohydrolase type 2a (Ppap2a), mRNA. 5/2002 Length = 871	phosphatidate phosphohydrolase type 2a
3485	9296	NM_022541	LLL	small zinc finger-like protein DDP2 (Ddp2), mRNA. 12/2000 Length = 494	small zinc finger-like protein DDP2
3486	9541	NM_022542	W, II, QQ	rhoB gene (Arhb), mRNA. 12/2000 Length = 2183	rhoB gene
3488	12192	NM_022545	M, HH	phosphoribosylpyrophosphate synthetase-associated protein (39 kDa) (Prpsap1), mRNA. 12/2000 Length = 1581	phosphoribosylpyrophosphate synthetase-associated protein (39 kDa)
3488	12193	NM_022545	M, EE	phosphoribosylpyrophosphate synthetase-associated protein (39 kDa) (Prpsap1), mRNA. 12/2000 Length = 1581	phosphoribosylpyrophosphate synthetase-associated protein (39 kDa)
3489	12422	NM_022546	H, T, DD, EE, KKK	Death-associated like kinase (Dapkl), mRNA. 12/2000 Length = 1514	Death-associated like kinase
3489	12423	NM_022546	D, DD, EE, KKK	Death-associated like kinase (Dapkl), mRNA. 12/2000 Length = 1514	Death-associated like kinase

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3490	12606	NM_022547	O, P, NN, OO, VV, EEE, III, JJJ, MMM, General Alternate	10-formyltetrahydrofolate dehydrogenase (Fthfd), mRNA. 12/2000 Length = 3109	10-formyltetrahydrofolate dehydrogenase
3501	12542	NM_022647	A, B	histone 2b (H2b), mRNA. 1/2001 Length = 378	ESTs, Highly similar to 0506206A histone H2B [Rattus norvegicus] [R.norvegicus]
3502	24442	NM_022667	JJ	Matrin F/G (Matr1), mRNA. 1/2001 Length = 2748	Matrin F/G
3514	24458	NM_022706	L, LL	GABA(A) receptor-associated protein like 2 (Gabarapl2), mRNA. 5/2002 Length = 975	GABA(A) receptor-associated protein like 2
3520	6891	NM_022934	C, Q, R, DD, EE	DnaJ-like protein (Hsj2), mRNA. 11/2002 Length = 1610	DnaJ-like protein
3526	20681	NM_022952	G, H	clathrin-associated protein 17 (Ap2s1), mRNA. 1/2001 Length = 797	clathrin-associated protein 17
3538	15367	NM_024149	X, Y	ADP-ribosylation factor 5 (Arf5), mRNA. 11/2002 Length = 1058	ADP-ribosylation factor 5
3540	21696	NM_024152	O, P, Q, R	ADP-ribosylation factor 6 (Arf6), mRNA. 11/2002 Length = 995	ADP-ribosylation factor 6
3559	23387	NM_024404	E	RNA binding protein p45AUF1 (Hnrpd), mRNA. 3/2001 Length = 1240	RNA binding protein p45AUF1
3559	23388	NM_024404	C	RNA binding protein p45AUF1 (Hnrpd), mRNA. 3/2001 Length = 1240	RNA binding protein p45AUF1
3559	25682	NM_024404	MM, TTT	RNA binding protein p45AUF1 (Hnrpd), mRNA. 3/2001 Length = 1240	RNA binding protein p45AUF1

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3572	15186	NM_030861	DD, EE	N-acetylglucosaminyltransferase I (Mgat1), mRNA. 4/2001 Length = 2546	N-acetylglucosaminyltransferase I
3572	15187	NM_030861	FF, TT, NNN	N-acetylglucosaminyltransferase I (Mgat1), mRNA. 4/2001 Length = 2546	N-acetylglucosaminyltransferase I
3572	15188	NM_030861	DD, EE, GG, OOO	N-acetylglucosaminyltransferase I (Mgat1), mRNA. 4/2001 Length = 2546	N-acetylglucosaminyltransferase I
3575	21801	NM_030987	ZZ, AAA	Guanine nucleotide-binding protein beta 1 (Gnb1), mRNA. 4/2002 Length = 2837	Guanine nucleotide-binding protein beta 1
3575	21802	NM_030987	O, P, VV, AAA	Guanine nucleotide-binding protein beta 1 (Gnb1), mRNA. 4/2002 Length = 2837	Guanine nucleotide-binding protein beta 1
3583	16561	NM_031020	DD, EE	p38 mitogen activated protein kinase (Mapk14), mRNA. 10/2002 Length = 3132	p38 mitogen activated protein kinase
3583	16562	NM_031020	E, T, DD	p38 mitogen activated protein kinase (Mapk14), mRNA. 10/2002 Length = 3132	p38 mitogen activated protein kinase
3583	16564	NM_031020	E, W, TT	p38 mitogen activated protein kinase (Mapk14), mRNA. 10/2002 Length = 3132	p38 mitogen activated protein kinase
3590	15138	NM_031051	G, H, Y	macrophage migration inhibitory factor (Mif), mRNA. 11/2002 Length = 551	macrophage migration inhibitory factor
3591	11899	NM_031052	OOO	mitochondrial intermediate peptidase (Mipep), mRNA. 11/2002 Length = 2337	mitochondrial intermediate peptidase

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3593	16104	NM_031058	D	mismatch repair protein (Msh2), mRNA. 11/2002 Length = 3002	mismatch repair protein
3593	16106	NM_031058	T	mismatch repair protein (Msh2), mRNA. 11/2002 Length = 3002	mismatch repair protein
3596	6348	NM_031077	PP, QQ	PCTAIRE-1 protein kinase, alternatively spliced (Pctk1), mRNA. 10/2002 Length = 3111	PCTAIRE-1 protein kinase, alternatively spliced
3604	20807	NM_031106	F, T, U, FFF	ribosomal protein L37 (Rpl37), mRNA. 11/2002 Length = 366	ribosomal protein L37
3612	23569	NM_031122	X, Y, BB, CC, DD, EE, KKK, NNN	suppression of tumorigenicity 13 (colon carcinoma) Hsp70-interacting protein (St13), mRNA. 4/2001 Length = 1694	suppression of tumorigenicity 13 (colon carcinoma) Hsp70-interacting protein
3616	15487	NM_031137	Q, R, PPP, QQQ	tripeptidylpeptidase II (Tpp2), mRNA. 4/2001 Length = 4566	tripeptidylpeptidase II
3616	15489	NM_031137	Q, R, PP, QQ, WW, ZZ, AAA	tripeptidylpeptidase II (Tpp2), mRNA. 4/2001 Length = 4566	tripeptidylpeptidase II
3617	17379	NM_031138	R, DD, EE, MM, WW, TTT, General Alternate	ubiquitin conjugating enzyme (LOC81816), mRNA. 4/2001 Length = 1737	ubiquitin conjugating enzyme
3619	21624	NM_031144	VV	cytoplasmic beta-actin (Actx), mRNA. 4/2001 Length = 1128	actin, beta
3619	21625	NM_031144	II	cytoplasmic beta-actin (Actx), mRNA. 4/2001 Length = 1128	actin, beta

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3621	15273	NM_031237	PPP, QQQ	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5) (Ube2d3), mRNA. 4/2001 Length = 1531	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)
3689	16178	NM_031785	T, V, JJ, KK	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1 (Atp6s1), mRNA. 5/2001 Length = 2089	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1
3696	17535	NM_031816	D	retinoblastoma binding protein 7 (Rbbp7), mRNA. 11/2002 Length = 1947	retinoblastoma binding protein 7
3698	23407	NM_031819	Q, R	FAT tumor suppressor (Drosophila) homolog (Fat), mRNA. 5/2001 Length = 14,746	FAT tumor suppressor (Drosophila) homolog
3705	10267	NM_031838	LL	ribosomal protein S2 (Rps2), mRNA. 11/2002 Length = 817	ribosomal protein S2
3705	10269	NM_031838	CC	ribosomal protein S2 (Rps2), mRNA. 11/2002 Length = 817	ribosomal protein S2
3706	10947	NM_031839	PP, QQ	arachidonic acid epoxygenase (Cyp2c23), mRNA. 11/2002 Length = 2153	arachidonic acid epoxygenase
3706	10949	NM_031839	FF, EEE, MMM	arachidonic acid epoxygenase (Cyp2c23), mRNA. 11/2002 Length = 2153	arachidonic acid epoxygenase
3721	19768	NM_031986	O, R	syntenin (Sdcbp), mRNA. 5/2001 Length = 2077	syntenin

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Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3738	24419	NM_033539	Y	eukaryotic translation elongation factor 1 alpha 2 (Eef1a2), mRNA. 11/2002 Length = 1404	eukaryotic translation elongation factor 1 alpha 1
3766	14670	NM_053439	UUU	RAN, member RAS oncogene family (Ran), mRNA. 11/2002 Length = 1084	RAN, member RAS oncogene family
3781	18401	NM_053532	K, X, Y, UUU	proteasome (prosome, macropain) subunit, beta type, 7 (Psmb7), mRNA. 11/2001 Length = 993	proteasome (prosome, macropain) subunit, beta type, 7
3796	21445	NM_053587	W, BB	S100 calcium-binding protein A9 (calgranulin B) (S100a9), mRNA. 11/2001 Length = 494	S100 calcium-binding protein A9 (calgranulin B)
3799	20902	NM_053593	C, G, H	cyclin-dependent kinase 4 (Cdk4), mRNA. 11/2001 Length = 1232	cyclin-dependent kinase 4
3820	24728	NM_053753	X, Y, EEE, MMM	Kupffer cell receptor (Kcfr), mRNA. 11/2001 Length = 1888	Kupffer cell receptor
3821	10909	NM_053756	U	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (Atp5g3), mRNA. 11/2001 Length = 723	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
3826	14016	NM_053770	A	Arg/Abl-interacting protein ArgBP2 (Argbp2), mRNA. 11/2001 Length = 6331	Arg/Abl-interacting protein ArgBP2
3826	14017	NM_053770	A	Arg/Abl-interacting protein ArgBP2 (Argbp2), mRNA. 11/2001 Length = 6331	Arg/Abl-interacting protein ArgBP2

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3830	19827	NM_053806	PP, QQ, YY, PPP, QQQ	potassium channel, subfamily K, member 6 (TWIK-2) (Kcnk6), mRNA. 11/2001 Length = 2243	ESTs, Weakly similar to OZF_RAT Zinc finger protein OZF (POZF-1) [R.norvegicus]
3835	20421	NM_053821	O, P, W	v-ral simian leukemia viral oncogene homolog B (ras related) (Ralb), mRNA. 11/2001 Length = 2074	v-ral simian leukemia viral oncogene homolog B (ras related)
3842	1570	NM_053857	O, P	eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1), mRNA. 11/2002 Length = 843	eukaryotic translation initiation factor 4E binding protein 1
3842	1571	NM_053857	W	eukaryotic translation initiation factor 4E binding protein 1 (Eif4ebp1), mRNA. 11/2002 Length = 843	eukaryotic translation initiation factor 4E binding protein 1
3843	18357	NM_053864	N	valosin-containing protein (Vcp), mRNA. 11/2002 Length = 2870	valosin-containing protein
3843	18358	NM_053864	LL	valosin-containing protein (Vcp), mRNA. 11/2002 Length = 2870	valosin-containing protein
3847	1453	NM_053887	II	mitogen activated protein kinase kinase 1 (Map3k1), mRNA. 11/2001 Length = 5180	mitogen activated protein kinase kinase kinase 1
3852	4588	NM_053923	II, General Alternate	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide (Pik3c2g), mRNA. 11/2001 Length = 5990	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide
3855	16190	NM_053961	U, FF, BBB	endoplasmic reticulum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	ESTs, Weakly similar to F Chain F, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 [R.norvegicus]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3857	16546	NM_053965	U, FF, LL, BBB, CCC, RRR, SSS	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (Slc25a20), mRNA. 11/2001 Length = 1231	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
3857	16547	NM_053965	RRR, SSS	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (Slc25a20), mRNA. 11/2001 Length = 1231	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
3858	6357	NM_053969	S	G protein pathway suppressor 1 (Gps1), mRNA. 11/2001 Length = 1794	G protein pathway suppressor 1
3861	15324	NM_053979	R	ADP-ribosylation factor-like 5 (Arl5), mRNA. 11/2001 Length = 2717	ADP-ribosylation factor-like 5
3867	17739	NM_053995	General Alternate	3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (Bdh), mRNA. 11/2001 Length = 1420	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)
3869	24655	NM_053998	RR	mel transforming oncogene (derived from cell line NK14)-RAB8 homolog (Mel), mRNA. 11/2001 Length = 840	mel transforming oncogene (derived from cell line NK14)-RAB8 homolog
3876	16043	NM_057100	N, Z, AA, JJ, KK, UUU	growth arrest specific 6 (Gas6), mRNA. 11/2002 Length = 2573	ESTs, Highly similar to growth arrest specific 6 [Rattus norvegicus] [R.norvegicus]
3877	17709	NM_057101	E, J, W, UU, III, JJJ, KKK, NNN	Cytochrome P450, subfamily XXI (steroid 21-hydroxylase) (Cyp21), mRNA. 10/2002 Length = 1964	Tenascin X

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLGC ID No.	Genbank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3881	23307	NM_057119	HHH	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10 (Sfrs10), mRNA. 11/2001 Length = 1978	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
3881	23309	NM_057119	VV	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10 (Sfrs10), mRNA. 11/2001 Length = 1978	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
3882	921	NM_057125	KKK	peroxisomal biogenesis factor 6 (Pex6), mRNA. 11/2001 Length = 3169	peroxisomal biogenesis factor 6
3887	15838	NM_057143	KK	fertility protein SP22 (SP22), mRNA. 11/2001 Length = 1097	fertility protein SP22
3887	15839	NM_057143	Q, R, JJ, KK, NNN	fertility protein SP22 (SP22), mRNA. 11/2001 Length = 1097	fertility protein SP22
3890	17477	NM_057194	W	phospholipid scramblase 1 (Plscr1), mRNA. 11/2002 Length = 1569	phospholipid scramblase 1
3893	14126	NM_057208	VV	tropomyosin 3, gamma (Tpm3), mRNA. 11/2001 Length = 1101	R.norvegicus mRNA for tropomyosin isoform 6, tropomyosin 3, gamma
3914	9952	NM_080902	C, General Alternate	hypoxia induced gene 1 (Hig1), mRNA. 1/2002 Length = 355	hypoxia induced gene 1
3922	18810	NM_130430	OOO	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 (Psm9), mRNA. 1/2002 Length = 1448	mitochondrial H ⁺ -ATP synthase alpha subunit

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3928	7863	NM_130823	II	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa (Atp6l), mRNA. 2/2002 Length = 1082	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa
3928	7865	NM_130823	OOO	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa (Atp6l), mRNA. 2/2002 Length = 1082	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16 kDa
3942	10660	NM_133423	WW	splicing factor YT521-B (YT521), mRNA. 3/2002 Length = 2968	splicing factor YT521-B
3945	9571	NM_133540	AA	natural killer cell group 7 sequence (Nkg7), mRNA. 11/2002 Length = 813	natural killer cell group 7 sequence
3950	745	NM_133567	HH	centaurin, alpha 1 (Centa1), mRNA. 3/2002 Length = 1281	centaurin, alpha 1
3952	1183	NM_133578	Q	MAP-kinase phosphatase (cpg21) (Cpg21), mRNA. 3/2002 Length = 2436	MAP-kinase phosphatase (cpg21)
3953	15029	NM_133583	NN, FFF, General Core Tox Markers	N-myc downstream-regulated gene 2 (Ndr2), mRNA. 3/2002 Length = 1998	N-myc downstream-regulated gene 2
3953	16993	NM_133583	A, B, H, NN, OO, FFF, III, JJJ, PPP, QQQ, General Core Tox Markers	N-myc downstream-regulated gene 2 (Ndr2), mRNA. 3/2002 Length = 1998	N-myc downstream-regulated gene 2

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3954	4312	NM_133586	M, X, TT, LLL, SSS, UUU	carboxylesterase 2 (intestine, liver) (Ces2), mRNA. 3/2002 Length = 1902	carboxylesterase 2 (intestine, liver)
3965	23321	NM_134407	C, K, W, BB, CC, NN, OO, GGG, III, JJJ, LLL	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (Akr7a2), mRNA. 3/2002 Length = 1272	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
3965	23322	NM_134407	L, BB, CC, NN, OO	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (Akr7a2), mRNA. 3/2002 Length = 1272	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
3974	61	NM_138510	General Alternate	20 alpha-hydroxysteroid dehydrogenase (LOC171516), mRNA. 4/2002 Length = 1215	20 alpha-hydroxysteroid dehydrogenase
3977	21439	NM_138533	S, General Core Tox Markers, General Alternate	F-spondin (LOC171569), mRNA. 4/2002 Length = 2325	F-spondin
3980	16922	NM_138549	S, Z, AA, General Alternate	synaptic glycoprotein SC2 (SC2), mRNA. 4/2002 Length = 1178	synaptic glycoprotein SC2
3980	25479	NM_138549	A, B, S, Z, AA, FF, General Alternate	synaptic glycoprotein SC2 (SC2), mRNA. 4/2002 Length = 1178	synaptic glycoprotein SC2
3985	5719	NM_138871	DD, EE	tudor repeat associator with PCTAIRE 2 (Pctaire2bp), mRNA. 4/2002 Length = 3874	tudor repeat associator with PCTAIRE 2
3990	5656	NM_138885	CCC	golgi-associated protein GCP360 (LOC192243), mRNA. 4/2002 Length = 10,170	golgi-associated protein GCP360

TABLE 1					
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Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3991	3015	NM_138895	T	polyubiquitin (Loc192255), mRNA. 4/2002 Length = 1115	polyubiquitin
3992	7635	NM_138896	K, M, ZZ, AAA	rotein carrying the RING-H2 sequence motif (Neurodap1), mRNA. 4/2002 Length = 4758	rotein carrying the RING-H2 sequence motif
3992	7636	NM_138896	ZZ, AAA	rotein carrying the RING-H2 sequence motif (Neurodap1), mRNA. 4/2002 Length = 4758	rotein carrying the RING-H2 sequence motif
3994	18083	NM_138907	BBB, RRR, SSS	mitochondrial acyl-CoA thioesterase 1 (Mte1), mRNA. 4/2002 Length = 1711	mitochondrial acyl-CoA thioesterase 1
3995	21915	NM_138910	Z, AA, OO	defender against cell death 1 (Dad1), mRNA. 11/2002 Length = 342	defender against cell death 1
3995	21916	NM_138910	OO	defender against cell death 1 (Dad1), mRNA. 11/2002 Length = 342	defender against cell death 1
3996	11840	NM_138911	H, Z, AA, DD	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (Stip1), mRNA. 4/2002 Length = 1632	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)
4001	16444	NM_139096	O, P, UU, VV	peptidylprolyl isomerase C-associated protein (Ppicap), mRNA. 5/2002 Length = 2151	peptidylprolyl isomerase C-associated protein
4005	17854	NM_139103	O, P	CD48 antigen (Cd48), mRNA. 5/2002 Length = 1422	CD48 antigen
4007	14463	NM_139110	Z, AA	G protein-coupled hepta-helical receptor Ig-Hepta (Ig-Hepta), mRNA. 5/2002 Length = 4951	G protein-coupled hepta-helical receptor Ig-Hepta

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4008	15239	NM_139114	M, V, FFF, General Core Tox Markers	ribosomal protein L15 (Rpl15), mRNA. 5/2002 Length = 691	ribosomal protein L15
4013	19150	NM_139324	V, UU, General Alternate	pincher (Ehd4), mRNA. 11/2002 Length = 3438	pinocytic chaperone; similar to Homo sapiens EHD4 and mouse Past2
4017	4949	NM_139338	D	Na+/Pi-cotransporter type IIc (LOC246234), mRNA. 11/2002 Length = 2075	Rattus norvegicus mRNA for Na+/Pi-cotransporter type IIc, complete cds
4018	6735	NM_139341	K	peptide/histidine transporter PHT2 (Pht2), mRNA. 11/2002 Length = 1979	Rattus norvegicus mRNA for peptide histidine transporter 1 homolog rPHT2, complete cds
4020	15703	NM_144750	E, FFF, General Alternate	Lysophospholipase (LOC246266), mRNA. 11/2002 Length = 2525	Rattus norvegicus mRNA for Lysophospholipase, complete cds
4021	11494	NM_144755	Q, W	kinase (LOC246273), mRNA. 11/2002 Length = 2004	ESTs, Weakly similar to A53621 AMP-activated protein kinase - rat [R.norvegicus]
4025	16345	NM_145724	RR	zinc finger protein Y1 (RLZF-Y) (Rlzf), mRNA. 11/2002 Length = 2472	Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds
4039	8278	NM_148892	Q, R	osteoclast stimulating factor 1 (Ostf1), mRNA. 11/2002 Length = 835	ESTs, Weakly similar to BRCA1-associated RING domain protein 1 [Rattus norvegicus] [R.norvegicus]
4044	20784	NM_153308	Z, AA, HH, WW	NMDA receptor glutamate-binding chain (Grina), mRNA. 10/2002 Length = 1742	ESTs, Moderately similar to S19586 N-methyl-D-aspartate receptor glutamate-binding chain - rat [R.norvegicus]
4071	18647	S69316	LL		ESTs, Weakly similar to HS9B_RAT Heat shock protein HSP 90-beta (HSP 84) [R.norvegicus]
4076	1460	S76054	G, H, VV, General Alternate		ESTs, Highly similar to K2C8_RAT Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin endo A) [R.norvegicus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4085	110	U01145	D, F		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
4086	347	U01914	Q, WW	A kinase anchor protein 8	A kinase anchor protein 8
4088	111	U02506	MM, SS, NNN, TTT		Rattus norvegicus clone 15 polymeric immunoglobulin receptor mRNA, 3'UTR microsatellite repeats
4091	2010	U05675	E, S, MM, KKK, TTT		Rattus norvegicus Sprague-Dawley fibrinogen B beta chain mRNA, complete cds
4094	2686	U08214	Q, R		ESTs, Highly similar to 2019405A upstream regulator element-binding protein [Rattus norvegicus] [R.norvegicus]
4100	22039	U13176	Q, R, ZZ, AAA		Rattus norvegicus clone ubc2e ubiquitin conjugating enzyme (E217kB) mRNA, complete cds
4105	1949	U19614	XX, YY		Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds, Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds
4114	1558	U28504	GG, JJJ, NNN	solute carrier family 17 vesicular glutamate transporter), member 1	solute carrier family 17 vesicular glutamate transporter), member 1
4114	1559	U28504	FF, GG, NNN	solute carrier family 17 vesicular glutamate transporter), member 1	solute carrier family 17 vesicular glutamate transporter), member 1
4118	1478	U32314	M, VV, DDD, GGG, LLL, UUU, General Core Tox Markers	Pyruvate carboxylase	Pyruvate carboxylase

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4118	1479	U32314	M, X, VV, DDD, GGG, LLL, UUU, General Core Tox Markers	Pyruvate carboxylase	Pyruvate carboxylase
4120	154	U32681	NN, PP, EEE, MMM	deleted in malignant brain tumors 1	deleted in malignant brain tumors 1
4120	155	U32681	BB, CC, NN, PP, QQ, EEE, MMM	deleted in malignant brain tumors 1	deleted in malignant brain tumors 1
4127	18038	U39943	CC, NN, OO, BBB, CCC, General Alternate		Rattus norvegicus cytochrome P450 pseudogene (CYP2J3P1) mRNA
4128	18036	U40004	G, H, OO, General Alternate		Rattus norvegicus cytochrome P450 pseudogene (CYP2J3P1) mRNA
4129	1623	U41164	N	Cys2/His2 zinc finger protein (rKr1)	Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds
4132	2685	U47312	Q, R, PP, QQ		ESTs, Highly similar to 2019405A upstream regulator element-binding protein [Rattus norvegicus] [R.norvegicus]
4134	734	U49055	C	CTD-binding SR-like protein rA8	CTD-binding SR-like protein rA8
4137	746	U51013	N, PP, QQ, XX, YY	centaurin, alpha 1	centaurin, alpha 1
4146	1439	U57391	WW	SH2-B PH domain containing signaling mediator 1	SH2-B PH domain containing signaling mediator 1
4156	904	U67082	DDD	Kruppel associated box (KRAB) zinc finger 1	Kruppel associated box (KRAB) zinc finger 1
4159	15516	U68544	N		Rattus norvegicus cyclophilin D mRNA, nuclear gene encoding mitochondrial protein, complete cds

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4169	1314	U75932	I, J, OOO, General Alternate	Protein kinase, cAMP dependent, regulatory, type 1	Protein kinase, cAMP dependent, regulatory, type 1
4179	9841	U94856	O, P, GG, PP, QQ, XX, YY	paraoxonase 1	paraoxonase 1
4179	9842	U94856	A, B, BB, CC, GG, HH, NN, OO, PP, QQ, BBB, CCC, HHH, PPP, QQQ	paraoxonase 1	paraoxonase 1
4184	20818	X02904	G	glutathione S-transferase, pi 2	glutathione S-transferase, pi 2
4186	1700	X03369	NN, UU		ESTs, Highly similar to TBB1_RAT TUBULIN BETA CHAIN (T BETA-15) [R.norvegicus], Rat mRNA for beta-tubulin T beta15
4196	19584	X13905	QQ, RR, UU		ESTs, Moderately similar to TVRTYP GTP-binding protein Rab1 - rat [R.norvegicus]
4231	1141	X59601	UU, KKK	plectin	plectin
4238	4441	X62146	II, JJ, KK, DDD, FFF, GGG, General Alternate		ESTs, Highly similar to RL11_HUMAN 60S ribosomal protein L11 [R.norvegicus]
4239	13646	X62166	G, H, JJ, KK, UU, GGG, HHH, General Alternate		ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) [R.norvegicus]
4241	15387	X62482	Z, AA, OO, JJJ, NNN		ESTs, Highly similar to R3RT25 ribosomal protein S25, cytosolic [validated] - rat [R.norvegicus]
4248	20844	X65228	General Alternate		ESTs, Highly similar to R3RT3A ribosomal protein L23a, cytosolic [validated] - rat [R.norvegicus]
4265	23302	X78949	Q, R, Z, AA, RR	prolyl 4-hydroxylase alpha subunit	prolyl 4-hydroxylase alpha subunit

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4270	537	X83231	D	pre-alpha-inhibitor, heavy chain 3	pre-alpha-inhibitor, heavy chain 3
4278	18031	X94551	RR	laminin, gamma 1	laminin, gamma 1
4286	3831	Y12635	O, P, Q, II, MM, VV, PPP, TTT	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta 56/58 kDa, isoform 2	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta 56/58 kDa, isoform 2
220	10157	AA819527	XX, YY	HHs:amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	ESTs, Highly similar to S23094 beta-amyloid protein precursor - rat [R.norvegicus]
1018	10155	AA956735	V	HHs:amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	ESTs, Highly similar to S23094 beta-amyloid protein precursor - rat [R.norvegicus]
2503	23013	AI230743	O, VV, HHH	actin-related protein 3	actin-related protein 3
4211	20872	X51707	F, K, II, JJ, KK, VV, EEE, FFF, GGG, MMM, General Alternate	ribosomal protein S19	ESTs, Highly similar to R3RT19 ribosomal protein S19, cytosolic [validated] - rat [R.norvegicus]
32	20843	AA799545	VV		ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) [R.norvegicus]
887	12301	AA944727	EE, PP, QQ, III, JJJ, NNN		ESTs, Weakly similar to A44437 regenerating liver inhibitory factor RL/IF-1 - rat [R.norvegicus]
1375	3693	AI011448	GG		ESTs, Highly similar to A49128 cell-fate determining gene Notch2 protein - rat [R.norvegicus]
1409	2250	AI012354	Q, R		ESTs, Highly similar to 0506206A histone H2B [Rattus norvegicus] [R.norvegicus]
1955	22598	AI137506	U, BB, EEE, MMM		ESTs, Weakly similar to A29035 thyroid hormone-regulated proteinase inhibitor - rat (fragment) [R.norvegicus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2165	6678	AI175454	Q, R		ESTs, Weakly similar to S44204 procollagen-proline dioxygenase (EC 1.14.11.2) alpha chain - rat [R.norvegicus]
2256	16175	AI177145	XX, YY		ESTs, Weakly similar to CAG7_RAT ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY) [R.norvegicus]
2506	20055	AI230762	V, EEE, MMM		ESTs, Weakly similar to A53742 calponin, acidic - rat [R.norvegicus]
2635	13294	AI233731	A, B, H, S, GGG, HHH		ESTs, Weakly similar to TCPA_RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) [R.norvegicus]
3409	18141	NM_019383	Y, JJ	ATP synthase subunit d (Atp5jd), mRNA. 11/2000 Length = 581	ATP synthase subunit d, ESTs, Moderately similar to T46317 hypothetical protein DKFZp434A0612.1 - human [H.sapiens]
3409	22727	NM_019383	GG	ATP synthase subunit d (Atp5jd), mRNA. 11/2000 Length = 581	ATP synthase subunit d
3511	19375	NM_022699	AA	ribosomal protein L30 (Rpl30), mRNA. 11/2002 Length = 392	EST, Moderately similar to R6RT30 ribosomal protein L30, cytosolic [validated] - rat [R.norvegicus]
3608	19161	NM_031111	WW	ribosomal protein S21 (Rps21), mRNA. 11/2002 Length = 359	ribosomal protein S21
3608	19162	NM_031111	CCC	ribosomal protein S21 (Rps21), mRNA. 11/2002 Length = 359	ribosomal protein S21
3862	15468	NM_053982	F	ribosomal protein S15a (Rps15a), mRNA. 11/2001 Length = 449	ribosomal protein S15a
3862	19544	NM_053982	KK	ribosomal protein S15a (Rps15a), mRNA. 11/2001 Length = 449	EST, Moderately similar to JC2234 ribosomal protein S15a, cytosolic [validated] - rat [R.norvegicus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
4023	9845	NM_145672	EEE, MMM	monokine induced by gamma interferon (Mig), mRNA. 11/2002 Length = 386	ESTs, Weakly similar to JN0572 neutrophil chemo-attractant Gro protein precursor - rat [R.norvegicus]
147	2830	AA818025	XX, YY	CD59 antigen	CD59 antigen
147	2831	AA818025	L, XX, YY	CD59 antigen	CD59 antigen
1611	3550	AI058606	I, J	signal peptidase complex (18kD)	signal peptidase complex (18kD)
1872	23574	AI104520	LL	Cytochrome c oxidase subunit VIa (liver)	Cytochrome c oxidase subunit VIa (liver)
2558	573	AI232087	A, B, M, OOO, UUU, General Core Tox Markers	hydroxyacid oxidase 3 (medium-chain)	hydroxyacid oxidase 3 (medium-chain)
2905	21011	H32189	F, PP, QQ, TT, DDD	Glutathione-S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
2922	21012	J02592	GG, NN, OO, EEE, LLL, MMM	Glutathione-S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
2925	17284	J02827	VV, XX, YY, EEE, MMM	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha	Branched chain alpha-ketoacid dehydrogenase subunit E1 alpha
2926	21014	J03914	N, BB, CC, NN	Glutathione-S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
2949	3548	L11319	I, J, EEE, MMM	signal peptidase complex (18kD)	signal peptidase complex (18kD)
2949	3549	L11319	O, HH, XX, YY, PPP, QQQ	signal peptidase complex (18kD)	signal peptidase complex (18kD)
3121	15616	NM_012699	Q	dnaJ homolog, subfamily b, member 9 (Dnajb9), mRNA. 11/2002 Length = 1936	DnaJ (Hsp40) homolog, subfamily B, member 9
3251	21013	NM_017014	F, N, DD, EE, TT, DDD	Glutathione-S-transferase, mu type 2 (Yb2) (Gstm2), mRNA. 11/2000 Length = 1055	Glutathione-S-transferase, mu type 2 (Yb2)

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3251	21015	NM_017014	F, K, N, TT, DDD	Glutathione-S-transferase, mu type 2 (Yb2) (Gstm2), mRNA. 11/2000 Length = 1055	Glutathione-S-transferase, mu type 2 (Yb2)
3293	21975	NM_017154	E, FF, LLL, RRR, SSS, UUU, General Alternate	xanthine dehydrogenase (Xdh), mRNA. 11/2002 Length = 4198	xanthine dehydrogenase.
3361	24362	NM_019156	M, N, SS	vitronectin (Vtn), mRNA. 11/2002 Length = 1588	vitronectin
3383	21443	NM_019262	NN	complement component 1, q subcomponent, beta polypeptide (C1qb), mRNA. 11/2002 Length = 1136	complement component 1, q subcomponent, beta polypeptide
3420	20816	NM_021261	O, P, NN, OO	thymosin, beta 10 (Tmsb10), mRNA. 11/2002 Length = 539	thymosin, beta 10
3430	17976	NM_021739	Z, AA	Ca ⁺⁺ /calmodulin-dependent protein kinase II, beta subunit (Camk2b), mRNA. 11/2002 Length = 1840	Ca ⁺⁺ /calmodulin-dependent protein kinase II, beta subunit
3681	18074	NM_031738	RR, UU	solute carrier family 29, member 2 (Slc29a2), mRNA. 11/2002 Length = 1678	solute carrier family 29 (nucleoside transporters), member 2
3709	16535	NM_031853	Q, R, U, YY	diazepam binding inhibitor (Dbi), mRNA. 11/2002 Length = 512	Diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
3819	18174	NM_053752	BBB, CCC	succinate-CoA ligase, GDP-forming, alpha subunit (Suc1g1), mRNA. 11/2001 Length = 1684	succinate-CoA ligase, GDP-forming, alpha subunit

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3819	18175	NM_053752	L, U, BBB, CCC, RRR	succinate-CoA ligase, GDP-forming, alpha subunit (Suc1g1), mRNA. 11/2001 Length = 1684	succinate-CoA ligase, GDP-forming, alpha subunit
3998	15134	NM_139081	E, K	Ornithine decarboxylase antizyme (Oaz), mRNA. 10/2002 Length = 1046	ESTs, Highly similar to OAZ_RAT Ornithine decarboxylase antizyme (ODC-Az) [R.norvegicus]
4257	23576	X72757	HH, LL	Cytochrome c oxidase subunit VIa (liver)	Cytochrome c oxidase subunit VIa (liver)
43	18333	AA799614	V		ESTs, Moderately similar to sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae) [Rattus norvegicus] [R.norvegicus]
242	22820	AA848315	GGG, General Alternate		ESTs, Weakly similar to guanosine monophosphate reductase [Rattus norvegicus] [R.norvegicus]
422	309	AA866460	BB, CC, OO, EEE, MMM		ESTs, Weakly similar to T42737 gp330 protein precursor - rat [R.norvegicus]
747	15577	AA924557	C, FF		ESTs, Highly similar to vesicle-associated calmodulin-binding protein [Rattus norvegicus] [R.norvegicus]
776	5110	AA925274	E, BB, UU, General Alternate		ESTs, Highly similar to OKRT2R protein kinase (EC 2.7.1.37), cAMP-dependent, type II-alpha regulatory chain - rat (fragment) [R.norvegicus]
992	5111	AA955729	CC, LL, UU		EST, ESTs, Highly similar to OKRT2R protein kinase (EC 2.7.1.37), cAMP-dependent, type II-alpha regulatory chain - rat (fragment) [R.norvegicus]
1038	1095	AA957676	D	thyroid hormone receptor interactor 10	thyroid hormone receptor interactor 10
1159	23502	AA998025	General Alternate		ESTs, Weakly similar to A60716 somatotropin intron-related protein RDE.25 - rat (fragment) [R.norvegicus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1284	18125	AI008787	FF, BBB		ESTs, Highly similar to S16788 probable reverse transcriptase - rat [R.norvegicus]
1326	6832	AI009685	N		ESTs, Weakly similar to S19597 transcription factor SOX4 - rat [R.norvegicus]
1491	7502	AI029647	XX		ESTs, Weakly similar to ACBP_RAT ACYL-COA-BINDING PROTEIN (ACBP) (DIAZEPAM BINDING INHIBITOR) (DBI) (ENDOZEPINE) (EP) [R.norvegicus]
2092	18126	AI171369	RRR		ESTs, Highly similar to S16788 probable reverse transcriptase - rat [R.norvegicus]
2131	15673	AI172107	G, LLL, SSS, UUU	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)
2340	22258	AI179357	HHH		ESTs, Weakly similar to A53798 58K membrane-associated protein - rat [R.norvegicus]
2683	14923	AI235223	SS		ESTs, Weakly similar to A60716 somatotropin intron-related protein RDE.25 - rat (fragment) [R.norvegicus]
2927	1869	J03959	M, GG, WW	urate oxidase	urate oxidase
2927	1870	J03959	M	urate oxidase	urate oxidase
3347	17782	NM_017344	ZZ, AAA	glycogen synthase kinase 3 alpha (Gsk3a), mRNA. 11/2002 Length = 2155	glycogen synthase kinase 3 alpha
3470	24535	NM_022399	M, U, FF	calreticulin (Calr), mRNA. 11/2002 Length = 1882	calreticulin
3470	24537	NM_022399	M, FF	calreticulin (Calr), mRNA. 11/2002 Length = 1882	calreticulin
3690	22828	NM_031787	YY	homeodomain-interacting protein kinase 3 (Hipk3), mRNA. 5/2001 Length = 4120	homeodomain-interacting protein kinase 3

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3824	1868	NM_053768	M	urate oxidase (Uox), mRNA. 4/2002 Length = 1361	urate oxidase
3853	19942	NM_053946	K, DD, EE, PP, QQ	implantation-associated protein (IAG2), mRNA. 11/2001 Length = 1219	implantation-associated protein
4289	1426	Z48225	K	eukaryotic translation initiation factor 2B	eukaryotic translation initiation factor 2B
835	6691	AA943028	UUU		ESTs, Highly similar to KFMS_RAT Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) [R.norvegicus]
1428	19591	AI012747	BBB		ESTs, Highly similar to BLMH_RAT Bleomycin hydrolase (BLM hydrolase) (BMH) (BH) [R.norvegicus]
1858	16915	AI104104	QQ, YY		ESTs, Highly similar to QYRTGP phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32), cytosolic - rat [R.norvegicus]
2876	19590	D87336	BBB, CCC, RRR		ESTs, Highly similar to BLMH_RAT Bleomycin hydrolase (BLM hydrolase) (BMH) (BH) [R.norvegicus]
2916	18638	H33922	XX, YY	RT1 class Ib gene	RT1 class Ib gene
3004	18618	M24026	Z, AA, EEE, MMM	RT1 class Ib gene	RT1 class Ib gene
3101	18636	NM_012645	II, XX, YY	RT1 class Ib gene (RT1Aw2), mRNA. 11/2002 Length = 1540	RT1 class Ib gene
3830	18628	NM_053806	RR, XX, YY	potassium channel, subfamily K, member 6 (TWIK-2) (Kcnk6), mRNA. 11/2001 Length = 2243	RT1 class Ib gene
438	4339	AA875121	UU	CCAAT binding factor of CBF-C/NFY-C	CCAAT binding factor of CBF-C/NFY-C
484	18489	AA891669	RR	RAB11B, member RAS oncogene family	ESTs

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
894	17471	AA944965	LL	Group-specific component (vitamin D-binding protein)	Group-specific component (vitamin D-binding protein)
1207	25149	AB009246	GG	stem cell growth factor	
1220	15292	AF012714	Q, MM, TTT, General Alternate	multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
1247	18731	AF093139	R	tip associating protein	tip associating protein
1265	17353	AI008020	BBB, CCC	Malic enzyme 1, soluble	Malic enzyme 1, soluble
1357	4213	AI010453	F, S, EE, SS, NNN	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
1763	19647	AI100867	JJ, KK	SH3/ankyrin domain gene 3	SH3/ankyrin domain gene 3
1790	19373	AI102044	LL, NNN	Drosophila polarity gene (frizzled) homologue, beta-carotene 15, 15'-dioxygenase	beta-carotene 15, 15'-dioxygenase
1898	15291	AI111401	Q, SS, General Alternate	multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
2027	6479	AI169690	BB, CC, DD, EE, LL, SS, DDD, III, JJJ, LLL, NNN, UUU	Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide
2083	8240	AI171267	II	SAC1 (supressor of actin mutations 1, homolog)-like (S. cerevisiae)	SAC1 (supressor of actin mutations 1, homolog)-like (S. cerevisiae)
2400	2052	AI227854	RR	gamma-aminobutyric acid (GABA) B receptor, 1	gamma-aminobutyric acid (GABA) B receptor, 1
2703	21414	AI235842	W, NN	Superoxide dismutase 2, mitochondrial	Superoxide dismutase 2, mitochondrial
2834	25233	AJ000556	T	Janus kinase 1	

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2839	21051	D00698	D, G, H, GG, DDD	Insulin-like growth factor I	Insulin-like growth factor I
2860	25281	D30804	G, H, K, X, Y, LLL, SSS, UUU	proteasome (prosome, macropain) subunit, alpha type 7	
2867	9134	D45247	G, H, K, BB, CC, GGG	proteasome beta type subunit 5	
2883	1921	E01524	I, L, WW, OOO, General Alternate	P450 (cytochrome) oxidoreductase	P450 (cytochrome) oxidoreductase
2923	1577	J02649	D	ATPase, H ⁺ , K ⁺ -transporting, alpha / (gastric H,K-ATPase catalytic subunit)	
2928	174	J04197	JJ, KK, SS	6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (liver and muscle)	6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (liver and muscle)
2937	1264	K01933	S, SS, WW, NNN	Haptoglobin	Haptoglobin
2956	1228	L14684	BBB, CCC	G elongation factor	G elongation factor
2961	854	L20823	RR	Epimorphin	Epimorphin
2965	395	L24374	SS	Matrix metalloproteinase 7 (matrilysin)	Matrix metalloproteinase 7 (matrilysin)
2984	4254	M12450	M, S, NNN	Group-specific component (vitamin D-binding protein)	Group-specific component (vitamin D-binding protein)
2993	21052	M15481	H, S, GGG, PPP, QQQ, General Alternate	Insulin-like growth factor I	Insulin-like growth factor I
2993	21053	M15481	G, H, PPP, QQQ	Insulin-like growth factor I	Insulin-like growth factor I
3006	25430	M26247	N, WW, UUU	Coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)	

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3019	20699	M35601	E, KKK	Fibrinogen, A alpha polypeptide	Fibrinogen, A alpha polypeptide
3019	20700	M35601	E, L, S, X, Y, NNN	Fibrinogen, A alpha polypeptide	Fibrinogen, A alpha polypeptide
3030	64	M60655	C, I, L, W, XX, YY, LLL, OOO, General Alternate	Adrenergic, alpha 1B-, receptor	Adrenergic, alpha 1B-, receptor
3043	25060	M81766	D	Retinoic acid receptor, beta	
3049	13488	M91599	V	Fibroblast growth factor receptor 4	
3049	13489	M91599	UUU	Fibroblast growth factor receptor 4	ESTs, Highly similar to JC1450 fibroblast growth factor receptor 4 - rat [R.norvegicus]
3070	4467	NM_012529	ZZ, AAA	creatine kinase, brain (Ckb), mRNA. 11/2002 Length = 1146	Creatine kinase, brain
3080	6477	NM_012559	E, N, LL, MM, KKK, NNN, TTT	Fibrinogen, gamma polypeptide (Fgg), mRNA. 11/2000 Length = 1358	Fibrinogen, gamma polypeptide
3080	6478	NM_012559	E, J, S, X, Y, DD, EE, KKK, NNN	Fibrinogen, gamma polypeptide (Fgg), mRNA. 11/2000 Length = 1358	Fibrinogen, gamma polypeptide
3081	17237	NM_012562	XX, YY	Fucosidase, alpha-L-1, tissue (Fuca), mRNA. 11/2002 Length = 1478	Fucosidase, alpha-L-1, tissue
3083	20744	NM_012571	C, I, J, X, EE, MM, UU, WW, KKK, TTT, General Alternate	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12 (Got1), mRNA. 11/2000 Length = 1937	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12
3093	18746	NM_012600	BBB	Malic enzyme 1, soluble (Me1), mRNA. 11/2000 Length = 1761	Malic enzyme 1, soluble

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3093	18747	NM_012600	T, X, Y, BBB, LLL, RRR, SSS, UUU	Malic enzyme 1, soluble (Me1), mRNA. 11/2000 Length = 1761	Malic enzyme 1, soluble
3093	18749	NM_012600	X, Y, BBB, LLL, RRR, SSS, UUU	Malic enzyme 1, soluble (Me1), mRNA. 11/2000 Length = 1761	Malic enzyme 1, soluble
3099	172	NM_012621	JJ, KK, WW, YY	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (Pfkfb1), mRNA. 11/2002 Length = 1898	6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (liver and muscle)
3108	16198	NM_012663	BB, CC	vesicle-associated membrane protein 2 (Vamp2), mRNA. 10/2002 Length = 2071	Vesicle-associated membrane protein (synaptobrevin 2)
3108	16199	NM_012663	Z, AA	vesicle-associated membrane protein 2 (Vamp2), mRNA. 10/2002 Length = 2071	Vesicle-associated membrane protein (synaptobrevin 2)
3124	24545	NM_012713	D	Protein kinase C beta (Prkcb1), mRNA. 11/2000 Length = 2599	Protein kinase C beta
3132	5317	NM_012737	BBB, CCC	Apolipoprotein A-IV (Apoa4), mRNA. 5/2002 Length = 1423	Apolipoprotein A-IV
3144	10247	NM_012797	V	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation) (Id1), mRNA. 10/2002 Length = 1124	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)
3144	10248	NM_012797	DD, EE, JJJ, General Core Tox Markers	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation) (Id1), mRNA. 10/2002 Length = 1124	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3154	11137	NM_012839	D, MM, FFF, TTT	cytochrome c, somatic (Cycs), mRNA. 11/2002 Length = 318	Cytochrome C, expressed in somatic tissues
3154	11138	NM_012839	T, JJ, KK, LL	cytochrome c, somatic (Cycs), mRNA. 11/2002 Length = 318	Cytochrome C, expressed in somatic tissues
3164	23651	NM_012881	EEE, MMM	secreted phosphoprotein 1 (Spp1), mRNA. 11/2002 Length = 1457	Sialoprotein (osteopontin)
3191	19391	NM_012998	U, FF, RRR	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide) (P4hb), mRNA. 11/2000 Length = 2460	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
3191	19392	NM_012998	D, BB	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide) (P4hb), mRNA. 11/2000 Length = 2460	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
3191	19393	NM_012998	FF	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide) (P4hb), mRNA. 11/2000 Length = 2460	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
3196	23543	NM_013013	V, UU	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Psap), mRNA. 11/2000 Length = 2175	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator)
3196	23544	NM_013013	MM, TTT	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator) (Psap), mRNA. 11/2000 Length = 2175	Prosaposin (sulfated glycoprotein, sphingolipid hydrolase activator)
3203	2667	NM_013048	F, T, LL, RR, EEE, MMM, General Alternate	Tocopherol transfer protein alpha (Ttpa), mRNA. 11/2000 Length = 2182	

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3209	16472	NM_013062	JJJ	FLK1 kinase insert domain receptor (VEGF receptor 2) (Kdr), mRNA. 11/2000 Length = 5892	FLK1 kinase insert domain receptor (VEGF receptor 2)
3219	24	NM_013101	Z, AA, RRR, SSS	Phosphodiesterase 4A (Pde4a), mRNA. 11/2000 Length = 2914	Phosphodiesterase 4A
3235	397	NM_013214	I, J, U, FF, BBB	acyl-CoA hydrolase (RBACH), mRNA. 11/2000 Length = 1523	brain acyl-CoA hydrolase
3235	20851	NM_013214	BBB, CCC, RRR, SSS	acyl-CoA hydrolase (RBACH), mRNA. 11/2000 Length = 1523	brain acyl-CoA hydrolase
3245	24897	NM_016993	QQ	B-cell leukemia/lymphoma 2 (Bcl2), mRNA. 11/2002 Length = 1179	B cell lymphoma 2 associated oncogene
3250	18988	NM_017013	V, NN, OO	glutathione-S-transferase, alpha type2 (Gsta2), mRNA. 11/2002 Length = 831	Glutathione-S-transferase, alpha type (Ya)
3262	682	NM_017051	EEE, MMM	Superoxide dismutase 2, mitochondrial (Sod2), mRNA. 11/2002 Length = 1492	Superoxide dismutase 2, mitochondrial
3268	11150	NM_017073	II, RR, TT, DDD	Glutamine synthetase (glutamate-ammonia ligase) (GluI), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)
3268	11151	NM_017073	N, TT	Glutamine synthetase (glutamate-ammonia ligase) (GluI), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3268	11152	NM_017073	II, LL, TT, UU, DDD, LLL, UUU	Glutamine synthetase (glutamate-ammonia ligase) (Glul), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)
3268	11153	NM_017073	G, K, II, TT, DDD, GGG, LLL	Glutamine synthetase (glutamate-ammonia ligase) (Glul), mRNA. 11/2000 Length = 2793	Glutamine synthetase (glutamate-ammonia ligase)
3288	20859	NM_017144	D, U, BBB, CCC, RRR, SSS	troponin 1, type 3 (Tnni3), mRNA. 11/2002 Length = 830	Troponin I
3331	12350	NM_017290	PP, QQ	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (Atp2a2), mRNA. 11/2002 Length = 5648	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
3339	20789	NM_017319	M, U, LL	glucose regulated protein, 58 kDa (Grp58), mRNA. 11/2002 Length = 1874	glucose regulated protein, 58 kDa
3397	889	NM_019346	Z, AA, SS	solute carrier family 14, member 1 (Slc14a1), mRNA. 11/2002 Length = 1412	solute carrier family 14, member 1
3406	20298	NM_019374	O, P, BB, CC	prodynorphin (Pdyn), mRNA. 11/2002 Length = 747	prodynorphin
3407	15680	NM_019376	Q, R, PPP, QQQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (Ywhag), mRNA. 11/2002 Length = 3410	14-3-3 protein gamma-subtype
3413	15911	NM_019907	ZZ, AAA	postsynaptic protein Crip1 (Crip1), mRNA. 11/2002 Length = 1435	postsynaptic protein Crip1

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3421	15335	NM_021264	GGG	ribosomal protein L35a (Rpl35a), mRNA. 11/2002 Length = 348	ribosomal protein L35a
3444	24321	NM_022177	G, J, S, WW, OOO, PPP, QQQ, General Core Tox Markers	Stromal cell-derived factor 1 (Sdf1), mRNA. 11/2002 Length = 1830	Stromal cell-derived factor 1
3477	4212	NM_022519	M, HH, SS	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (Serpina1), mRNA. 4/2002 Length = 1380	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
3477	25681	NM_022519	SS	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (Serpina1), mRNA. 4/2002 Length = 1380	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
3479	5666	NM_022529	D, JJ, KK	mitochondrial ribosomal protein L23 (Mrpl23), mRNA. 1/2002 Length = 540	mitochondrial ribosomal protein L23
3528	15755	NM_022960	C, U, X, DD, EE, DDD, LLL, OOO, RRR, SSS, UUU	aquaporin 9 (Aqp9), mRNA. 11/2002 Length = 1495	neutral solute channel aquaporin 9
3631	19096	NM_031352	L	drebrin-like (Dbnl), mRNA. 11/2002 Length = 1750	drebrin-like
3636	24710	NM_031512	W	Interleukin 1 beta (Il1b), mRNA. 11/2002 Length = 1329	Interleukin 1 beta

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3643	4010	NM_031543	EE, MM, TTT	Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. 11/2002 Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
3643	4011	NM_031543	K, O, P, FF, II, NN, OO, QQ, EEE, MMM	Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. 11/2002 Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
3643	4012	NM_031543	T, EE, FF, MM, EEE, MMM, TTT	Cytochrome P450, subfamily 2e1 (ethanol-inducible) (Cyp2e1), mRNA. 11/2002 Length = 1624	Cytochrome P450, subfamily 2e1 (ethanol-inducible)
3651	1919	NM_031576	I, L, WW	P450 (cytochrome) oxidoreductase (Por), mRNA. 11/2002 Length = 2441	P450 (cytochrome) oxidoreductase
3651	1920	NM_031576	C, I, L, MM, WW, OOO, TTT, General Alternate	P450 (cytochrome) oxidoreductase (Por), mRNA. 11/2002 Length = 2441	P450 (cytochrome) oxidoreductase
3665	9428	NM_031656	RR	syntaxin 8 (Stx8), mRNA. 11/2002 Length = 859	syntaxin-like protein 3135
3666	17448	NM_031668	C, PPP, QQQ, General Alternate	MYB binding protein 1a (Mybbp1a), mRNA. 11/2002 Length = 3834	MYB binding protein (P160) 1a
3731	17933	NM_032615	U, BBB, CCC, RRR, SSS	membrane interacting protein of RGS16 (Mir16), mRNA. 11/2002 Length = 1203	membrane interacting protein of RGS16
3731	17934	NM_032615	U, V, BBB, CCC	membrane interacting protein of RGS16 (Mir16), mRNA. 11/2002 Length = 1203	membrane interacting protein of RGS16

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3731	17935	NM_032615	RRR, SSS	membrane interacting protein of RGS16 (Mir16), mRNA. 11/2002 Length = 1203	membrane interacting protein of RGS16
3746	13164	NM_053318	E, S, PP, QQ, WW	hemopexin (Hpx), mRNA. 11/2002 Length = 1484	hemopexin
3773	16394	NM_053485	O, P	calcium binding protein A6 (calcyclin) (S100a6), mRNA. 11/2001 Length = 291	calcium binding protein A6 (calcyclin)
3782	14380	NM_053536	W	Kruppel-like factor 15 (Klf15), mRNA. 11/2002 Length = 2458	Kruppel-like factor 15 (kidney)
3806	13005	NM_053623	LL, BBB, CCC, RRR	fatty acid Coenzyme A ligase, long chain 4 (Facl4), mRNA. 11/2002 Length = 4862	fatty acid-Coenzyme A ligase, long chain 4
3833	16311	NM_053818	G, H	glycine transporter 1 (Glyt1), mRNA. 11/2001 Length = 2558	glycine transporter 1
3838	20868	NM_053843	O, P, NN, OO, VV	Fc receptor, IgG, low affinity III (Fcgr3), mRNA. 11/2002 Length = 1318	Fc receptor, IgG, low affinity III
3838	20869	NM_053843	O, P, V, NN, OO, VV	Fc receptor, IgG, low affinity III (Fcgr3), mRNA. 11/2002 Length = 1318	Fc receptor, IgG, low affinity III
3932	17560	NM_133283	N	mitogen activated protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376	mitogen activated protein kinase kinase 2
3932	17564	NM_133283	I, J, DD, EE	mitogen activated protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376	mitogen activated protein kinase kinase 2

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3932	21848	NM_133283	I, J, RRR, UUU	mitogen activated protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376	mitogen activated protein kinase kinase 2
3932	21849	NM_133283	U, RRR	mitogen activated protein kinase kinase 2 (Map2k2), mRNA. 11/2002 Length = 1376	mitogen activated protein kinase kinase 2
3944	15542	NM_133539	G, H	mitochondrial ribosomal protein L17 (Mrpl17), mRNA. 5/2002 Length = 1102	mitochondrial ribosomal protein L17
3944	15543	NM_133539	G, H	mitochondrial ribosomal protein L17 (Mrpl17), mRNA. 5/2002 Length = 1102	mitochondrial ribosomal protein L17
3962	15017	NM_134349	M, S, DD, EE, NNN	microsomal glutathione S-transferase 1 (Mgst1), mRNA. 11/2002 Length = 883	microsomal glutathione S-transferase 1
3998	25250	NM_139081	LL	Ornithine decarboxylase antizyme (Oaz), mRNA. 10/2002 Length = 1046	
4052	1937	R46934	HH	amelogenin	amelogenin
4093	1583	U07201	E, GG, III, JJJ	Asparagine synthetase	Asparagine synthetase
4095	58	U09870	W, General Alternate	major vault protein	major vault protein
4106	202	U20181	N	iron-regulatory protein 2	iron-regulatory protein 2
4123	433	U37142	RR	Brevican	Brevican
4136	396	U49694	NNN	brain acyl-CoA hydrolase	brain acyl-CoA hydrolase
4145	1286	U55938	F, UU	Sialyltransferase 8 (GT3 alpha 2,8-sialyltransferase) C	Sialyltransferase 8 (GT3 alpha 2,8-sialyltransferase) C
4149	912	U59184	QQ, UU, General Core Tox Markers	Bcl2-associated X protein	Bcl2-associated X protein

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4163	25083	U72632	RR	amine oxidase, copper containing 3	
4174	906	U83112	X	forkhead box M1	forkhead box M1
4190	21054	X06107	G, H, M, S, GGG	Insulin-like growth factor I	Insulin-like growth factor I
4198	15652	X14210	BB, CC, EEE, III, JJJ, MMM	ribosomal protein S4, X-linked	
4204	173	X15580	L, Z, AA, JJ, KK, WW	6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (liver and muscle)	6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (liver and muscle)
4208	25686	X51536	G, H, JJ, KK, GGG, HHH	ribosomal protein S3	
4210	25687	X51706	H, EEE, MMM, General Alternate	ribosomal protein L9	
4226	5667	X58200	G, H, EEE, MMM, General Core Tox Markers, General Alternate	ribosomal protein L23	
4237	25718	X62145	G, H, JJ, HHH	ribosomal protein L8	
4244	25089	X63594	I, J	Inhibitor of nuclear factor of kappa light chain gene enhancer in B-cells, alpha	
4244	25090	X63594	J	Inhibitor of nuclear factor of kappa light chain gene enhancer in B-cells, alpha	
4251	580	X68812	N	solute carrier family 8 (sodium/calcium exchanger), member 1	solute carrier family 8 (sodium/calcium exchanger), member 1
4281	1620	X97374	D, Z, AA	Prepronociceptin (neuropeptide nociceptin) (N23K)	Prepronociceptin (neuropeptide nociceptin) (N23K)

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4287	20426	Z12158	SS, WW	Pyruvate dehydrogenase (lipoamide) alpha 1	
4291	1541	Z50144	F	kynurenine aminotransferase II	kynurenine aminotransferase II
4291	1542	Z50144	F, XX, YY	kynurenine aminotransferase II	kynurenine aminotransferase II
1	25098	AA108277	Q		
2	4433	AA684641	R		ESTs
4	4438	AA684919	D, V, UU		ESTs
5	4439	AA685175	BB, CC, NN, OO		ESTs, Moderately similar to ribosome binding protein 1 isoform mRRp61 [Mus musculus] [M.musculus]
6	16704	AA686132	RRR, SSS, UUU		
11	18289	AA686704	SS		
12	19222	AA799279	L		ESTs, Highly similar to mitochondrial carrier homolog 2 [Mus musculus] [M.musculus]
13	18396	AA799330	Q, R, W		ESTs, Weakly similar to T47122 cell division protein pelota [imported] - fruit fly (Drosophila melanogaster) [D.melanogaster]
15	15083	AA799396	R		ESTs
16	20042	AA799420	T, V, KKK		ESTs
17	18159	AA799448	D, III, JJJ		ESTs
17	18160	AA799448	X, Y		ESTs
19	4206	AA799474	F		ESTs, Highly similar to CY1_HUMAN Cytochrome c1, heme protein, mitochondrial precursor [H.sapiens]
21	18290	AA799497	WW		ESTs
28	17687	AA799531	ZZ, AAA, PPP, General Alternate		ESTs, Weakly similar to M18.3.p [Caenorhabditis elegans] [C.elegans]
28	17688	AA799531	A, B, ZZ, AAA, HHH, PPP, QQQ, General Core Tox Markers		ESTs, Weakly similar to M18.3.p [Caenorhabditis elegans] [C.elegans]
29	18327	AA799537	L, QQ		ESTs
31	24628	AA799542	KK		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
34	17577	AA799566	V, Z, AA, RR	incisor protein	incisor protein
35	11353	AA799569	II, XX, YY		ESTs
38	20971	AA799576	D		ESTs, Highly similar to T46259 hypothetical protein DKFZp761E0323.1 - human (fragment) [H.sapiens]
40	20975	AA799599	DDD		ESTs
41	16696	AA799607	DDD		ESTs
48	22909	AA799654	NNN		ESTs
48	22910	AA799654	DD, EE, NNN, OOO		ESTs
49	11314	AA799656	C, MM, WW, ZZ, AAA, TTT		ESTs
50	16383	AA799671	Z, AA		
51	17062	AA799680	HH, UU		ESTs
53	2040	AA799700	MM, TTT	HMm:selenophosphate synthetase 2	ESTs, Highly similar to SPS2_MOUSE Selenide,water dikinase 2 (Selenophosphate synthetase 2) (Selenium donor protein 2) [M.musculus]
54	20994	AA799717	F		ESTs, Highly similar to RPB9_HUMAN DNA-directed RNA polymerase II 14.5 kDa polypeptide (RPB9) (RPB14.5) [H.sapiens]
55	18346	AA799718	N, SS		ESTs
56	8768	AA799726	W, PP, QQ		ESTs
59	8977	AA799741	Y		ESTs, Weakly similar to ATP-dependent RNA helicase [Caenorhabditis elegans] [C.elegans]
60	18349	AA799744	W, General Alternate		ESTs
61	17494	AA799751	W		ESTs
62	4133	AA799762	L, BB, CC, FF, OOO, General Core Tox Markers, General Alternate		ESTs
64	6425	AA799784	DDD		ESTs

TABLE 1					
Attorney Doc# 44921-5038-01WO Document No. 1935323.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
68	14504	AA799804	W, BB, NN, XX, YY		ESTs
69	11423	AA799812	OO, PP, III		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens]
72	12060	AA799890	L, TT, DDD		ESTs
73	18180	AA799891	KK, HHH		ESTs
76	23202	AA799971	I, J, General Alternate		ESTs, Moderately similar to hypothetical protein FLJ10986 [Homo sapiens] [H.sapiens]
76	23203	AA799971	JJ, KK, XX, YY, General Alternate		ESTs, Moderately similar to hypothetical protein FLJ10986 [Homo sapiens] [H.sapiens]
77	18400	AA799991	CC, ZZ, AAA, DDD, LLL		ESTs
81	23343	AA800016	Q, R		ESTs, Weakly similar to Yeast ABD1 protein like [Caenorhabditis elegans] [C.elegans]
83	23344	AA800034	U, OO		ESTs
84	19177	AA800062	O, P		ESTs
85	13568	AA800169	I		ESTs
88	16420	AA800191	XX		ESTs
89	18430	AA800197	F		ESTs
91	3692	AA800210	DDD		ESTs
92	7947	AA800224	MM, ZZ, AAA, TTT		ESTs, Weakly similar to C27H6.4.p [Caenorhabditis elegans] [C.elegans]
97	24228	AA800318	E, BB, EEE, GGG, MMM, PPP, QQQ		ESTs, Moderately similar to IC1_MOUSE Plasma protease C1 inhibitor precursor (C1 Inh) (C1Inh) [M.musculus]
98	12064	AA800429	TT, General Core Tox Markers		ESTs
99	14545	AA800456	LLL		ESTs
101	12069	AA800572	V		ESTs
102	19073	AA800576	A		ESTs
103	2070	AA800597	Z, AA		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
104	13930	AA800613	M, W, GG, MM, TTT		EST
105	21368	AA800626	DD, EE		ESTs
106	4843	AA800651	W, OOO, General Alternate		ESTs
108	5257	AA800673	UU		ESTs, Highly similar to KIAA0164 gene product [Homo sapiens] [H.sapiens]
109	23368	AA800678	E, DD, EE, KKK, OOO		ESTs
110	3604	AA800712	BB, CC		ESTs
111	17649	AA800735	Z, AA		ESTs, Weakly similar to VIL1_MOUSE Villin 1 [M.musculus]
112	21380	AA800739	Q, HHH, General Alternate		ESTs, Weakly similar to KT12_YEAST KTI12 PROTEIN [S.cerevisiae]
113	21389	AA800772	DDD		ESTs
114	12797	AA800790	O, P, NN, OO		ESTs
115	19103	AA800797	C, FFF, III, JJJ, OOO, General Core Tox Markers		ESTs
116	11662	AA800803	F		ESTs, Weakly similar to YNP5_CAEEL HYPOTHETICAL 28.3 KDA PROTEIN T05G5.5 IN CHROMOSOME III [C.elegans]
119	8207	AA800850	N, Z, AA		ESTs
121	21407	AA800912	C, EE, ZZ, AAA		ESTs
123	14600	AA801076	BB, CC, NN, OO		ESTs
125	15027	AA801212	PP, QQ		ESTs
127	16889	AA817692	RR		
129	11633	AA817715	FF		ESTs, Weakly similar to T32897 hypothetical protein C42C1.10 - Caenorhabditis elegans [C.elegans]
130	24237	AA817726	A, BB, NN, OO		ESTs
131	6304	AA817729	SS		ESTs
132	15094	AA817753	E		ESTs
134	1690	AA817829	CC		ESTs

TABLE 1					
Attorney Docket 44921-5033-01WO Document No. 1935323.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
135	1802	AA817841	W, DDD, UUU		ESTs
137	1846	AA817844	FFF, General Alternate		ESTs
138	1900	AA817849	Z, II		ESTs
140	2781	AA817925	O		ESTs
141	6308	AA817951	SS		ESTs
142	2485	AA817954	K, PPP, QQQ		ESTs
144	10623	AA817987	N, FF, II, QQ, YY, UUU	Sulfotransferase hydroxysteroid gene 2	Sulfotransferase hydroxysteroid gene 2
146	6698	AA818020	WW		ESTs
149	2897	AA818039	R, EE, OOO, General Alternate		ESTs
150	19926	AA818062	PP, QQ		ESTs
151	5996	AA818065	F, N, II, UUU		ESTs
154	6001	AA818090	YY		EST
155	3233	AA818105	L		ESTs, Weakly similar to hypothetical protein LOC57019 [Homo sapiens] [H.sapiens]
156	6003	AA818107	SS		ESTs
157	6007	AA818123	GGG, General Core Tox Markers		ESTs, Weakly similar to T13616 hypothetical protein 8D8.8 - fruit fly (Drosophila melanogaster) [D.melanogaster]
158	3476	AA818142	YY		ESTs, Weakly similar to F13B9.8.p [Caenorhabditis elegans] [C.elegans]
159	6015	AA818158	A, B, JJ, FFF, GGG, HHH, General Core Tox Markers		ESTs
162	3757	AA818202	HHH, PPP, QQQ		ESTs
164	6030	AA818252	T		ESTs
165	4017	AA818287	D, KKK		ESTs
166	5923	AA818355	F, M, General Core Tox Markers		ESTs
167	7714	AA818394	LL		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
168	12160	AA818412	O, P, X, TT, DDD	cytochrome P450, 2b19	cytochrome P450, 2b19
169	7806	AA818421	Q		ESTs
170	6222	AA818474	HH		ESTs
171	8237	AA818512	DD, EE, NNN		ESTs
172	6226	AA818521	PP, QQ		ESTs
173	8360	AA818534	UU		ESTs, Highly similar to COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana); DNA segment, Chr 6, ERATO Doi 35, expressed; COP9 complex S7a; COP9 (constitutive photomorphogenic), subunit 7a (Arabidopsis) [Mus musculus]
174	17434	AA818574	L		ESTs
175	6231	AA818595	QQ		ESTs
177	8728	AA818615	MM, TTT, General Alternate		ESTs
179	6056	AA818664	E		ESTs
181	4250	AA818700	LLL		ESTs
182	6060	AA818702	UU, General Core Tox Markers		ESTs
183	11864	AA818717	RR		ESTs
184	4291	AA818741	I, LLL, SSS		ESTs
185	6619	AA818743	HH		ESTs, Weakly similar to ACF7_MOUSE Actin cross-linking family protein 7 (Microtubule actin crosslinking factor) (MACF) [M.musculus]
186	4330	AA818747	B, H, JJJ, OOO, General Core Tox Markers		ESTs
188	6066	AA818781	LL		ESTs
190	6073	AA818818	T		EST
192	4921	AA818900	K		ESTs
193	4952	AA818907	Q		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
194	19729	AA818910	III, JJJ, NNN, General Core Tox Markers		ESTs
195	17408	AA818971	N, PPP, QQQ		ESTs
196	10985	AA818998	General Alternate		ESTs
198	16958	AA819021	G		EST
199	5608	AA819041	General Alternate		ESTs
200	6132	AA819055	N, PPP		ESTs, Weakly similar to G35070 apolipoprotein H-related protein 13G1 - mouse [M.musculus]
201	6135	AA819065	MM, TTT		ESTs
202	5863	AA819111	KK		ESTs
205	11988	AA819193	TT		ESTs
207	15147	AA819268	W		ESTs
208	6438	AA819269	General Alternate		ESTs
213	6252	AA819381	EE		ESTs
214	9402	AA819383	JJ, HHH, LLL		ESTs
215	6267	AA819438	D		EST
216	19438	AA819450	LL		EST
217	6275	AA819459	PP, QQ		ESTs
221	18723	AA819547	DD, EE, III, JJJ		ESTs, Moderately similar to JC5821 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) CI-B14 chain - human [H.sapiens]
223	10988	AA819640	E, RR		ESTs
225	6723	AA819653	Q, R, PP, QQ		ESTs, Weakly similar to S44652 f42h10.6 protein - Caenorhabditis elegans [C.elegans]
226	6176	AA819657	T		EST
227	6295	AA819672	DD, MM, WW, TTT		ESTs
228	10695	AA819679	E, II		ESTs
229	6296	AA819680	BB, CC		ESTs
230	6297	AA819681	WW		ESTs, Highly similar to RIKEN cDNA 1200014P03 [Mus musculus] [M.musculus]
232	11021	AA819767	W, AA, DD, General Core Tox Markers		ESTs

TABLE 1					
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Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
234	6190	AA819812	FFF, General Core Tox Markers		ESTs
235	6200	AA819853	NN		ESTs, Highly similar to TNFC_MOUSE Lymphotoxin- beta (LT-beta) (Tumor necrosis factor C) (TNF-C) [M.musculus]
238	9815	AA848218	Q, R		ESTs
239	24629	AA848238	PPP, QQQ		ESTs
241	17315	AA848309	D		ESTs
243	15030	AA848378	LL		ESTs
244	6614	AA848389	OO, EEE, MMM		ESTs, Weakly similar to Iron- containing alcohol dehydrogenases [Caenorhabditis elegans] [C.elegans]
245	23521	AA848407	A, B, HH		ESTs
246	21125	AA848437	III, JJJ, KKK, General Core Tox Markers		ESTs
247	23505	AA848496	Q, R		ESTs, Moderately similar to IF4B_HUMAN Eukaryotic translation initiation factor 4B (eIF- 4B) [H.sapiens]
248	2324	AA848545	ZZ, AAA		ESTs, Weakly similar to T19253 hypothetical protein C14A4.11 - Caenorhabditis elegans [C.elegans]
249	12088	AA848597	DD, EE		ESTs
250	21135	AA848646	B		EST
251	18244	AA848776	EEE, MMM		ESTs
252	21150	AA848826	Z, AA, III, JJJ		ESTs
253	14604	AA848828	F		ESTs
254	12102	AA848902	UU General Alternate		ESTs, Weakly similar to S12207 hypothetical protein (B2 element) - mouse [M.musculus]
255	14207	AA848904			ESTs
256	2924	AA848948	C		ESTs, Weakly similar to F18H3.1.p [Caenorhabditis elegans] [C.elegans]
257	12108	AA848963	CC, KKK		ESTs, Moderately similar to S70630 xeroderma pigmentosum group C - mouse [M.musculus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
			OOO, General Core Tox Markers, General Alternate		
259	21173	AA848990			ESTs
261	22631	AA849030	UUU		ESTs
262	2056	AA849210	YY		ESTs
			C, MM, TTT		ESTs, Moderately similar to cell cycle progression 2 protein [Homo sapiens] [H.sapiens]
264	12119	AA849354			
265	12120	AA849365	JJ		ESTs
			General Core Tox Markers		ESTs, Weakly similar to YLC4_CAEEL Hypothetical 81.0 kDa protein C35D10.4 in chromosome III [C.elegans]
266	18908	AA849426			
			General Core Tox Markers		ESTs, Weakly similar to YLC4_CAEEL Hypothetical 81.0 kDa protein C35D10.4 in chromosome III [C.elegans]
266	18909	AA849426			
			FF, OOO, General Core Tox Markers		
267	17339	AA849497			ESTs
			C, I, J, KKK		
268	11726	AA849518			ESTs
			I, J, KKK, NNN		
268	11727	AA849518			ESTs
269	18743	AA849531	K		ESTs
					ESTs, Weakly similar to guanosine-3',5'-bis(diphosphate)-pyrophosphohydrolase like [Caenorhabditis elegans] [C.elegans]
271	6862	AA849729	BB, CC		
272	12989	AA849743	D		ESTs
273	21275	AA849796	F, II		ESTs
			NN, EEE, MMM		
276	21285	AA849898			EST
					ESTs, Moderately similar to NB8M_HUMAN NADH-ubiquinone oxidoreductase B18 subunit (Complex I-B18) (CI-B18) (Cell adhesion protein SQM1) [H.sapiens]
280	21327	AA850130	F		
281	21333	AA850136	K		ESTs
			U, FF, UU, BBB, RRR, SSS		
282	21341	AA850195			ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935823.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
283	21353	AA850247	E, General Alternate		ESTs
286	19502	AA850601	OO		ESTs
288	6471	AA850706	FFF, General Alternate		ESTs
290	5754	AA850738	Z		ESTs
291	3400	AA850771	V		ESTs
293	19575	AA850814	JJJ, KKK		ESTs, Weakly similar to F22F7.1.p [Caenorhabditis elegans] [C.elegans]
295	21762	AA850886	L		ESTs
297	21773	AA850951	XX		ESTs
298	9514	AA850978	L, Z, AA		ESTs
300	8872	AA851050	G, K, X, TT, HHH, UUU	glutathione reductase	glutathione reductase
301	22518	AA851065	ZZ, AAA		ESTs
304	4163	AA851210	RRR, SSS, UUU		ESTs, Weakly similar to T33304 hypothetical protein R01B10.5 - Caenorhabditis elegans [C.elegans]
305	17699	AA851233	JJ		ESTs, Highly similar to RIKEN cDNA 4930548G07 [Mus musculus] [M.musculus]
306	18961	AA851238	C	fasting-inducible integral membrane protein TM6P1	fasting-inducible integral membrane protein TM6P1
307	4134	AA851240	General Core Tox Markers; General Alternate		ESTs
308	21694	AA851248	Y		ESTs
309	21466	AA851273	EE, HHH		ESTs, Weakly similar to retinoic acid receptor responder (tazarotene induced) 2 [Homo sapiens] [H.sapiens]
310	17766	AA851299	TT, LLL, UUU		ESTs
313	22979	AA851372	TT		ESTs, Moderately similar to hypothetical protein MGC2749 [Homo sapiens] [H.sapiens]
314	21482	AA851407	CCC		ESTs
316	21510	AA851620	T		ESTs
319	21529	AA851748	F, W, HH		ESTs
322	23243	AA851803	L, OO, TT, UU		ESTs

TABLE 1					
Attorney Docket 44921-5033-01WO Document No. 1935823.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
324	18243	AA851920	F		ESTs, Moderately similar to RIKEN cDNA 2310040G17; expressed sequence AI425883 [Mus musculus] [M.musculus]
327	18580	AA851963	BB, NN, EEE, MMM		ESTs
329	21572	AA852011	A, B		ESTs
330	21574	AA852038	W, DD		ESTs
331	1904	AA852046	DD, EE		Rat VL30 element mRNA
332	15207	AA858448	NN, OO, PP		ESTs
333	15211	AA858449	N		ESTs
335	15283	AA858548	RR		ESTs
336	21856	AA858550	WW		ESTs
339	23069	AA858572	TT		ESTs
341	24161	AA858588	C, I, J, W, WW, OOO, General Alternate		ESTs
343	17382	AA858607	I, J, NN, OO, DDD		ESTs
344	1801	AA858636	General Alternate		ESTs, Highly similar to mini chromosome maintenance deficient 7 (S. cerevisiae) [Mus musculus] [M.musculus]
346	6344	AA858649	F		ESTs, Weakly similar to F17C11.8.p [Caenorhabditis elegans] [C.elegans]
347	6345	AA858657	XX, YY		ESTs
352	13229	AA858760	JJ		ESTs
353	6389	AA858815	General Core Tox Markers, General Alternate		ESTs
354	11161	AA858817	O, P		ESTs, Moderately similar to T46271 hypothetical protein DKFZp564P1263.1 - human [H.sapiens]
355	6390	AA858821	GGG		ESTs
357	6409	AA858910	FF		ESTs
358	14191	AA858924	M, XX, OOO		ESTs
359	14234	AA858928	UUU		ESTs
360	6413	AA858954	RR		EST
361	14210	AA858955	L		EST

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
362	18765	AA859019	YY, PPP, QQQ		ESTs, Weakly similar to G35070 apolipoprotein H-related protein 13G1 - mouse [M.musculus]
362	18766	AA859019	PPP, QQQ		ESTs, Weakly similar to G35070 apolipoprotein H-related protein 13G1 - mouse [M.musculus]
363	4591	AA859029	UUU, General Core Tox Markers, General Alternate		ESTs
364	6431	AA859085	W, X, BB, CC, LL, NN		ESTs
365	17361	AA859114	C		ESTs
373	15157	AA859343	PP, QQ		ESTs
378	11827	AA859468	PP, QQ, LLL, SSS		ESTs
380	18862	AA859520	CCC		ESTs
381	4178	AA859536	EEE, MMM		ESTs
382	15150	AA859562	SSS		ESTs
383	15	AA859577	EEE, MMM		ESTs
384	14353	AA859585	C, KK, QQ, General Core Tox Markers		ESTs
385	11852	AA859593	W		ESTs
387	4809	AA859616	LLL		ESTs, Weakly similar to FYVE zinc finger [Caenorhabditis elegans] [C.elegans]
388	11608	AA859633	A, Q, R		ESTs
391	19067	AA859663	OOO, General Alternate		ESTs
392	19726	AA859665	RR		EST

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
394	21707	AA859722	C, E, R, BB, CC, DD, MM, QQ, WW, III, JJJ, KKK, NNN, TTT, General Core Tox Markers		ESTs
395	20034	AA859796	BBB, CCC		ESTs, Weakly similar to S61982 probable membrane protein YOL002c - yeast (<i>Saccharomyces cerevisiae</i>) [<i>S.cerevisiae</i>]
397	22396	AA859806	Y, UU, ZZ, AAA		ESTs
398	11079	AA859829	I, J		ESTs
399	22739	AA859877	ZZ, AAA		ESTs
400	22773	AA859885	X, Y		ESTs
401	22813	AA859897	LL		ESTs
402	16320	AA859899	F, K, LLL, UUU, General Alternate		ESTs
403	15165	AA859919	TT		ESTs
403	15166	AA859919	TT		ESTs
404	22927	AA859920	UU, PPP, QQQ, General Alternate		ESTs
405	26034	AA859921	TT		
406	22978	AA859931	D		ESTs, Moderately similar to hypothetical protein MGC2749 [<i>Homo sapiens</i>] [<i>H.sapiens</i>]
413	16322	AA866240	D		EST
413	16323	AA866240	BBB		EST
417	15927	AA866321	PP, QQ		ESTs
418	21690	AA866362	N, V		ESTs
419	15980	AA866426	I, T, DD, EE, XX, YY, LLL		ESTs
420	15987	AA866435	L, N, X, DDD, UUU		EST
421	16854	AA866454	M		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
423	9391	AA866477	Z, AA		ESTs, Moderately similar to COXM_MOUSE Cytochrome c oxidase polypeptide VIIb, mitochondrial precursor [M.musculus]
425	16118	AA874924	O, P		ESTs
429	7040	AA874978	K, T		ESTs
432	16242	AA875019	X, Y		ESTs, Highly similar to ZAP3_MOUSE Nuclear protein ZAP3 [M.musculus]
433	15573	AA875023	Z, AA		ESTs
436	16416	AA875098	FF, NN, OO, EEE, HHH, MMM		ESTs, Highly similar to RIKEN cDNA 1110002O23 [Mus musculus] [M.musculus]
437	16495	AA875107	R, RR		ESTs, Moderately similar to JE0379 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUFA3 - human [H.sapiens]
439	15313	AA875126	Q, MM, JJJ, TTT		ESTs
440	15713	AA875143	Z, AA, ZZ, AAA		ESTs
441	10936	AA875146	ZZ, AAA	HMm:ubiquitin conjugating enzyme 6	ESTs, Highly similar to ubiquitin conjugating enzyme 6; Ubc6p homolog [Mus musculus] [M.musculus]
443	14285	AA875194	SS		ESTs
446	15384	AA875217	K		ESTs
449	15401	AA875257	I, J		ESTs
451	15421	AA875286	SS		ESTs, Highly similar to prostate tumor over expressed gene 1 [Homo sapiens] [H.sapiens]
452	15509	AA875425	CCC		ESTs
453	7936	AA875495	L, Z, AA		ESTs
454	19381	AA875506	V		ESTs, Weakly similar to 0806162N protein URFA6L [Mus musculus] [M.musculus]
456	15558	AA875537	C, Q, W, QQ, UU		ESTs, Highly similar to SFR2_MOUSE Splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component, 35 kDa) (PR264 protein) [M.musculus]
457	15617	AA875620	Q		ESTs
458	15629	AA875629	RR		ESTs
459	15630	AA875630	EE		ESTs
460	15638	AA875633	K, XX, YY		ESTs
466	11940	AA891108	A		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935323.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
467	21909	AA891161	I, LL, RRR		ESTs
468	15833	AA891171	BBB, CCC		ESTs, Moderately similar to N4BM_HUMAN NADH-ubiquinone oxidoreductase subunit B14.5b (Complex I-B14.5b) (CI-B14.5b) [H.sapiens]
469	18582	AA891207	JJ, KK, PP, QQ, HHH		ESTs
470	21917	AA891220	E, W, DD, EE, SS, LLL, SSS, UUU		ESTs
471	209	AA891222	Z, AA		ESTs
474	15152	AA891314	T		ESTs
475	16446	AA891423	BB, CC, NNN, OOO		ESTs
478	19238	AA891542	Z, AA		ESTs
479	21905	AA891546	ZZ, AAA		ESTs
481	11949	AA891580	ZZ, AAA		ESTs
484	18490	AA891669	G, H		ESTs
486	17052	AA891689	X, Y		ESTs
488	18584	AA891694	Q, R		ESTs
489	1133	AA891717	N, DDD		ESTs, Highly similar to USF1_MOUSE Upstream stimulatory factor 1 (Major late transcription factor 1) [M.musculus]
490	17039	AA891727	E, NNN		ESTs
491	17255	AA891734	O, P, VV		ESTs
492	11959	AA891735	BB, CC, III, JJJ		ESTs
493	17693	AA891737	S, T, NN, OO, KKK		ESTs
494	17256	AA891739	W, XX		ESTs, Weakly similar to F52H3.5.p [Caenorhabditis elegans] [C.elegans]
495	18287	AA891742	N		ESTs
496	13686	AA891749	MM, SS, WW, TTT		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
498	9905	AA891774	E, F, G, L, O, P, V, W, FF, EEE, III, JJJ, MMM, General Core Tox Markers		ESTs
499	17289	AA891785	X, Y, XX		ESTs, Weakly similar to A54756 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42), cytosolic - rat [R.norvegicus]
499	17290	AA891785	II, XX, YY		ESTs, Weakly similar to A54756 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42), cytosolic - rat [R.norvegicus]
500	22124	AA891790	Q		ESTs
503	17311	AA891818	R		ESTs
506	14289	AA891838	S		ESTs, Weakly similar to F10E7.5.p [Caenorhabditis elegans] [C.elegans]
507	20523	AA891842	O, P, W, NN, EEE, III, JJJ, MMM		ESTs
508	20616	AA891851	D		ESTs
511	22314	AA891877	MM, UU, TTT		ESTs
512	17321	AA891881	P		ESTs
514	17308	AA891902	O, P		ESTs
516	17811	AA891922	LL		ESTs
517	19319	AA891937	TT		ESTs, Highly similar to S66254 dolichyl-diphosphooligosaccharide--protein glycotransferase (EC 2.4.1.119) 50K chain - human [H.sapiens]
518	23107	AA891938	V		ESTs, Moderately similar to I49635 mouse Dhml protein - mouse [M.musculus]
520	17437	AA891943	D		ESTs
521	22862	AA891944	C, I, WW, OOO, General Alternate		ESTs
522	1159	AA891949	E, L, Y		ESTs
523	9826	AA891950	III, JJJ, KKK		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
524	4473	AA891965	U		ESTs, Highly similar to fructosamine 3 kinase [Mus musculus] [M.musculus]
525	4474	AA891969	D		ESTs
526	17374	AA891978	K, T		ESTs
528	2106	AA892006	SS	HMm:ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1	ESTs, Highly similar to VAA1_MOUSE Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (V-ATPase A subunit 1) (Vacuolar proton pump alpha subunit 1) (V-ATPase 69 kDa subunit 1) [M.musculus]
528	2107	AA892006	O, P, ZZ, AAA	HMm:ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1	ESTs, Highly similar to VAA1_MOUSE Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (V-ATPase A subunit 1) (Vacuolar proton pump alpha subunit 1) (V-ATPase 69 kDa subunit 1) [M.musculus]
529	15087	AA892010	PPP, QQQ, RRR		ESTs, Weakly similar to T22242 hypothetical protein F45G2.10 - Caenorhabditis elegans [C.elegans]
530	23047	AA892027	Z, AA, II		ESTs
531	3847	AA892036	ZZ, AAA		ESTs, Highly similar to T13964 probable histone deacetylase (EC 3.5.1.-) HDA2 - mouse [M.musculus]
532	13420	AA892042	LL, UU		ESTs
533	22865	AA892083	Q, R		ESTs
536	14595	AA892128	U, FF, WW, BBB, RRR		ESTs
538	12010	AA892137	DD, EE, KKK, NNN		ESTs, Highly similar to open reading frame 12 [Mus musculus] [M.musculus]
539	14330	AA892146	NN		ESTs
540	11384	AA892149	ZZ, AAA		ESTs
542	20917	AA892238	Q, R		ESTs
544	15666	AA892248	II		
544	15667	AA892248	II		
546	11981	AA892257	Y		ESTs
547	18165	AA892259	O, P, VV		ESTs, Highly similar to ICSB_MOUSE INTERFERON CONSENSUS SEQUENCE BINDING PROTEIN (ICSBP) [M.musculus]

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935823.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
549	11982	AA892284	U, ZZ, AAA		ESTs
551	4244	AA892300	T, III, JJJ, KKK		ESTs
557	15492	AA892376	F, L		ESTs
558	3474	AA892378	SS		ESTs, Weakly similar to F13B9.8.p [Caenorhabditis elegans] [C.elegans]
560	2013	AA892390	NN	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
563	4495	AA892399	ZZ, AAA		ESTs
565	17439	AA892446	Z, AA		ESTs
568	11991	AA892483	V		ESTs
571	23888	AA892520	O, GG		ESTs
571	23889	AA892520	BB		ESTs
574	16507	AA892547	GGG, HHH		ESTs, Highly similar to hypothetical protein CL25022 [Homo sapiens] [H.sapiens]
575	4507	AA892551	K		EST
576	11202	AA892554	III, JJJ, KKK		ESTs
576	11203	AA892554	BB, CC, OO, QQ, III, JJJ		ESTs
577	13574	AA892557	M, S, DDD, PPP, QQQ, General Alternate		ESTs
577	13575	AA892557	D, M, S		ESTs
578	18906	AA892561	F, X, GGG		ESTs
579	7906	AA892570	PP, QQ		ESTs
581	19085	AA892598	C, M, MM, KKK, OOO, TTT, General Core Tox Markers		ESTs, Weakly similar to putative nucleotide binding protein, estradiol-induced [Homo sapiens] [H.sapiens]

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
581	19086	AA892598	C, MM, FFF, TTT, General Core Tox Markers		ESTs, Weakly similar to putative nucleotide binding protein, estradiol-induced [Homo sapiens] [H.sapiens]
582	16825	AA892602	Z, AA		ESTs
583	2119	AA892607	GG		ESTs
584	20088	AA892666	E, L		ESTs
585	4523	AA892754	UU		ESTs
586	23783	AA892773	W, III, JJJ, General Core Tox Markers, General Alternate		ESTs
587	4527	AA892774	R, PP, QQ, LLL		ESTs
589	4590	AA892778	SS, III, JJJ, NNN, PPP, QQQ, General Core Tox Markers, General Alternate		ESTs
590	17421	AA892789	BBB, CCC		ESTs
591	19251	AA892796	GG		ESTs
595	17332	AA892829	K, ZZ, AAA	HMm:3'-phosphoadenosine 5' phosphosulfate synthase 1	ESTs, Highly similar to 2204316A ATP sulfurylase-adenosine phosphosulfate kinase [Mus musculus] [M.musculus]
596	19443	AA892832	M, GG, HH, III, JJJ, General Alternate		ESTs
600	17589	AA892851	E, W, PP, QQ, FFF, III, JJJ		ESTs
600	17590	AA892851	A, E, W, KK, UU, ZZ, AAA, III, JJJ, General Alternate		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
601	18887	AA892860	K, DDD		ESTs
602	9053	AA892861	III, JJJ, KKK, OOO, General Core Tox Markers		ESTs
603	7756	AA892864	RRR, SSS		ESTs
604	4531	AA892868	PP, QQ		EST
605	16366	AA892888	BB, CC, GG, HH, NN, EEE, LLL, MMM		EST
605	16367	AA892888	V, BB, CC, GG, HH, NN, DDD, EEE, MMM		EST
606	12848	AA892916	E, BB, CC		ESTs, Weakly similar to JC7260 strictosidine synthase (EC 4.3.3.2) homolog 2 - fruit fly (<i>Drosophila melanogaster</i>) [<i>D.melanogaster</i>]
607	2727	AA892918	C, I		ESTs
610	14465	AA892950	MM, TTT		ESTs, Moderately similar to A Chain A, Crystal Structure Of The Accessory Subunit Of Murine Mitochondrial Polymerase Gamma [<i>M.musculus</i>]
611	8438	AA892986	I, J, HH, LLL, OOO, SSS, UUU, General Alternate		ESTs
613	3853	AA892999	A, B		ESTs
615	3131	AA893032	E, G, H, I, J, III, JJJ, KKK, OOO, General Core Tox Markers		ESTs
616	12020	AA893035	M	HP33	HP33

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935823.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
618	13332	AA893080	E, NN, OO, PP, III, KKK, OOO, General Core Tox Markers, General Alternate		ESTs
619	21305	AA893082	F, NNN		ESTs
620	17691	AA893088	RR		ESTs
621	19745	AA893199	VV, BBB, CCC, General Alternate		ESTs, Highly similar to RIKEN cDNA 1500004D14 [Mus musculus] [M.musculus]
622	2356	AA893202	Z, AA		ESTs
623	4243	AA893217	O, P		ESTs
625	548	AA893235	A, B, E, DD, EE		ESTs, Highly similar to G0S2_MOUSE Putative lymphocyte G0/G1 switch protein 2 (G0S2-like protein) [M.musculus]
627	10538	AA893239	T	2-hydroxyphytanoyl-CoA lyase	2-hydroxyphytanoyl-CoA lyase
629	17752	AA893244	U, X, Y, II, VV, LLL, SSS, UUU, General Alternate		ESTs
632	3783	AA893320	Z, AA		ESTs
635	17800	AA893436	DD		ESTs
636	12312	AA893453	E, H, S, KK, GGG, III, JJJ, OOO, General Core Tox Markers		ESTs
637	21980	AA893454	E, I, L, JJ, KK, LL, UU, HHH, OOO		ESTs
638	2480	AA893471	C, XX, YY, DDD		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935328.1					
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
641	17698	AA893596	JJ, KK		ESTs, Highly similar to RIKEN cDNA 4930548G07 [Mus musculus] [M.musculus]
642	4540	AA893603	ZZ, AAA		ESTs
643	22150	AA893607	ZZ, AAA, UUU		ESTs
645	17838	AA893641	ZZ, AAA		ESTs, Highly similar to synembryn [Mus musculus] [M.musculus]
646	14495	AA893658	GG, EEE, MMM		ESTs
647	4544	AA893664	ZZ, AAA	TEMO	TEMO
649	12028	AA893670	ZZ, AAA		ESTs
653	3035	AA893821	ZZ, AAA		ESTs
654	17891	AA893885	F		ESTs
655	17896	AA893905	UU, General Alternate		ESTs
655	17897	AA893905	G, H, I, J, General Alternate		ESTs
656	23240	AA893939	FFF		ESTs, Highly similar to DSS1_HUMAN Deleted in split hand/split foot protein 1 (Split hand/foot deleted protein 1) [M.musculus]
657	23731	AA894004	O, P, VV, UUU		ESTs, Highly similar to CAPG_MOUSE Macrophage capping protein (Myc basic motif homolog-1) (Actin-capping protein GCAP39) [M.musculus]
658	22584	AA894009	General Alternate		ESTs
659	10540	AA894027	II, JJ, FFF		
660	3895	AA894029	O, P, V, VV		ESTs
663	17953	AA894090	JJ, KK, ZZ, AAA		ESTs
664	2979	AA894099	N		ESTs, Highly similar to vacuolar protein sorting protein 4a; RIKEN cDNA 4930589C15 gene [Mus musculus] [M.musculus]

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
665	3216	AA894101	NNN		ESTs, Moderately similar to PNAD_MOUSE PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) [M.musculus]
665	3217	AA894101	L		ESTs, Moderately similar to PNAD_MOUSE PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) [M.musculus]
668	21989	AA894188	Q, R		ESTs
671	3928	AA894233	Z, AA, RR		ESTs
671	3929	AA894233	JJ		ESTs
674	26051	AA894316	BBB, CCC		ESTs
675	19120	AA894318	ZZ, AAA		ESTs
676	23332	AA894321	D		ESTs, Weakly similar to I49759 hepatocyte growth factor-regulated tyrosine kinase substrate Hrs [imported] - mouse [M.musculus]
677	1578	AA894338	III, JJJ		ESTs, Weakly similar to T24832 hypothetical protein T11F9.11 - Caenorhabditis elegans [C.elegans]
678	17788	AA899045	X		ESTs, Moderately similar to ESTD_HUMAN Esterase D [H.sapiens]
679	21230	AA899057	O, P, Q, R		ESTs
680	4107	AA899109	RR		ESTs
681	18477	AA899120	D, E		
682	12195	AA899121	RR		ESTs, Highly similar to hypothetical protein FLJ20602 [Homo sapiens] [H.sapiens]
683	4607	AA899152	W, SS		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
684	12203	AA899256	Z		ESTs, Moderately similar to IF4G_HUMAN Eukaryotic translation initiation factor 4 gamma (eIF-4-gamma) (eIF-4G) (eIF4G) (P220) [H.sapiens]
685	4196	AA899304	FF, XX, BBB, CCC		ESTs
688	22051	AA899498	F, RRR, UUU		ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]
688	22052	AA899498	K		ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]
689	22308	AA899535	C, OOO		ESTs
690	18588	AA899635	TT, DDD		ESTs, Highly similar to 2020285A BRG1 protein [Mus musculus] [M.musculus]
691	12094	AA899681	U, LL, CCC, DDD		ESTs, Weakly similar to C16C10.11.p [Caenorhabditis elegans] [C.elegans]
692	21354	AA899721	U, FF, LL, BBB, RRR, SSS, UUU		ESTs
693	4663	AA899723	Q, R		EST
695	20038	AA899797	BBB, RRR		EST
696	4095	AA899814	O, P, VV		ESTs
697	2559	AA899828	C, UU		ESTs
698	4674	AA899847	JJ, WW, HHH		ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse (fragment) [M.musculus]
700	22060	AA899898	General Alternate		ESTs
701	4689	AA899899	DDD		ESTs
702	18890	AA899964	U, NN, BBB, RRR, UUU		ESTs
703	8988	AA900148	S		ESTs
707	4730	AA900326	G, H		ESTs
708	15992	AA900422	FF		ESTs
709	4746	AA900452	NNN		EST

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
712	17368	AA900548	OO		ESTs, Weakly similar to T30021 hypothetical protein K08F11.4 - <i>Caenorhabditis elegans</i> [C.elegans]
713	12210	AA900593	UU, WW, KKK		ESTs
714	19258	AA900613	AA		ESTs
717	16067	AA900976	LLL, SSS, UUU		ESTs, Highly similar to S78418 ribosomal protein RL32, mitochondrial [validated] - rat (tentative sequence) (fragment) [R.norvegicus]
718	4801	AA900981	C		EST
719	4822	AA901041	W		ESTs
721	11467	AA901069	D		
722	22897	AA901107	V, NN		ESTs
722	22898	AA901107	V		ESTs
724	4866	AA901350	M, General Alternate		ESTs
725	4879	AA923852	MM, TTT		ESTs
726	3963	AA923955	Q, R, LLL, SSS		ESTs
728	4894	AA923998	Q, R		ESTs
729	17644	AA924036	ZZ		ESTs
730	16370	AA924059	A, B		ESTs
731	14297	AA924092	K		ESTs, Weakly similar to T29507 hypothetical protein W05H7.3 - <i>Caenorhabditis elegans</i> [C.elegans]
734	4171	AA924144	R		ESTs, Weakly similar to T28H10.2.p [Caenorhabditis elegans] [C.elegans]
735	22969	AA924151	KK		ESTs
736	22235	AA924152	Z		ESTs, Weakly similar to guanylyltransferase [Caenorhabditis elegans] [C.elegans]
737	20771	AA924169	VV		ESTs
739	4933	AA924301	NN		ESTs
741	22914	AA924335	O, P		ESTs
745	18434	AA924413	G, H, General Alternate		ESTs, Moderately similar to hypothetical protein MNCb-0169 [Mus musculus] [M.musculus]
746	4954	AA924444	RR		ESTs
748	24310	AA924578	M		ESTs
749	18780	AA924586	XX		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
750	18891	AA924598	U, OO, BBB, RRR, UUU		ESTs
751	2683	AA924604	LL		ESTs
752	4997	AA924673	D		ESTs
756	5011	AA924751	ZZ, AAA		ESTs
757	23030	AA924763	I, J, NNN		ESTs
758	5026	AA924783	LLL, General Core Tox Markers, General Alternate		EST
759	21735	AA924787	DDD		ESTs
760	12372	AA924803	V		ESTs
761	4067	AA924813	WW		ESTs
763	2888	AA924902	U, DDD		ESTs
764	19444	AA924993	NN		ESTs
765	12379	AA925004	D		ESTs
766	22534	AA925045	L, HH		ESTs
767	21458	AA925049	FFF		ESTs
769	5073	AA925061	AA		ESTs, Moderately similar to S20710 hypothetical protein, 16K mouse [M.musculus]
770	20063	AA925063	Z, PP, QQ		ESTs, Weakly similar to T33571 hypothetical protein Y59C2A.2 - Caenorhabditis elegans [C.elegans]
771	23147	AA925137	S		ESTs, Weakly similar to RCA1_YEAST MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 (TAT-BINDING HOMOLOG 12) [S.cerevisiae]
772	23448	AA925167	C, L, HH, GGG		ESTs
773	4904	AA925186	E		ESTs
779	5131	AA925341	UU		ESTs
780	23978	AA925352	III, JJJ		ESTs
782	5141	AA925393	J		Rat mRNA for acetyl-coenzyme A carboxylase (EC 6.4.1.2.) 3' untranslated region
783	5150	AA925432	S		ESTs
786	20805	AA925478	AAA		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
787	24225	AA925490	III, JJJ, General Core Tox Markers, General Alternate		ESTs
788	3993	AA925540	Y		ESTs
790	8092	AA925542	W		ESTs
792	17156	AA925556	O, P		ESTs, Highly similar to B46132 c-Jun leucine zipper interactive (cDNA JZA-20) - mouse (fragment) [M.musculus]
793	4271	AA925603	U, FF, YY, BBB, RRR, SSS		ESTs
795	5213	AA925767	FF		ESTs
796	10588	AA925826	JJ, KK		ESTs
797	18441	AA925849	E		EST
798	3791	AA925854	AA, General Core Tox Markers, General Alternate		ESTs
799	3794	AA925868	HHH		ESTs
800	22224	AA925869	BBB		ESTs
801	23464	AA925876	UU		ESTs
802	12196	AA925983	X, Y		ESTs, Highly similar to hypothetical protein FLJ20602 [Homo sapiens] [H.sapiens]
803	5241	AA925986	Y		ESTs
804	5242	AA925994	S		ESTs
805	23068	AA926036	FFF		ESTs
806	5251	AA926037	SS		ESTs
807	4007	AA926066	GG		ESTs
808	23468	AA926067	JJ, KK		ESTs
809	22967	AA926080	DDD		ESTs
810	5256	AA926088	L		ESTs
811	5258	AA926089	DDD		ESTs, Highly similar to KIAA0164 gene product [Homo sapiens] [H.sapiens]
813	17496	AA926109	KKK, OOO, General Core Tox Markers		ESTs
814	17157	AA926129	E, O, VV		ESTs

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
816	22928	AA926262	FFF, GGG, General Core Tox Markers		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
819	12401	AA926354	P		ESTs
820	22870	AA926360	OOO, General Core Tox Markers, General Alternate		ESTs
822	21827	AA933158	M, DD, EE		ESTs, Highly similar to SKIW_HUMAN Helicase SKI2W (Helicase-like protein) (HLP) [H.sapiens]
823	22008	AA942670	UUU		ESTs
825	6039	AA942716	VV		ESTs, Highly similar to hematological and neurological expressed sequence 1 [Mus musculus] [M.musculus]
827	23005	AA942770	EE, NN, RR, EEE, MMM		ESTs
828	21318	AA942774	A, B		ESTs
830	6615	AA942889	OO, EEE, MMM		ESTs, Weakly similar to Iron-containing alcohol dehydrogenases [Caenorhabditis elegans] [C.elegans]
831	23055	AA942929	General Core Tox Markers, General Alternate		ESTs
832	22121	AA942961	V		ESTs, Highly similar to S57500 signal recognition particle - mouse [M.musculus]
833	11168	AA943009	T		ESTs
834	22130	AA943020	ZZ, AAA		ESTs
837	21987	AA943110	KK		ESTs
840	22187	AA943229	MM, TTT		EST
843	24140	AA943501	D		ESTs
844	22242	AA943506	W		ESTs
846	10394	AA943564	ZZ		ESTs, Weakly similar to Y53C10A.5.p [Caenorhabditis elegans] [C.elegans]
847	21962	AA943588	General Alternate		ESTs, Highly similar to cDNA sequence AB012808; organic cation transporter BOCT [Mus musculus] [M.musculus]

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
849	22092	AA943734	Z, AA		ESTs, Weakly similar to T13C5.6.p [Caenorhabditis elegans] [C.elegans]
851	19220	AA943740	JJJ		ESTs
852	12277	AA943800	NN, III, JJJ		ESTs
853	13027	AA943835	SS		ESTs
856	9549	AA943891	KK		ESTs
858	19129	AA943990	GG		ESTs
860	23527	AA944061	SS		ESTs, Weakly similar to T28052 hypothetical protein ZK858.7 - Caenorhabditis elegans [C.elegans]
861	11255	AA944079	AA		ESTs
862	2658	AA944155	V		ESTs
863	22368	AA944157	OOO, General Core Tox Markers		ESTs
864	22370	AA944158	H, U, BBB, FFF, General Core Tox Markers, General Alternate		ESTs
867	22378	AA944212	I, J		ESTs
868	8321	AA944233	ZZ, AAA		ESTs
869	13507	AA944244	BBB, CCC		ESTs
871	18855	AA944347	D		ESTs
872	4511	AA944348	GG		ESTs
873	16910	AA944352	Z, AA		ESTs, Moderately similar to SUR2_MOUSE Surfeit locus protein 2 (Surf-2) [M.musculus]
874	17901	AA944355	V		ESTs
875	22416	AA944380	U, FF, BBB, RRR, SSS		ESTs, Weakly similar to T26648 hypothetical protein Y38A8.1 - Caenorhabditis elegans [C.elegans]
877	15606	AA944401	V, DD, III, NNN		ESTs, Moderately similar to B Chain B, Vhs Domain Of Tom1 Protein From H. Sapiens [H.sapiens]
878	22681	AA944413	B, W, II		ESTs
879	19229	AA944419	R		ESTs
883	5138	AA944485	WW		ESTs
888	12140	AA944752	KKK		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
891	12306	AA944898	C, F, DD, GG, MM, SS, UU, KKK, TTT		ESTs
892	22519	AA944906	VV		ESTs
893	23029	AA944935	I, J, KKK, NNN		ESTs
895	23985	AA944998	H		ESTs, Weakly similar to A35068 complement factor H-related protein 3A4/5G4 - mouse (fragment) [M.musculus]
896	22548	AA945031	Z		ESTs
897	2813	AA945052	RRR	3-hydroxy-3-methylglutaryl CoA lyase	3-hydroxy-3-methylglutaryl CoA lyase
898	22554	AA945076	G, FFF, HHH, General Core Tox Markers		ESTs
899	13557	AA945090	DD		ESTs
900	22558	AA945123	GGG, General Core Tox Markers		EST
906	12309	AA945193	W		ESTs, Weakly similar to C5MS complement C5 precursor - mouse [M.musculus]
907	22574	AA945268	General Alternate		ESTs
910	6592	AA945325	JJ, KK		ESTs
910	6593	AA945325	KK		ESTs
913	22601	AA945574	S		ESTs
918	22266	AA945601	Q, R, X, NNN		ESTs
918	22267	AA945601	X, Y		ESTs
919	22050	AA945604	RRR, SSS		ESTs
925	22625	AA945704	Q		ESTs
926	21382	AA945708	Y, DDD, LLL, OOO		ESTs
927	23035	AA945712	F, VV, UUU, General Alternate		ESTs
928	18661	AA945751	C, UUU		ESTs
929	18993	AA945763	DDD		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
930	22645	AA945765	P		ESTs
932	16489	AA945784	C		ESTs
933	14419	AA945792	Z, AA		ESTs
934	2671	AA945826	XX, YY		ESTs
935	6720	AA945828	EE, UU, III, JJ, KKK		ESTs
936	18939	AA945875	TT		ESTs, Weakly similar to S12207 hypothetical protein (B2 element) mouse [M.musculus]
937	11256	AA945898	AAA		ESTs
938	22713	AA945904	GG		ESTs
939	8860	AA945915	II, General Alternate		ESTs
940	13482	AA945938	VV		ESTs
941	22690	AA945970	NN, OO		ESTs, Weakly similar to RIKEN cDNA 4933419D20 [Mus musculus] [M.musculus]
942	12318	AA946031	D		ESTs
943	12585	AA946034	JJ, HHH		ESTs
945	18337	AA946046	Z, AA		ESTs
946	22715	AA946120	F	liver regeneration p-53 related protein	liver regeneration p-53 related protein
947	22729	AA946167	UU, DDD, UUU		ESTs
948	8639	AA946221	W		ESTs
949	22755	AA946323	HH		ESTs
950	22069	AA946349	J		ESTs
953	22770	AA946428	PP, QQ		ESTs
954	21968	AA946434	M, Z, AA, KKK		ESTs
955	22772	AA946444	RR		ESTs
956	21878	AA946448	DDD		ESTs
957	21947	AA946451	NN, OO		ESTs, Moderately similar to CGI-105 protein [Homo sapiens] [H.sapiens]
958	17499	AA946467	W, NN, OO		ESTs
959	22042	AA946476	EEE, MMM		ESTs
960	12963	AA946486	P		ESTs
962	22953	AA946509	K		ESTs, Highly similar to JC6524 26S proteasome regulatory complex chain p44.5 - human [H.sapiens]
963	23750	AA946530	WW		ESTs
964	19143	AA946531	WW		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
965	23578	AA955042	V		ESTs, Highly similar to FOL2_MOUSE Folate receptor beta precursor (FR-beta) (Folate receptor 2) (Folate-binding protein 2) [M.musculus]
967	23360	AA955104	D		ESTs
968	23471	AA955162	J		ESTs
969	23320	AA955164	GG, KK, CCC		ESTs
970	23478	AA955181	WW		ESTs
971	23492	AA955211	D		ESTs
972	11231	AA955240	HHH		ESTs, Highly similar to HSPC025; eIEF associated protein HSPC021 [Homo sapiens] [H.sapiens]
973	23512	AA955282	EE		ESTs
974	16509	AA955287	Z, AA		ESTs
975	23520	AA955305	GG		ESTs
976	15383	AA955358	FF		ESTs
977	16823	AA955369	II		ESTs
979	23555	AA955443	C, BB		ESTs
980	23557	AA955447	ZZ, AAA		ESTs, Highly similar to Werner helicase interacting protein, isoform 1; putative helicase RUVBL [Homo sapiens] [H.sapiens]
983	23268	AA955506	WW		ESTs
984	23369	AA955523	DD, EE		ESTs
985	9984	AA955536	V		ESTs, Weakly similar to ELL_MOUSE RNA POLYMERASE II ELONGATION FACTOR ELL (ELEVEN-NINETEEN LYSINE-RICH LEUKEMIA PROTEIN) [M.musculus]
986	23626	AA955540	B, DD, General Alternate		ESTs
987	23629	AA955552	I, J		ESTs
988	12928	AA955564	W, QQ		ESTs, Weakly similar to T21697 hypothetical protein F40E10.6 - Caenorhabditis elegans [C.elegans]
989	23657	AA955630	PPP, QQQ		ESTs
990	23673	AA955684	HH		ESTs
991	23674	AA955691	SS		ESTs
996	14509	AA955871	QQQ		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935828.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
996	14510	AA955871	H, GGG, General Alternate		ESTs
997	24251	AA955887	C, MM, TTT		ESTs
999	4191	AA955926	BB, CC		ESTs, Highly similar to CDK9_HUMAN Cell division protein kinase 9 (Serine/threonine protein kinase PITALRE) (C-2K) [H.sapiens]
1000	17844	AA955927	C, WW, General Core Tox Markers		ESTs
1001	24277	AA955962	General Alternate		ESTs
1002	23285	AA955976	FFF		ESTs
1003	19938	AA955980	L		ESTs
1007	497	AA956278	O, P		ESTs
1011	23766	AA956456	DDD		ESTs
1012	23773	AA956476	P		ESTs
1013	23792	AA956502	D		EST
1014	23799	AA956530	GG		ESTs, Highly similar to hypothetical protein ET [Homo sapiens] [H.sapiens]
1015	22899	AA956555	T		ESTs
1016	23835	AA956668	S		ESTs
1019	12447	AA956769	K, DDD		ESTs
1020	24152	AA956785	UU		ESTs
1024	23928	AA957010	II, UUU		ESTs
1026	23936	AA957044	D		ESTs
1027	23971	AA957160	T		ESTs
1029	24012	AA957335	JJ, HHH		ESTs
1032	24051	AA957452	Z		ESTs
1033	24069	AA957500	F		ESTs
1034	22476	AA957585	AA, II		ESTs
1035	24091	AA957612	D		EST
1037	2230	AA957643	JJ, KK		ESTs
1040	26094	AA957818	RR		
1041	8725	AA957935	DD, EE		ESTs
1041	8726	AA957935	General Alternate		ESTs
1043	20333	AA958005	DDD		ESTs
1044	18653	AA962998	K		ESTs
1045	2725	AA963000	F		ESTs
1048	12513	AA963257	T		ESTs
1050	2049	AA963369	Q		ESTs
1051	2677	AA963443	J		ESTs
1052	2158	AA963505	K		ESTs
1053	2163	AA963560	EE		EST

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1054	2170	AA963590	T		EST
1055	23031	AA963661	KKK		ESTs
1056	2481	AA963664	F		ESTs
					ESTs, Highly similar to P2G4_MOUSE Proliferation-associated protein 2G4 (Proliferation-associated protein 1) (Protein p38-2G4) [M.musculus]
1057	24246	AA963703	G		
1059	18138	AA963815	FF		ESTs
1061	24322	AA964068	KK		ESTs
1063	15474	AA964114	CCC		ESTs
1065	2304	AA964212	E		EST
1066	5936	AA964214	UU		ESTs
			A, B, General Alternate		
1067	2319	AA964259			ESTs
1068	2320	AA964263	NN, OO		ESTs
1069	2335	AA964302	T		ESTs
1070	2342	AA964336	MM, TTT		ESTs
1071	2095	AA964362	DDD		ESTs
			H, PPP, QQQ		ESTs, Highly similar to G01932 queuine tRNA-ribosyltransferase (EC 2.4.2.29) - human [H.sapiens]
1072	2350	AA964368			
1073	2649	AA964377	V		ESTs
1074	2373	AA964455	JJ		ESTs
1076	19452	AA964500	Y, CCC		EST
1077	2383	AA964514	OO		ESTs
1078	11274	AA964535	II		ESTs
1079	2393	AA964544	TT		ESTs
					ESTs, Moderately similar to SH3-domain GRB2-like B1 (endophilin) [Mus musculus] [M.musculus]
1080	23714	AA964563	HHH		
1081	19145	AA964613	KKK		ESTs
1082	2424	AA964617	K, L		ESTs
			PP, QQ, III, JJJ		
1085	2430	AA964641			ESTs
			D, L, Q, R, S		
1086	2433	AA964653			ESTs
			PP, QQ, General Alternate		
1087	2444	AA964692			ESTs
			U, FF, BBB, RRR		
1088	2457	AA964752			ESTs
1089	2459	AA964755	A, B, VV		ESTs

TABLE 1					
Attorney Docket 44921-5038-01WO Document No. 1935623.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1091	2468	AA964807	General Core Tox Markers, General Alternate		ESTs, Weakly similar to K05C4.2.p [Caenorhabditis elegans] [C.elegans]
1092	11324	AA964832	F, Y, General Alternate		ESTs
1094	2486	AA964871	S, MM, TT, WW, TTT, General Alternate		ESTs
1096	12361	AA965031	JJ, General Core Tox Markers, General Alternate		ESTs
1098	2691	AA965075	General Alternate		ESTs
1099	2566	AA965118	SS		ESTs
1100	2568	AA965120	UU		ESTs, Weakly similar to S48963 hypothetical protein YHR121w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]
1101	2569	AA965122	A, K, KK, UU, WW, ZZ, FFF, GGG, HHH, OOO, General Core Tox Markers		ESTs, Weakly similar to T24832 hypothetical protein T11F9.11 - Caenorhabditis elegans [C.elegans]
1102	2581	AA965162	GG		ESTs, Weakly similar to I64799 sepiapterin reductase (EC 1.1.1.153) - rat (fragment) [R.norvegicus]
1103	2584	AA965168	X, Y		EST
1104	16680	AA965190	KKK		ESTs
1106	2620	AA965278	RR		EST
1107	2794	AA996412	N		ESTs
1108	15907	AA996422	General Alternate		ESTs
1109	8527	AA996461	K, FF		ESTs
1110	6783	AA996463	General Alternate		ESTs
1113	2860	AA996581	Z, AA		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1114	2874	AA996640	S		EST
1115	2787	AA996688	Q, R		ESTs
1116	2898	AA996697	ZZ, AAA		ESTs
			C, I, J, KKK, General Core Tox Markers		
1117	2905	AA996727			ESTs
1118	2918	AA996797	S, SS		ESTs
1119	2922	AA996816	GG		ESTs
1120	12589	AA996864	K		ESTs
1122	2940	AA996886	D		ESTs
1123	16496	AA996955	L		ESTs
1124	2978	AA996974	T		ESTs, Highly similar to 1802387B transcription factor IIE:SUBUNIT=small 34kD [Homo sapiens] [H.sapiens]
			PPP, QQQ, General Core Tox Markers		
1126	20694	AA997048			ESTs
1129	3132	AA997191	I, J		EST
			MM, OOO, TTT, General Core Tox Markers		
1130	3145	AA997237			ESTs
1131	17343	AA997242	AA		ESTs
1132	3152	AA997253	WW		EST
			General Core Tox Markers, General Alternate		
1134	19249	AA997342			Rattus norvegicus Ratsg2 mRNA, complete cds
1136	3168	AA997394	DDD		EST
1138	3189	AA997438	III, JJJ, General Core Tox Markers		ESTs, Weakly similar to low density lipoprotein receptor-related protein 6; low density lipoprotein-related protein 6 [Mus musculus] [M.musculus]
1139	17246	AA997522	CCC		ESTs, Highly similar to 2120310B RNA polymerase II elongation factor [Mus musculus] [M.musculus]
1140	16619	AA997544	TT, DDD		EST
1141	21872	AA997577	FF		ESTs
1143	12616	AA997599	OOO		ESTs

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1144	3032	AA997671	General Alternate		Rattus norvegicus putative G-protein coupled receptor RA1c mRNA, complete cds
1146	3452	AA997721	BB, DD, PP, QQ, JJJ, NNN	chemokine orphan receptor 1	chemokine orphan receptor 1
1147	3057	AA997731	RR		EST
1149	3265	AA997784	BB, CC		EST
1150	3268	AA997793	E		ESTs
1152	16071	AA997821	ZZ, AAA		ESTs
1155	3302	AA997905	L, WW, SSS, UUU		ESTs
1156	3308	AA997929	Q, R		ESTs
1157	3722	AA997979	DD, KKK		ESTs
1158	3332	AA998006	ZZ, AAA		ESTs
1160	3346	AA998043	WW		ESTs
1162	3362	AA998092	OO, XX		ESTs
1163	24095	AA998102	RR		ESTs
1165	2084	AA998151	X, Y		ESTs, Highly similar to ORN_HUMAN Oligoribonuclease, mitochondrial precursor (Small fragment nuclease) (CGI-114) [H.sapiens]
1167	16533	AA998174	UU		ESTs
1168	6789	AA998207	F		ESTs
1169	3725	AA998222	EE, NNN		ESTs
1170	3730	AA998234	DD		ESTs
1171	17470	AA998264	X, Y, LLL, UUU		ESTs, Moderately similar to JC2070 NADPH dehydrogenase (flavin) (EC 1.6.8.2) - human [H.sapiens]
1172	3744	AA998266	NN, OO		ESTs
1173	19458	AA998345	GGG		EST
1178	17009	AA998506	General Core Tox Markers, General Alternate		ESTs
1179	3526	AA998556	WW		ESTs
1181	12644	AA998621	UUU		ESTs
1182	3411	AA998638	FFF, GGG		ESTs
1183	22737	AA998660	BBB		ESTs
1184	14404	AA998666	EE		ESTs
1185	3618	AA998701	DDD		EST
1186	3460	AA998752	BBB, CCC		ESTs
1187	13549	AA998807	W		ESTs
1189	3690	AA999006	HH		ESTs

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1190	16821	AA999042	DD, EE, PP, QQ		ESTs
1191	3705	AA999054	HHH		ESTs
1193	3715	AA999103	K		ESTs
1194	3720	AA999138	RRR, SSS		ESTs
1195	3079	AA999169	QQ		ESTs
1201	25124	AB001453	RR		
1204	25134	AB004277	LL		
1213	12019	AB019693	M	HP33	HP33
1218	25160	AF004661	RR		
1219	2012	AF008439	NN	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
1224	18624	AF025308	II		
1226	20283	AF029357	Z, AA		
1227	25170	AF030087	DDD		
1228	23044	AF034218	I, L, NN, OO, PP, QQ, III, JJJ	hyaluronidase 2	hyaluronidase 2
1228	23045	AF034218	J, L, DD, EE	hyaluronidase 2	hyaluronidase 2
1229	7005	AF034237	W, PPP, QQQ		ESTs
1231	20188	AF034900	Z, AA		
1239	3031	AF079864	OOO, General Core Tox Markers, General Alternate		Rattus norvegicus putative G-protein coupled receptor RA1c mRNA, complete cds
1240	25203	AF079873	R	zinc finger protein 162	
1242	21957	AF087437	D, K, ZZ, AAA	core binding factor beta	ESTs
1245	25216	AF091563	D, Z, AA		
1250	21757	AI007656	MM, TTT		ESTs
1252	22733	AI007668	C, DD, EE		ESTs
1253	22746	AI007672	B, W, CC		ESTs
1256	11361	AI007821	General Alternate		ESTs
1257	1804	AI007824	N, T, DD, EE		

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1257	1805	AI007824	DD, KKK, NNN		
1261	11728	AI007884	I, J, WW, KKK, NNN		ESTs
1263	4037	AI007942	UUU		ESTs
1269	23556	AI008205	Q, R		ESTs
1270	4063	AI008258	WW		ESTs
1272	13009	AI008380	WW		ESTs
1273	26123	AI008396	GGG, HHH, General Alternate		
1274	14737	AI008416	L		ESTs
1275	23917	AI008441	LLL		ESTs, Highly similar to G01922 phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - human [H.sapiens]
1276	4084	AI008504	F, BB, CC		ESTs
1278	24359	AI008536	F		ESTs, Highly similar to synbindin; syndecan binding protein 2 [Mus musculus] [M.musculus]
1281	12438	AI008736	UU		ESTs
1282	4103	AI008740	TT		ESTs
1283	24112	AI008773	TT		ESTs
1288	4115	AI008890	O, P, Q, R		ESTs
1289	8130	AI008894	HH		ESTs, Highly similar to T00358 hypothetical protein KIAA0684 - human (fragment) [H.sapiens]
1290	3365	AI008919	W, GG, General Core Tox Markers		ESTs
1291	6818	AI008931	L		ESTs
1294	13936	AI009021	OOO, General Core Tox Markers, General Alternate		ESTs
1295	4951	AI009026	BB, CC, OOO, General Core Tox Markers		ESTs

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1297	4261	AI009079	VV		ESTs
1298	24665	AI009098	CC, FF		ESTs
1299	22151	AI009115	Y, PP		ESTs
1301	15366	AI009132	F		ESTs, Highly similar to RIKEN cDNA 2510048O06 [Mus musculus] [M.musculus]
1302	21595	AI009142	M		ESTs
1303	16904	AI009156	PPP, QQQ		ESTs
1305	12704	AI009194	UU		ESTs
1307	3755	AI009208	A, B		ESTs
1308	3992	AI009222	L		ESTs
1310	15905	AI009274	S		ESTs
1311	7524	AI009350	F, R		ESTs, Weakly similar to C37H5.3.p [Caenorhabditis elegans] [C.elegans]
1312	6382	AI009362	General Alternate		ESTs
1316	4154	AI009467	MM, TTT		ESTs
1318	6826	AI009493	G, H		ESTs
1321	10532	AI009602	CC, III, JJJ		ESTs
1322	6831	AI009644	K, RR		ESTs
1323	21750	AI009663	FF		ESTs
1324	19358	AI009675	T, XX, YY		EST
1325	22840	AI009676	C, DD, KKK, NNN, RRR		ESTs
1327	21192	AI009732	C, HH		ESTs
1329	15089	AI009752	General Core Tox Markers, General Alternate		ESTs
1331	6845	AI009781	SS		ESTs
1332	15593	AI009805	UUU		ESTs, Moderately similar to transmembrane 9 superfamily member 1 [Mus musculus] [M.musculus]
1334	24082	AI009815	BB, CC		ESTs
1335	22619	AI009825	CC, EE, PP, SS, III		ESTs
1336	26133	AI009950	E, BB, III, JJJ		EST
1337	3657	AI010023	II		ESTs
1338	6869	AI010025	CCC		EST
1339	16824	AI010027	II		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1340	15258	AI010104	VV		ESTs
1341	14491	AI010147	III, JJJ		ESTs
1342	6881	AI010169	KK		ESTs
					ESTs, Highly similar to RANG_MOUSE Ran-specific GTPase-activating protein (Ran binding protein 1) (RANBP1) [M.musculus]
1345	3534	AI010261	XX, YY		ESTs
1346	14455	AI010277	S		ESTs
1349	7069	AI010301	OOO		ESTs
1350	6801	AI010316	X		ESTs
					ESTs, Weakly similar to C16C10.11.p [Caenorhabditis elegans] [C.elegans]
1351	12095	AI010339	U		ESTs
1352	16307	AI010416	GG		ESTs
			A, B, W, General Alternate		ESTs
1353	5466	AI010423	W		ESTs
1354	18657	AI010435	DD, EE		EST
1355	6918	AI010445	DD, FF, UU, WW, KKK		ESTs
1358	6919	AI010461	WW		ESTs
1361	6927	AI010542	E		EST
1364	6957	AI010707	K		ESTs
1365	22884	AI010755	V, KKK		ESTs
1366	6986	AI010885			ESTs, Weakly similar to R08B4.3.p [Caenorhabditis elegans] [C.elegans]
1367	8966	AI010944	ZZ, AAA		ESTs
1368	6995	AI011003	SS, WW, General Alternate		ESTs
1370	15679	AI011058	MM, KKK, TTT		ESTs
1372	6044	AI011285	F	synaptic vesicle glycoprotein 2 b	synaptic vesicle glycoprotein 2 b
1373	4268	AI011350	ZZ, AAA		ESTs
1374	7042	AI011387	General Core Tox Markers		ESTs
1378	3934	AI011510	OOO, General Alternate		ESTs
1380	7066	AI011556	O		ESTs
1386	21060	AI011746	GG		ESTs
1387	21468	AI011749	II		ESTs
1389	12745	AI011799			ESTs

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1390	2388	AI011806	K		ESTs, Weakly similar to T31718 hypothetical protein F44E7.9 - <i>Caenorhabditis elegans</i> [C.elegans]
1394	13920	AI011930	WW		ESTs
1395	4205	AI011982	General Alternate		ESTs
1396	12751	AI012074	W		ESTs
1398	9349	AI012143	D		ESTs, Weakly similar to Y33K_HUMAN Hypothetical 33.4 kDa protein [H.sapiens]
1399	2341	AI012144	AAA		ESTs
1400	3697	AI012160	GG		ESTs
1405	2441	AI012231	A, B		ESTs
1406	13569	AI012281	V		ESTs
1407	3957	AI012311	AAA, DDD	poly(ADP-ribose) glycohydrolase	poly(ADP-ribose) glycohydrolase
1410	24200	AI012356	E, CC, DD, UU, III, JJJ, KKK, NNN		ESTs
1411	19638	AI012366	RR		EST
1412	7471	AI012379	NNN		ESTs
1413	12758	AI012385	RR		ESTs
1416	7247	AI012438	HHH		ESTs
1419	2670	AI012552	III, JJJ, General Core Tox Markers, General Alternate		ESTs
1420	9723	AI012556	GG		ESTs, Moderately similar to dolichyl-phosphate mannosyltransferase polypeptide 3 [Homo sapiens] [H.sapiens]
1421	5652	AI012562	ZZ, AAA		ESTs
1422	17489	AI012566	P	unconventional myosin Myr2 I heavy chain	unconventional myosin Myr2 I heavy chain
1425	3961	AI012598	MM, TTT		ESTs, Weakly similar to S37744 endo-exonuclease yNucR - yeast (<i>Saccharomyces cerevisiae</i>) [S.cerevisiae]
1429	7171	AI012761	JJ, KK		ESTs
1431	8594	AI012932	GG		ESTs, Highly similar to hypothetical protein FLJ10099 [Homo sapiens] [H.sapiens]
1434	14033	AI012979	WW, AAA		ESTs

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1435	10641	AI012995	Z, AA		ESTs
					ESTs, Moderately similar to N4AM_HUMAN NADH-ubiquinone oxidoreductase subunit B14.5a (Complex I-B14.5a) (CI-B14.5a) [H.sapiens]
1436	17054	AI013031	II		
			KK, General Core Tox Markers, General Alternate		
1438	7199	AI013044			ESTs
					ESTs, Moderately similar to hypothetical protein FLJ14621 [Homo sapiens] [H.sapiens]
1439	3191	AI013075	A, B		
			Q, R, III, JJJ		
1440	21073	AI013090			ESTs
1443	7248	AI013362	T		ESTs
1444	26147	AI013387	Y		
1445	12793	AI013395	RR		ESTs
1446	19467	AI013397	Z, AA		ESTs
			I, J, BB, OO, LLL, General Alternate		
1449	7225	AI013657			ESTs
1450	15130	AI013676	V		ESTs
1451	17167	AI013690	O, P		ESTs
					ESTs, Weakly similar to Human mRNA KIAA0066 predicted protein like [Caenorhabditis elegans] [C.elegans]
1454	7281	AI013755	L		
1455	2058	AI013756	QQ		ESTs
			A, B, FF, GGG, OOO, General Core Tox Markers		
1457	2799	AI013778			ESTs
1458	4066	AI013782	E		ESTs
			PP, QQ, BBB		
1460	3260	AI013875			ESTs
1463	8585	AI013886	K		ESTs
1464	21454	AI013888	Z, AA		ESTs
1465	21074	AI013890	NN, OO		ESTs
1467	11547	AI013912	II		ESTs
1468	15786	AI013924	PP, SS		ESTs
			EEE, MMM		
1470	12779	AI013978			ESTs
1471	15936	AI013993	DD, EE		ESTs
1472	23646	AI014072	M		ESTs

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1473	7214	AI014145	YY		ESTs
1474	12431	AI014149	K		ESTs
1475	6277	AI014154	XX		ESTs
1476	7344	AI028942	OOO, General Core Tox Markers, General Alternate		ESTs
1477	7345	AI028948	N		ESTs
1478	7362	AI029026	M, EE		ESTs
1479	21933	AI029057	E, KKK, UUU		ESTs
1481	6792	AI029066	D		ESTs
1482	7384	AI029143	NN, OO		ESTs
1483	7393	AI029191	FF		ESTs
1484	7402	AI029211	D		EST
1485	3647	AI029285	ZZ, AAA		ESTs
1487	7639	AI029292	L, Z, AA		ESTs
1488	7448	AI029434	JJ, KK		ESTs
1490	2668	AI029455	CCC		ESTs
1492	15594	AI029672	CCC		ESTs, Moderately similar to transmembrane 9 superfamily member 1 [Mus musculus] [M.musculus]
1493	7514	AI029694	JJ, KK		ESTs
1494	7517	AI029709	BBB		ESTs, Moderately similar to hypothetical protein FLJ20399 [Homo sapiens] [H.sapiens]
1495	7380	AI029723	Q, R, W		ESTs
1498	2108	AI029960	ZZ, AAA	HMm:ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1	ESTs, Highly similar to VAA1_MOUSE Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (V-ATPase A subunit 1) (Vacuolar proton pump alpha subunit 1) (V-ATPase 69 kDa subunit 1) [M.musculus]
1499	2310	AI029969	BB, OO		ESTs
1500	7574	AI029976	D		ESTs
1501	7582	AI029996	I, J, OOO, General Core Tox Markers		ESTs
1502	7583	AI030001	EE, KKK		EST
1503	7586	AI030024	H		ESTs
1504	14492	AI030091	OO		ESTs

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1505	7617	AI030170	OOO, General Core Tox Markers		ESTs
1506	7618	AI030172	Z, AA		ESTs
1508	7003	AI030259	W, EE, OOO, General Core Tox Markers		ESTs, Moderately similar to hypothetical protein MGC12904 [Homo sapiens] [H.sapiens]
1509	6553	AI030271	RRR		ESTs
1510	5856	AI030284	DDD		ESTs
1511	6192	AI030301	LL, SS		ESTs
1512	7681	AI030449	S		ESTs, Moderately similar to methyltransferase-like 1 (S. cerevisiae) [Mus musculus] [M.musculus]
1513	10710	AI030494	GG, HH, JJJ, KKK		ESTs
1514	2997	AI030545	U, EEE, MMM		ESTs
1516	7736	AI030681	E		EST
1517	7745	AI030706	MM, TTT		ESTs
1519	21172	AI030799	KK		ESTs
1520	2911	AI030835	I, J, T, General Core Tox Markers		ESTs
1521	10748	AI030839	D		EST
1522	19560	AI030921	D		EST
1526	7825	AI031023	VV		ESTs
1527	7831	AI031035	RRR		ESTs
1528	5350	AI043611	M		ESTs
1530	7860	AI043662	M, SS		ESTs
1531	19617	AI043664	D, RR		EST
1532	7882	AI043720	TT		EST
1533	7584	AI043724	JJ, General Alternate		ESTs
1534	5263	AI043745	SS, TT		ESTs
1535	2901	AI043752	FFF		ESTs
1537	7893	AI043761	General Core Tox Markers		EST
1538	7903	AI043805	FFF, General Core Tox Markers		ESTs
1539	10805	AI043840	Z, AA		EST
1541	3899	AI043904	B		ESTs

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Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1542	7926	AI043913	K, X, Y, SSS, UUU		ESTs
1543	7938	AI043953	JJ, KK		EST
1544	17625	AI043961	D		EST
1546	19121	AI044101	NN		ESTs
1547	5386	AI044137	RR		
1548	5396	AI044176	EE		EST
1549	5419	AI044225	D		ESTs
1551	4892	AI044292	E, NN		ESTs
1553	5464	AI044345	F, FFF		ESTs
1554	5465	AI044348	XX, PPP, QQQ, General Alternate		ESTs, Moderately similar to hypothetical protein FLJ11218 [Homo sapiens] [H.sapiens]
1555	21228	AI044404	II		ESTs
1556	18986	AI044478	C		ESTs
1557	5523	AI044568	KKK, NNN		ESTs
1559	9889	AI044621	U, GG		ESTs
1560	9893	AI044643	RR		ESTs
1562	19300	AI044706	F, S		EST
1567	22179	AI044906	D		ESTs
1568	9924	AI044915	RR		ESTs
1569	4047	AI044947	Q, R		ESTs
1570	5662	AI044987	AA		ESTs
1571	6740	AI045003	General Alternate		ESTs, Moderately similar to hypothetical protein DJ167A19.1 [Homo sapiens] [H.sapiens]
1572	9940	AI045008	X, Y		ESTs
1573	24290	AI045040	RRR, SSS, UUU, General Alternate		ESTs, Weakly similar to T15251, hypothetical protein K07B1.4 - Caenorhabditis elegans [C.elegans]
1574	5684	AI045056	L		ESTs
1575	3406	AI045083	N		ESTs, Moderately similar to Y256_HUMAN HYPOTHETICAL PROTEIN KIAA0256 [H.sapiens]
1576	5696	AI045116	S		ESTs
1577	20444	AI045118	General Alternate		ESTs
1579	5703	AI045136	S		ESTs
1580	9963	AI045144	J, S		EST, Moderately similar to A34372 complement C6 precursor - human [H.sapiens]
1585	20524	AI045201	E, JJJ, NNN		ESTs
1587	18932	AI045451	F		ESTs
1588	5809	AI045488	RR		EST

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1589	10008	AI045546	AA		ESTs, Highly similar to Y233_HUMAN Hypothetical protein KIAA0233 [H.sapiens]
1590	5824	AI045555	X		ESTs
1591	12825	AI045672	MM, TTT		ESTs, Weakly similar to T25443 hypothetical protein B0261.4 - Caenorhabditis elegans [C.elegans]
1592	5873	AI045767	GGG		ESTs
1595	5886	AI045807	EE		ESTs
1596	5890	AI045836	D		ESTs
1597	8701	AI045945	KK		ESTs
1598	10053	AI045948	WW		ESTs
1599	6825	AI045972	CC, III, UUU		ESTs
1601	10055	AI058291	NN, OO		EST, Weakly similar to Glutaredoxin, Zinc finger, C3HC4 type (RING finger) [Caenorhabditis elegans] [C.elegans]
1602	16765	AI058319	General Core Tox Markers		ESTs
1604	8025	AI058365	O, P		ESTs, Moderately similar to uncharacterized bone marrow protein BM033 [Homo sapiens] [H.sapiens]
1606	8627	AI058453	RR		ESTs
1608	8065	AI058509	W		ESTs
1609	8068	AI058524	M		ESTs
1610	8177	AI058603	BBB		ESTs
1612	8113	AI058669	RR		ESTs
1613	10084	AI058674	T		ESTs, Highly similar to MTR3_MOUSE Myotubularin-related protein 3 [M.musculus]
1614	3090	AI058730	II, VV		ESTs
1615	10093	AI058746	DDD		ESTs
1616	8143	AI058759	AA, FFF		ESTs
1617	10103	AI058821	L		EST
1618	18178	AI058881	N		ESTs
1619	4789	AI058889	MM, TTT		ESTs
1621	5549	AI058942	LLL		ESTs
1622	8600	AI058956	KKK, General Core Tox Markers		ESTs
1623	8202	AI058990	Q, R		ESTs
1624	8206	AI059010	W		ESTs
1625	4155	AI059014	MM, TTT		ESTs
1626	8220	AI059046	HH		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1627	8221	AI059061	JJ, KK		ESTs
1629	8230	AI059117	JJ, KK		ESTs
1630	8232	AI059122	D		ESTs
1632	8283	AI059290	K		ESTs
1633	8285	AI059298	XX		ESTs
1634	8303	AI059352	LL, General Alternate		ESTs
1635	8314	AI059386	Q, W		ESTs
1638	10200	AI059444	Z, UUU		ESTs
1639	14518	AI059477	N		ESTs, Moderately similar to POL3_MOUSE Retrovirus-related POL polyprotein (Endonuclease) [M.musculus]
1640	8344	AI059511	A, B		EST
1641	19230	AI059604	II, UUU		ESTs
1642	8392	AI059638	RR		ESTs
1643	8422	AI059723	N, UUU		EST
1644	9383	AI059824	HH		ESTs
1645	8457	AI059835	HH		ESTs
1646	10270	AI059856	DD, EE, HH, PP, QQ		ESTs
1647	10281	AI059947	General Alternate		ESTs
1648	8490	AI059962	B, UUU, General Alternate		ESTs
1650	8494	AI059968	II		ESTs
1651	8500	AI059983	LL		ESTs
1653	8520	AI060052	OOO, General Alternate		ESTs, Moderately similar to RIKEN cDNA B230118H07 [Mus musculus] [M.musculus]
1654	8522	AI060071	E, BB, III, JJJ		ESTs
1655	10315	AI060178	X, Y		ESTs
1656	23776	AI060224	II		ESTs
1657	8116	AI060271	V		ESTs, Weakly similar to T28787 hypothetical protein C41D11.5 - Caenorhabditis elegans [C.elegans]
1658	18322	AI060279	WW, DDD		ESTs
1659	10332	AI060283	QQ		EST
1660	3498	AI069912	MM, TTT		ESTs
1661	8715	AI069920	I, J, DD, WW, General Alternate		ESTs
1662	10359	AI069975	C		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1663	10363	AI069986	A, B		ESTs, Weakly similar to S.pombe hypothetical protein C1D4.09C like [Caenorhabditis elegans] [C.elegans]
1664	8710	AI070058	AA		ESTs
1666	8789	AI070073	M		ESTs
1668	8808	AI070132	ZZ, AAA, PPP, QQQ, General Core Tox Markers, General Alternate		ESTs
1670	8809	AI070134	PP, QQ		ESTs
1672	7743	AI070233	V, NN		ESTs
1673	24372	AI070241	XX		ESTs
1674	16905	AI070275	GG		ESTs
1675	10396	AI070294	X, Y		ESTs
1676	4437	AI070308	Q, R	HMm:genes associated with retinoid-IFN-induced mortality 19	ESTs, Highly similar to genes associated with retinoid-IFN-induced mortality 19; RIKEN cDNA 2700054G14 gene [Mus musculus] [M.musculus]
1677	8864	AI070319	K		ESTs
1679	8874	AI070336	VV		ESTs
1680	23137	AI070408	Q, R		ESTs
1681	10418	AI070411	JJ, KK		EST
1682	14424	AI070421	Q, II		ESTs
1683	9767	AI070459	XX, YY		ESTs, Highly similar to PSD7_MOUSE 26S proteasome non-ATPase regulatory subunit 7 (26S proteasome regulatory subunit S12) (Proteasome subunit p40) (Mov34 protein) [M.musculus]
1685	8931	AI070531	FF		ESTs
1690	10472	AI070809	PPP, QQQ		ESTs
1691	9012	AI070879	FFF, OOO, General Core Tox Markers		EST

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1692	9016	AI070903	A, B, GGG, HHH, PPP, General Core Tox Markers		EST
1693	8720	AI071023	N		ESTs, Weakly similar to YG5I_YEAST Hypothetical 29.9 kDa protein in APL6-MES1 intergenic region [S.cerevisiae]
1695	11006	AI071155	D		ESTs
1696	18792	AI071177	General Core Tox Markers		ESTs
1697	9583	AI071185	A, B, CC, NN, OO		ESTs
1699	16799	AI071197	T		ESTs
1701	11019	AI071240	X, Y		EST
1702	9079	AI071251	L, NN		ESTs, Moderately similar to A57050 K-glypican precursor - mouse [M.musculus]
1703	11024	AI071285	D, V		ESTs
1705	11057	AI071509	SS		ESTs
1706	9668	AI071538	W		ESTs
1707	9669	AI071563	E		ESTs
1708	5695	AI071566	PP, QQ		ESTs, Weakly similar to SYBSR threonine synthase (EC 4.2.99.2) yeast (Saccharomyces cerevisiae) [S.cerevisiae]
1709	22929	AI071578	B, Z, II, FFF, GGG, HHH, OOO, General Core Tox Markers		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
1709	22930	AI071578	FFF, GGG, OOO, General Core Tox Markers		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
1710	9720	AI071727	O, P		EST
1711	11097	AI071749	D		EST
1712	9735	AI071773	YY		ESTs
1714	9772	AI071886	FF		EST

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
1716	8711	AI071934	N		ESTs
1717	9788	AI071958	T		ESTs
1719	9800	AI072014	ZZ		ESTs, Weakly similar to U2af50-P1 [Drosophila melanogaster] [D.melanogaster]
1720	9805	AI072034	W, LLL, RRR, SSS, UUU		ESTs
1722	13426	AI072081	I, J, RR		ESTs
1724	9196	AI072121	II		ESTs, Weakly similar to 2118405G hexaprenyl pyrophosphate synthetase [Saccharomyces cerevisiae] [S.cerevisiae]
1725	20123	AI072214	H, V, General Alternate		ESTs, Weakly similar to T26686 hypothetical protein Y38F1A.6 - Caenorhabditis elegans [C.elegans]
1726	9245	AI072278	General Core Tox Markers		ESTs, Weakly similar to T08793 hypothetical protein DKFZp586F0422.1 - human (fragment) [H.sapiens]
1728	14231	AI072358	GG, HH		ESTs
1729	10866	AI072380	K		ESTs
1730	18877	AI072393	JJ		ESTs
1732	17680	AI072403	VV		ESTs, Highly similar to S43484 heterogeneous nuclear ribonucleoprotein F - human [H.sapiens]
1733	9292	AI072485	General Core Tox Markers, General Alternate		ESTs
1734	10893	AI072559	N		EST
1735	10902	AI072603	PPP, QQQ		ESTs
1736	9331	AI072633	General Core Tox Markers		ESTs
1738	9336	AI072643	GGG		EST
1739	6548	AI072658	PP, QQ		ESTs
1740	9348	AI072667	T		EST
1741	9368	AI072706	L		ESTs, Moderately similar to RGR_MOUSE RPE-retinal G protein-coupled receptor [M.musculus]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1742	9372	AI072712	KK, BBB, RRR, SSS		ESTs
1743	10918	AI072733	I, J, DD, EE, JJJ		EST
1744	16813	AI072746	VV		EST
1745	9384	AI072751	HH		ESTs
1746	9385	AI072755	JJ, KK		ESTs
1748	9432	AI072914	KKK		EST
1749	15518	AI072945	ZZ, AAA		ESTs
1750	22269	AI072965	RR		ESTs
1751	10940	AI072998	V		EST
1752	9469	AI073023	D		ESTs
1753	9471	AI073035	ZZ, AAA		ESTs
1754	10944	AI073039	E, RR		ESTs
1755	9475	AI073059	FFF, SSS, UUU		ESTs
1756	7074	AI073086	FFF		ESTs
1757	5091	AI073092	C, LL		ESTs
1758	10958	AI073105	DD, EE		ESTs
1759	10968	AI073207	RR		ESTs
1760	5340	AI073239	Z, AA		ESTs
1761	23124	AI100785	M, OOO, General Alternate		ESTs, Highly similar to germ cell-less homolog (Drosophila) [Mus musculus] [M.musculus]
1762	9190	AI100835	I, DDD		ESTs
1764	10594	AI100878	Q, R		ESTs, Highly similar to hypothetical protein EST00098 [Homo sapiens] [H.sapiens]
1765	4444	AI100882	B, V, BB, CC		ESTs, Highly similar to HSCO protein [Mus musculus] [M.musculus]
1767	5687	AI101006	NN		ESTs
1768	11942	AI101094	RR		ESTs
1770	24165	AI101113	D, V		ESTs
1771	17705	AI101150	T, LL, TT		ESTs
1772	21913	AI101181	L		ESTs
1773	7868	AI101229	OO, OOO, General Core Tox Markers		ESTs
1774	2220	AI101258	XX, YY		ESTs
1775	11742	AI101262	General Core Tox Markers		ESTs
1776	5421	AI101270	NN, OO, VV	HMm:Rho, GDP dissociation inhibitor (GDI) beta	ESTs, Highly similar to I49687 GDP-dissociation inhibitor - mouse [M.musculus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1777	7870	AI101319	Y		ESTs
			G, General Alternate		ESTs, Weakly similar to W06D4.4.p [Caenorhabditis elegans] [C.elegans]
1779	4650	AI101582	T, RRR, SSS, UUU		
1780	5597	AI101622	PP, QQ		ESTs
1781	2295	AI101674	C		ESTs
1783	5074	AI101695			ESTs
					ESTs, Highly similar to ubiquitin-like 5 [Mus musculus] [M.musculus], ESTs, Moderately similar to F46F11.4.p [Caenorhabditis elegans] [C.elegans]
1784	11213	AI101864	V, XX		
1785	2042	AI101921	O, P, PP		ESTs
					ESTs, Highly similar to cDNA sequence AB012808; organic cation transporter BOCT [Mus musculus] [M.musculus]
1786	21965	AI101977	S		
			III, LLL, OOO, UUU, General Core Tox Markers		ESTs
1787	14208	AI102017	Q, R		ESTs
1793	21592	AI102065	T		ESTs
1794	18565	AI102073	LL		ESTs
1795	6213	AI102190	Z, AA		ESTs
1796	11463	AI102236	PPP, QQQ		ESTs
1797	10227	AI102248			ESTs
					ESTs, Moderately similar to B154_MOUSE BRAIN PROTEIN I54 [M.musculus]
1798	22099	AI102258	UUU		ESTs
1799	9522	AI102382	RRR		ESTs
1800	3320	AI102482	RR		ESTs
1804	11563	AI102560	NNN		ESTs
1805	19769	AI102570	E, III, JJJ		
1806	21056	AI102574	LLL		ESTs
1809	17510	AI102595	ZZ, AAA		ESTs
					ESTs, Highly similar to proline rich protein expressed in brain [Mus musculus] [M.musculus]
1810	15515	AI102612	M, ZZ, AAA		ESTs
1811	19011	AI102618	E, SS		ESTs
1812	23837	AI102620	KKK		ESTs
			W, General Alternate		
1816	8837	AI102849			ESTs

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1817	11228	AI102871	U, General Core Tox Markers		ESTs
1820	11723	AI102896	K		ESTs
1821	6541	AI102905	JJ, NN, OO		ESTs
1822	22628	AI102955	T, KKK		ESTs
1823	24229	AI102972	N		ESTs
1824	13222	AI102977	C, DD, EE		ESTs
1825	8784	AI103007	RRR		ESTs, Weakly similar to T20117 hypothetical protein C50F4.11 - Caenorhabditis elegans [C.elegans]
1826	10659	AI103059	BB, CC, NNN		ESTs
1827	2316	AI103084	LL		ESTs, Moderately similar to selective hybridizing clone [Mus musculus] [M.musculus]
1829	15128	AI103098	V		ESTs
1831	17753	AI103246	MM, TTT		ESTs, Highly similar to JC6067 CCAAT-binding factor CBF1 - mouse [M.musculus]
1832	24181	AI103320	General Alternate		ESTs, Weakly similar to Y40B1B.7.p [Caenorhabditis elegans] [C.elegans]
1834	1807	AI103365	YY		
1835	5197	AI103376	BB, CC		ESTs, Weakly similar to T31650 hypothetical protein Y57A10A.cc - Caenorhabditis elegans [C.elegans]
1838	4355	AI103410	MM, TTT, General Alternate		ESTs
1840	17168	AI103441	OO		ESTs
1841	15841	AI103465	MM, TTT		ESTs, Moderately similar to RP29_HUMAN Ribonuclease P protein subunit p29 [H.sapiens]
1844	21579	AI103572	W		ESTs
1848	2752	AI103641	Q, R		ESTs
1849	17553	AI103643	X, Y		ESTs
1851	4856	AI103708	O		ESTs
1855	17762	AI103854	H		ESTs, Highly similar to S37488 gene T10 protein - mouse [M.musculus]
1856	7434	AI103954	Z, AA		ESTs
1859	26213	AI104113	T		
1861	20542	AI104173	KKK		
1862	11738	AI104213	LL		ESTs

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1864	21752	AI104250	LL		ESTs, Highly similar to presenilins associated rhomboid-like protein; hypothetical protein PRO2207 [Homo sapiens] [H.sapiens]
1865	5907	AI104261	N		ESTs
1866	7184	AI104297	F, II		ESTs
1868	7223	AI104373	LLL, UUU		ESTs, Highly similar to RIKEN cDNA 2810428115 [Mus musculus] [M.musculus]
1871	7006	AI104405	W		ESTs
1874	18235	AI104523	Z		ESTs
1877	15019	AI104552	PP, QQ		ESTs
1878	4782	AI104570	D		ESTs
1880	2484	AI104675	NN, OO, GGG, General Core Tox Markers		ESTs
1883	8273	AI104908	NN, EEE, MMM		ESTs
1885	23836	AI105088	CCC		ESTs, Highly similar to RAN guanine nucleotide release factor [Mus musculus] [M.musculus]
1888	5246	AI105144	Z, AA		ESTs
1889	11492	AI105145	HH, OOO, General Core Tox Markers		ESTs
1891	17768	AI105196	HH, KKK		ESTs
1892	2196	AI105243	J		ESTs
1894	13231	AI105376	Z, AA		ESTs
1895	22931	AI105417	M, FFF, GGG, General Core Tox Markers		ESTs, Moderately similar to S29993 P311 protein - mouse [M.musculus]
1896	22948	AI105421	C		ESTs
1899	9141	AI111407	JJ, KK		ESTs
1900	4013	AI111441	PP, QQ		ESTs
1902	8305	AI111695	Z, AA		ESTs
1903	3309	AI111725	UUU		ESTs
1904	9047	AI111825	HH		ESTs
1906	24275	AI111854	RRR		ESTs, Weakly similar to T33164 hypothetical protein T26C12.1 - Caenorhabditis elegans [C.elegans]

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1907	2539	AI111960	I, J, General Alternate		ESTs, Weakly similar to FKB5_MOUSE 51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) [M.musculus]
1909	19219	AI112059	RR		ESTs
1910	12909	AI112074	RR		ESTs
1911	4914	AI112086	A, B, II, NN, OO, XX, EEE, FFF, MMM, OOO, General Core Tox Markers		ESTs
1912	22522	AI112092	V, BB, CC, LL, NN, OO, EEE, MMM		ESTs
1913	4143	AI112107	OOO, General Core Tox Markers		ESTs
1914	14560	AI112111	A, B, Q, R		ESTs
1915	4161	AI112141	O, P		ESTs, Weakly similar to A55169 pre-T-cell receptor alpha chain precursor - mouse [M.musculus]
1916	9754	AI112194	OOO, General Core Tox Markers	seizure related gene 6	seizure related gene 6
1919	9654	AI112416	DDD		ESTs
1920	2482	AI112802	II		ESTs
1921	11376	AI112863	O, P		ESTs
1922	12965	AI112926	Q, R, MM, TTT		ESTs, Moderately similar to ALKB_HUMAN Alkylated DNA repair protein alkB homolog [H.sapiens]
1923	14512	AI112964	G, GGG, General Core Tox Markers		ESTs
1924	12969	AI112969	Q		ESTs
1927	6555	AI113020	M, SS		ESTs
1931	17253	AI136523	D, E		ESTs

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1932	9595	AI136630	PP, LLL, SSS, UUU		ESTs
1933	8985	AI136672	RR		ESTs
1934	11301	AI136709	HH		ESTs
1935	9373	AI136714	BBB, DDD		ESTs
1937	3488	AI136830	GG		ESTs, Weakly similar to B0432.8.p [Caenorhabditis elegans] [C.elegans]
1938	23851	AI136862	GG, HH, UUU		ESTs, Highly similar to carcinoma related gene [Mus musculus] [M.musculus]
1941	12142	AI136972	E		ESTs
1945	22722	AI137211	JJ, FFF		ESTs
1946	14915	AI137232	C		ESTs, Weakly similar to Yeast YIP1 protein like [Caenorhabditis elegans] [C.elegans]
1948	22234	AI137344	A, B, NNN, General Core Tox Markers, General Alternate		ESTs
1949	9192	AI137345	U, HH, XX, YY		ESTs
1951	19064	AI137443	E, HH	HMM:endonuclease G	ESTs, Highly similar to NUCG_MOUSE Endonuclease G, mitochondrial precursor (Endo G) [M.musculus]
1953	21164	AI137488	LL, BBB, RRR, SSS, General Alternate		ESTs
1956	17369	AI137572	NN		ESTs, Weakly similar to T30021 hypothetical protein K08F11.4 - Caenorhabditis elegans [C.elegans]
1957	6638	AI137579	General Alternate		ESTs
1961	5104	AI137783	RR		ESTs
1963	14459	AI137930	E, EE, XX, YY		ESTs
1964	13153	AI137935	J		ESTs
1965	12030	AI137976	FFF		ESTs

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1969	23183	AI144586	M, FF, HHH, General Alternate	eveclin-1	eveclin-1
1970	23187	AI144591	PP, QQ		ESTs
1971	5993	AI144612	SS		ESTs
1972	2264	AI144741	HH		ESTs
1973	6291	AI144797	I, LL		ESTs
1974	7887	AI144832	S, PPP		ESTs, Highly similar to SYR_HUMAN ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS) [H.sapiens]
1975	10529	AI144877	M		ESTs
1976	8880	AI144936	UUU		ESTs
1978	13018	AI145424	KK		ESTs
1979	5235	AI145569	S		ESTs, Weakly similar to YJ05_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 [C.elegans]
1980	24170	AI145601	NNN, General Core Tox Markers, General Alternate		ESTs
1982	23631	AI145650	O, P		ESTs
1983	8634	AI145722	MM, TTT, General Alternate		ESTs, Weakly similar to T31511 hypothetical protein Y116A8C.9 - Caenorhabditis elegans [C.elegans]
1984	8339	AI145761	General Core Tox Markers, General Alternate		ESTs, Weakly similar to T21659 hypothetical protein F32D8.4 - Caenorhabditis elegans [C.elegans]
1985	5874	AI145801	M, GGG, General Core Tox Markers, General Alternate		ESTs
1987	18522	AI145870	M, General Core Tox Markers		ESTs, Moderately similar to RIKEN cDNA 1110025H10 [Mus musculus] [M.musculus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
1989	11576	AI146177	FFF, OOO, General Core Tox Markers		ESTs
1992	18473	AI168975	X, TT		ESTs, Weakly similar to Yeast hypothetical 52.9 KD protein like [Caenorhabditis elegans]
1993	11551	AI168981	O, P		ESTs
1994	2060	AI168996	WW		ESTs
1995	22559	AI169007	FFF		ESTs
1997	21523	AI169104	II		ESTs, Highly similar to A26774 platelet factor 4 precursor - rat [R.norvegicus]
1999	16484	AI169116	QQQ		ESTs
2000	10984	AI169156	NN, EEE, MMM, General Core Tox Markers		ESTs
2001	23075	AI169166	General Core Tox Markers		ESTs
2004	12979	AI169177	NNN		ESTs, Highly similar to S33363 gly96 protein - mouse [M.musculus]
2005	806	AI169231	O, P		ESTs, Highly similar to G33_RAT GENE 33 POLYPEPTIDE [R.norvegicus]
2006	5038	AI169239	Z, AA		ESTs
2007	15323	AI169255	RR		ESTs
2008	24162	AI169279	XX, YY, General Core Tox Markers		ESTs
2010	22986	AI169291	S		ESTs
2011	7497	AI169302	JJ, PPP, QQQ		ESTs, Highly similar to S27393 sphingomyelin phosphodiesterase (EC 3.1.4.12), acidic, splice form 1 precursor - mouse [M.musculus]
2012	13910	AI169308	NNN		ESTs
2020	24163	AI169430	K, L		ESTs, Weakly similar to T29315 hypothetical protein F36D4.5 - Caenorhabditis elegans [C.elegans]
2022	6623	AI169595	FF		ESTs

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2024	24592	AI169622	T, PP, QQ	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic
2028	11429	AI169706	G		ESTs
2029	20466	AI169735	LL, GGG, UUU, General Alternate		Rat cytochrome P450IIB3 (P450IIB subfamily) mRNA, complete cds
2032	4274	AI169829	E		ESTs
2035	3916	AI169947	A, H, II, FFF, HHH, PPP, QQQ, General Core Tox Markers		ESTs
2036	5954	AI169984	YY, PPP, QQQ		ESTs
2038	5899	AI170038	A, General Core Tox Markers		ESTs
2039	21185	AI170056	B		ESTs
2040	21254	AI170059	D		ESTs
2041	22014	AI170117	RRR		ESTs
2044	15102	AI170298	RR		ESTs
2047	2729	AI170363	Z, AA		ESTs
2048	5297	AI170379	W		ESTs
2049	22707	AI170384	LLL		ESTs
2050	19728	AI170394	FFF		ESTs
2051	18744	AI170407	PP, QQ		ESTs
2052	7106	AI170446	AA		ESTs
2057	17778	AI170538	ZZ, AAA		ESTs, Highly similar to RIKEN cDNA 2610206B05 [Mus musculus] [M.musculus]
2059	6164	AI170597	HH, General Alternate		ESTs, Moderately similar to hypothetical protein AF053356_CDS3 [Homo sapiens] [H.sapiens]
2060	13364	AI170606	PP, QQ, TT		ESTs, Weakly similar to DRNG_RAT DEOXYRIBONUCLEASE GAMMA PRECURSOR (DNASE GAMMA) (DEOXYRIBONUCLEASE I-LIKE 3) (DNASEY) [R.norvegicus]

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2061	6272	AI170617	Z		ESTs, Highly similar to DAZ associated protein 1 [Homo sapiens] [H.sapiens]
2063	12698	AI170665	XX		ESTs
2064	5057	AI170671	RR, SS		ESTs
2065	10593	AI170673	ZZ		ESTs
2068	9757	AI170693	A, B, Q, R, U, BBB, CCC		ESTs
2069	11686	AI170715	RR		ESTs, Weakly similar to DD21_MOUSE Nucleolar RNA helicase II (Nucleolar RNA helicase Gu) (RH II/Gu) (DEAD-box protein 21) [M.musculus]
2070	23612	AI170751	L		ESTs
2072	4868	AI170763	III, JJJ		ESTs
2073	18905	AI170770	YY		ESTs, Highly similar to NUCM_HUMAN NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial precursor (Complex I-49KD) (CI-49KD) [H.sapiens]
2074	3803	AI170773	X, Y, Z		Rattus norvegicus 250 kDa estrous-specific protein mRNA, partial cds
2075	3023	AI170795	G		ESTs
2076	1902	AI170809	A, B, Z, AA, PPP, QQQ		ESTs
2077	22204	AI170820	C, MM, TTT		ESTs
2079	2811	AI171090	FF, BBB, CCC, RRR, SSS	3-hydroxy-3-methylglutaryl CoA lyase	3-hydroxy-3-methylglutaryl CoA lyase
2079	2812	AI171090	BBB, CCC	3-hydroxy-3-methylglutaryl CoA lyase	3-hydroxy-3-methylglutaryl CoA lyase
2080	2131	AI171091	II		ESTs, Weakly similar to T19999 hypothetical protein C47D12.2 - Caenorhabditis elegans [C.elegans]
2082	18660	AI171262	KKK, NNN		ESTs
2086	11426	AI171305	HH, NN, OO, III, JJJ		ESTs, Moderately similar to PTN3_HUMAN Protein tyrosine phosphatase, non-receptor type 3 (Protein-tyrosine phosphatase H1) (PTP-H1) [H.sapiens]

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Seq. ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2087	3695	AI171307	T		ESTs
			III, JJJ, General Core Tox Markers		
2089	17591	AI171354			ESTs
			BBB, CCC		ESTs, Moderately similar to HSPC154 protein [Homo sapiens] [H.sapiens]
2091	6243	AI171367			ESTs
2095	11813	AI171487	Z, AA		ESTs
2099	15345	AI171587	L, Z		ESTs
			I, J, L, Z, OOO		ESTs
2100	9128	AI171611			ESTs
2101	24073	AI171632	X, Y		ESTs
					ESTs, Weakly similar to BVECAG apaG protein - Escherichia coli [E.coli]
2102	11504	AI171652	E, KKK		ESTs
2103	14357	AI171662	ZZ, AAA		ESTs
2107	2216	AI171745	ZZ		ESTs
2109	16005	AI171764	RR, FFF		ESTs
			CC, UU, III, JJJ, KKK, NNN		ESTs
2111	21209	AI171772			ESTs
2112	22745	AI171788	E		ESTs
2113	11708	AI171807	L, AA		ESTs
					ESTs, Weakly similar to FAD-1 like protein [Caenorhabditis elegans] [C.elegans]
2114	11514	AI171855	Z, AA		ESTs
2116	6524	AI171952	TT		ESTs
2119	6637	AI171975	DDD		ESTs
					ESTs, Moderately similar to I48672 p8 MTCP-1 - mouse [M.musculus]
2120	22239	AI171982	Z, AA		ESTs
2121	6645	AI171998	II		ESTs
			ZZ, AAA, PPP, QQQ		ESTs, Highly similar to Coordinates Of Rat Map Kinase Erk2 With An Arginine Mutation At Position 52 [R.norvegicus]
2125	3971	AI172050			
			X, DD, EE, SS, NNN, General Alternate		ESTs
2126	19012	AI172056			
			G, III, JJJ, UUU		ESTs
2127	11205	AI172057			ESTs
2128	1411	AI172075	O, P		ESTs
2134	11438	AI172189	CC		ESTs
			N, RR, CCC		ESTs
2136	11888	AI172217			ESTs

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2139	15016	AI172285	General Core Tox Markers		ESTs
2142	15382	AI172302	DDD, FFF		ESTs, Weakly similar to S43056 hypothetical protein - mouse [M.musculus]
2146	17049	AI172417	GGG, HHH, General Core Tox Markers		ESTs, Weakly similar to B.subtilis YQJC protein like [Caenorhabditis elegans] [C.elegans]
2149	26222	AI172506	D		
2150	13434	AI172552	General Alternate		EST
2151	13097	AI172600	PPP, QQQ		ESTs
2152	8795	AI172618	Q, R		ESTs
2153	22947	AI175008	LL		ESTs
2155	8053	AI175033	E		ESTs
2156	2331	AI175045	C		ESTs
2157	7134	AI175063	General Alternate		ESTs
2158	4989	AI175087	O, P		ESTs
2161	10637	AI175203	Z, AA		ESTs, Weakly similar to A53237 I(3)S12 protein - fruit fly (Drosophila melanogaster) (fragment) [D.melanogaster]
2164	4187	AI175346	S		ESTs
2168	14717	AI175477	S		ESTs
2169	13353	AI175508	BB, III, JJJ, KKK, NNN, General Core Tox Markers, General Alternate		ESTs
2171	23536	AI175558	General Alternate		ESTs
2172	15113	AI175590	G, M		ESTs, Weakly similar to T15628 hypothetical protein C25H3.9 - Caenorhabditis elegans [C.elegans]
2173	2261	AI175619	WW		ESTs, Weakly similar to A53237 I(3)S12 protein - fruit fly (Drosophila melanogaster) (fragment) [D.melanogaster]
2174	14501	AI175778	QQ		ESTs

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2175	22906	AI175790	C, Z, DD, MM, WW, KKK, TTT		ESTs
2176	7262	AI175833	VV		ESTs
2179	13490	AI175948	ZZ, AAA		ESTs, Highly similar to JC1450 fibroblast growth factor receptor 4 - rat [R.norvegicus]
2182	22311	AI176007	MM, AAA, TTT		ESTs, Highly similar to PM5P_HUMAN Protein pM5 precursor [H.sapiens]
2183	6739	AI176016	PPP, QQQ		ESTs
2184	3114	AI176018	WW		ESTs, Weakly similar to T16696 hypothetical protein R07E4.4 - Caenorhabditis elegans [C.elegans]
2186	21467	AI176061	WW, PPP, QQQ		ESTs, Weakly similar to retinoic acid receptor responder (tazarotene induced) 2 [Homo sapiens] [H.sapiens]
2188	4585	AI176121	Q, R		ESTs
2189	6686	AI176130	ZZ		ESTs
2190	8742	AI176136	QQ		ESTs
2191	18581	AI176160	E		ESTs
2192	14159	AI176169	V		ESTs
2194	22011	AI176212	UU		ESTs, Weakly similar to T23D8.3.p [Caenorhabditis elegans] [C.elegans]
2196	21130	AI176298	W		ESTs
2198	13502	AI176320	L		ESTs
2199	18936	AI176358	II, XX, YY		Rattus norvegicus MHC class I RT1.E protein mRNA, complete cds, haplotype u
2200	3014	AI176362	W		ESTs
2201	15015	AI176363	BBB		ESTs
2202	8387	AI176365	OOO, General Core Tox Markers		ESTs
2204	6138	AI176420	UU		ESTs
2207	26029	AI176460	M, T, KKK		
2208	11488	AI176477	U		ESTs, Highly similar to 2016304A motor protein [Homo sapiens] [H.sapiens]
2212	8609	AI176505	SS		ESTs
2213	15959	AI176540	Z		ESTs

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2215	22139	AI176548	N, BBB, CCC, UUU		ESTs, Weakly similar to T15B7.2.p [Caenorhabditis elegans] [C.elegans]
2217	2161	AI176592	W, AA, BB, CC, III, JJJ, KKK, NNN, General Alternate		ESTs
2219	2536	AI176616	V, III, JJJ, OOO, General Core Tox Markers		ESTs
2220	15847	AI176638	Z, AA		ESTs
2221	15179	AI176675	ZZ		ESTs
2222	24313	AI176680	SSS, UUU		ESTs
2223	13697	AI176718	JJJ		ESTs
2224	23547	AI176734	JJJ		ESTs, Highly similar to hypothetical protein FLJ20580 [Homo sapiens] [H.sapiens]
2225	11536	AI176739	III, JJJ, KKK, OOO, General Core Tox Markers		ESTs, Moderately similar to KIAA1002 protein; clone FLB5224 [Homo sapiens] [H.sapiens]
2226	11505	AI176767	QQ		ESTs, Weakly similar to BVECAG apaG protein - Escherichia coli [E.coli]
2227	10187	AI176781	General Alternate		ESTs
2228	18525	AI176792	GG, JJ, KK, FFF, GGG		ESTs
2229	21740	AI176810	E, BB, GG, PP, III		ESTs
2230	2557	AI176820	DD, EE, UU, III, JJJ		ESTs
2231	23449	AI176828	C, L, HH		ESTs
2232	9712	AI176836	III		ESTs, Weakly similar to T21364 hypothetical protein F25H5.6 - Caenorhabditis elegans [C.elegans]

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2233	23299	AI176839	KK, FFF, General Alternate		ESTs
2234	6821	AI176841	Z		ESTs
2235	19309	AI176858	SS		ESTs
2236	5579	AI176863	E, UU		ESTs
2237	12792	AI176883	DD, EE		ESTs, Weakly similar to BEM-1/BUD5 suppressor-like [Caenorhabditis elegans] [C.elegans]
2238	7697	AI176942	A, B, BB, GGG, General Core Tox Markers		ESTs
2239	5460	AI176944	GGG		ESTs
2240	16917	AI176951	II		ESTs
2243	15146	AI176969	W, LLL, SSS		ESTs
2244	6861	AI176970	I, ZZ		ESTs
2245	14738	AI176993	L, GGG		ESTs
2247	2596	AI177031	PPP, QQQ		ESTs
2248	3969	AI177055	LLL, SSS, UUU		ESTs
2249	4383	AI177056	DD, EE		ESTs
2250	6473	AI177091	FFF		ESTs
2252	5943	AI177105	GGG, General Core Tox Markers		ESTs, Weakly similar to OAF_DROME Out at first protein [Contains: Out at first short protein] [D.melanogaster]
2253	2487	AI177117	RR		ESTs
2254	14920	AI177120	K		ESTs
2255	6262	AI177125	III, JJJ		ESTs
2259	24221	AI177166	N		ESTs
2261	3528	AI177189	JJ, KK, HHH		ESTs
2262	7163	AI177256	Y		ESTs
2263	13539	AI177280	VV		ESTs, Weakly similar to GMCR_MOUSE Granulocyte-macrophage colony-stimulating factor receptor alpha chain precursor (GM-CSF-R-alpha) (GMR) [M.musculus]
2267	7975	AI177374	WW		ESTs
2268	1903	AI177377	B, X, Y		ESTs

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2270	3071	AI177404	R, General Alternate		ESTs
2271	18095	AI177482	S	SH-PTP2 protein tyrosine phosphatase, non-receptor type 11	SH-PTP2 protein tyrosine phosphatase, non-receptor type 11
2276	14275	AI177748	ZZ, AAA		ESTs
2277	14425	AI177755	E, DD, EE, KKK, NNN		ESTs, Moderately similar to PBEF_HUMAN Pre-B cell enhancing factor precursor [H.sapiens]
2278	10611	AI177790	F, II, FFF		ESTs
2279	22037	AI177797	AA, General Alternate		ESTs
2280	547	AI177871	F, II, FFF		ESTs, Highly similar to CDK1_MOUSE Cyclin-dependent kinase 2-associated protein 1 (CDK2-associated protein 1) (Putative oral cancer suppressor) (Deleted in oral cancer-1) (DOC-1) [M.musculus]
2281	8638	AI177875	F		ESTs
2282	5275	AI177898	PP, QQ		ESTs, Weakly similar to T25144 hypothetical protein T22H6.6 - Caenorhabditis elegans [C.elegans]
2286	17706	AI178052	LL		ESTs
2289	3943	AI178179	FF		ESTs, Weakly similar to hypothetical protein FLJ21868 [Homo sapiens] [H.sapiens]
2292	17847	AI178214	C, FF, General Core Tox Markers		ESTs
2294	5813	AI178231	General Core Tox Markers		ESTs
2297	19720	AI178259	XX, YY		
2298	4073	AI178272	Y, SS		ESTs, Weakly similar to S51973 hypothetical protein YAL046c - yeast (Saccharomyces cerevisiae) [S.cerevisiae]
2299	7318	AI178278	E		ESTs, Weakly similar to S47857 basic protein, cytosolic - fruit fly (Drosophila melanogaster) [D.melanogaster]

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2301	14561	AI178503	DD, EE, YY		ESTs
2302	18800	AI178504	O, P		ESTs
2303	13580	AI178507	OO		ESTs
2304	22197	AI178527	L, OOO, General Core Tox Markers		ESTs
2305	5921	AI178556	ZZ, AAA		ESTs
2306	13581	AI178602	SS		ESTs
2308	4097	AI178635	O, VV		ESTs
2310	5200	AI178699	Q, R		ESTs
2311	5381	AI178734	ZZ		ESTs
2312	13166	AI178736	UU		ESTs
2314	17239	AI178763	F, II		ESTs
2316	21224	AI178778	YY		ESTs, Moderately similar to T14273 zinc finger protein 106 - mouse [M.musculus]
2317	9674	AI178784	C		ESTs
2318	14520	AI178785	General Alternate		ESTs, Moderately similar to POL3_MOUSE Retrovirus-related POL polyprotein (Endonuclease) [M.musculus]
2321	4576	AI178872	LL		ESTs
2327	4791	AI179106	HH		ESTs
2329	22436	AI179139	Z, AA		ESTs
2330	2818	AI179144	General Core Tox Markers, General Alternate		ESTs
2333	8477	AI179167	W, DD, EE, NNN		ESTs
2334	21568	AI179185	C, DD, EE		ESTs
2335	26270	AI179218	RR		
2336	6303	AI179243	PPP, QQQ		Rat Rev-ErbA-alpha protein mRNA, complete cds
2337	22802	AI179291	LLL, UUU		ESTs
2339	8849	AI179315	W		ESTs
2341	19783	AI179388	L		ESTs, Highly similar to RIKEN cDNA 0610040D20 [Mus musculus] [M.musculus]
2342	13614	AI179407	M		ESTs, Moderately similar to RB17_MOUSE Ras-related protein Rab-17 [M.musculus]
2343	11291	AI179413	S		ESTs
2344	15042	AI179422	A, B		ESTs
2345	13619	AI179464	C, Q, R, HH		ESTs

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2346	22852	AI179478	V		ESTs
2347	2768	AI179481	BBB, CCC		ESTs
2348	23515	AI179498	L		ESTs, Highly similar to SEC23B (S. cerevisiae) [Mus musculus] [M.musculus]
2350	22961	AI179519	V, RR		ESTs
2351	13054	AI179560	General Alternate		ESTs
2352	15533	AI179569	RR		
2354	11484	AI179612	R	myeloid differentiation primary response gene 116	myeloid differentiation primary response gene 116
2356	17865	AI179636	Y		ESTs, Highly similar to RIKEN cDNA 0610009B22 [Mus musculus] [M.musculus]
2358	7918	AI179750	FFF		ESTs
2359	6647	AI179795	Z, AA		ESTs
2360	14496	AI179833	L		ESTs
2361	3524	AI179840	RRR, SSS		ESTs
2365	3049	AI179892	J	glucocorticoid-inducible protein	glucocorticoid-inducible protein
2366	18239	AI179942	B, CC		ESTs
2367	9157	AI179947	HH		ESTs, Highly similar to 42 kD cGMP-dependent protein kinase anchoring protein; hypothetical testis-specific [Mus musculus] [M.musculus]
2375	16706	AI180032	CC		ESTs
2378	15447	AI180108	L		ESTs
2379	2246	AI180113	JJ, KK		ESTs
2382	18465	AI180187	BB, CC, PP		ESTs
2383	3587	AI180253	Q		ESTs
2384	6955	AI180259	T		ESTs, Highly similar to RIKEN cDNA 1110036B12 [Mus musculus] [M.musculus]
2385	3134	AI180292	EEE, MMM		ESTs, Moderately similar to A23521 serum amyloid A3 precursor - mouse [M.musculus]
2391	7073	AI180416	UUU		ESTs
2392	3067	AI180426	HH		ESTs, Weakly similar to T26786 hypothetical protein Y40B1B.8 - Caenorhabditis elegans [C.elegans]
2393	23262	AI227688	HH, ZZ, AAA		ESTs
2394	11631	AI227690	SS		ESTs

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2395	23944	AI227705	W		ESTs, Weakly similar to T21344 hypothetical protein F25H2.1 - <i>Caenorhabditis elegans</i> [C.elegans]
2396	13670	AI227734	OOO, General Alternate		ESTs
2397	6765	AI227761	C		ESTs, Highly similar to EFER_HUMAN Eferin [H.sapiens]
2398	21890	AI227815	RR		ESTs, Highly similar to UBX domain-containing 2 [Mus musculus] [M.musculus]
2399	24300	AI227829	RR, SS		ESTs, Weakly similar to BD3_MOUSE BRAIN PROTEIN D3 [M.musculus]
2401	13981	AI227872	W		ESTs
2402	7324	AI227885	F, II		ESTs
2405	21288	AI227935	F, GG, HH, LL		ESTs
2406	2226	AI227941	R		ESTs
2408	4275	AI227972	N, PPP, QQQ		ESTs, Moderately similar to T17453 ERG-associated protein ESET - mouse [M.musculus]
2410	22901	AI228052	ZZ, AAA		ESTs
2412	18491	AI228195	PP, QQ, PPP, QQQ		ESTs
2414	14539	AI228254	T		ESTs
2415	24256	AI228256	T		ESTs
2416	14540	AI228269	YY		ESTs, Weakly similar to F09G2.8.p [Caenorhabditis elegans] [C.elegans]
2417	6715	AI228284	General Core Tox Markers, General Alternate		ESTs
2418	12946	AI228291	DD, OOO, General Core Tox Markers		ESTs
2420	8917	AI228301	EE, FF, III, JJJ, NNN		ESTs
2421	15879	AI228313	K, L, N, TT		ESTs
2422	13729	AI228348	HHH		ESTs
2424	4424	AI228422	T		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2425	17892	AI228438	RR		ESTs
2426	13746	AI228502	Z, AA, RR		ESTs
2427	13749	AI228540	OOO, General Core Tox Markers		ESTs
2428	16053	AI228596	J, Z		ESTs, Weakly similar to T16757 hypothetical protein R144.3 - <i>Caenorhabditis elegans</i> [C.elegans]
2430	22106	AI228628	ZZ, AAA		ESTs
2431	6072	AI228630	A, K, L, N, General Core Tox Markers		ESTs, Weakly similar to T20360 hypothetical protein D2030.9b - <i>Caenorhabditis elegans</i> [C.elegans]
2433	6788	AI228646	RRR, UUU		ESTs
2434	12252	AI228649	PPP, QQQ, General Alternate		ESTs, Weakly similar to Yeast YAE2 hypothetical protein [Caenorhabditis elegans] [C.elegans]
2435	3557	AI228672	KK		ESTs
2436	13757	AI228676	OOO, General Core Tox Markers		ESTs, Weakly similar to C32D5.6.p [Caenorhabditis elegans] [C.elegans]
2438	20388	AI228811	BBB, CCC		EST
2439	6721	AI228813	RR		ESTs
2440	16998	AI228829	UUU		EST
2441	11875	AI228846	D		ESTs
2442	6633	AI228931	C, TT		ESTs
2443	2210	AI228963	FF		ESTs, Weakly similar to T26088 hypothetical protein W02B12.7 - <i>Caenorhabditis elegans</i> [C.elegans]
2444	13785	AI228970	MM, TTT		ESTs
2445	19513	AI229035	UU		ESTs
2446	23824	AI229059	ZZ, AAA		ESTs, Moderately similar to retinoic acid induced 12; Clone 13u [Mus musculus] [M.musculus]
2447	22824	AI229074	M		ESTs
2448	19063	AI229166	RR		ESTs, Highly similar to mitochondrial ribosomal protein S14; 1810032L21Rik [Mus musculus] [M.musculus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2450	2748	AI229179	PPP, QQQ		ESTs
2453	15490	AI229253	PPP, QQQ		Rattus norvegicus zinc finger protein (pMLZ-4) mRNA, 3' untranslated region
2454	24013	AI229260	JJ, KK, HHH		ESTs
2455	5107	AI229291	X, Y		ESTs
2458	19721	AI229387	RR, SS		EST
2459	13838	AI229416	MM, ZZ, TTT		ESTs
2460	21237	AI229430	SS		Rattus norvegicus Tclone4 mRNA
2462	6945	AI229467	G, H		ESTs
2463	17183	AI229487	I, J		ESTs, Weakly similar to mitochondrial ribosomal protein L2a [Drosophila melanogaster] [D.melanogaster]
2464	13846	AI229493	K		ESTs
2465	15426	AI229497	R, DD, EE, III, JJJ		ESTs, Moderately similar to JE0381 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDUF10 - human [H.sapiens]
2466	15193	AI229508	DDD		ESTs
2469	7067	AI229655	KKK, General Alternate		ESTs
2470	2231	AI229664	JJ, KK		ESTs
2474	21446	AI229854	E		ESTs
2475	11934	AI229905	CC		ESTs, Weakly similar to T26088 hypothetical protein W02B12.7 - Caenorhabditis elegans [C.elegans]
2477	12551	AI230056	O, NN, OO, General Alternate		ESTs
2478	23048	AI230073	II		ESTs, Weakly similar to T33304 hypothetical protein R01B10.5 - Caenorhabditis elegans [C.elegans]
2480	2732	AI230136	V		ESTs
2482	6629	AI230165	General Alternate		ESTs, Weakly similar to Deoxyribose-phosphate aldolase [Caenorhabditis elegans] [C.elegans]
2487	14450	AI230262	XX		ESTs
2489	13762	AI230326	C		ESTs
2491	2372	AI230373	Z		ESTs

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2493	13899	AI230424	RR, SS		ESTs, Weakly similar to zinc finger protein 364 [Mus musculus] [M.musculus]
2494	6560	AI230440	JJ, KK, HHH		ESTs
2497	20895	AI230549	General Alternate		ESTs
2498	13446	AI230625	W, MM, TTT		ESTs
2499	18393	AI230632	A, B		ESTs
2500	14481	AI230697	BB, CC		ESTs
2501	18529	AI230716	W		ESTs
2502	17879	AI230741	S, General Alternate		ESTs
2504	9171	AI230747	RR		ESTs
2508	4731	AI230773	C, W, MM, NNN, TTT, General Alternate		ESTs
2511	23730	AI230915	RR		ESTs
2513	23182	AI230981	III, JJJ, NNN		ESTs
2515	19315	AI231010	V		EST
2516	16087	AI231011	Z		ESTs
2517	19082	AI231038	BB, CC		ESTs
2519	633	AI231127	UU, FFF, GGG, General Core Tox Markers		ESTs
2522	13949	AI231193	ZZ		ESTs, Moderately similar to SEC_HUMAN SEC protein [H.sapiens]
2524	3019	AI231218	QQ		ESTs
2525	6743	AI231219	H, General Alternate		ESTs
2528	4272	AI231309	U, FF, LL, BBB, PPP, QQQ, RRR, SSS, UUU		ESTs
2529	3050	AI231321	Z, AA	glucocorticoid-inducible protein	glucocorticoid-inducible protein

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2531	13966	AI231421	FFF, HHH, General Alternate		ESTs
2532	12343	AI231433	R		ESTs
2533	13967	AI231439	UUU		ESTs
2535	3581	AI231471	LL, LLL		ESTs, Moderately similar to RIKEN cDNA 1110017G11; RIKEN cDNA 1110017G11 gene [Mus musculus] [M.musculus]
2538	16321	AI231506	A, B		ESTs
2541	17172	AI231572	WW		ESTs, Weakly similar to T45057 hypothetical protein Y39B6B.aa [imported] - Caenorhabditis elegans [C.elegans]
2543	18402	AI231778	DD, EE, KKK		ESTs
2546	6193	AI231797	LL		ESTs
2547	2339	AI231798	S		ESTs, Highly similar to T-complex expressed gene 2 [Mus musculus] [M.musculus]
2548	14007	AI231808	AA, GGG, General Core Tox Markers		ESTs
2549	7001	AI231814	V		ESTs
2550	15173	AI231846	HH, MM, TTT		ESTs
2555	24273	AI232033	AA		ESTs
2556	22995	AI232047	C		ESTs
2559	12366	AI232088	SS		ESTs
2560	2587	AI232103	G, S, GGG, PPP, QQQ		ESTs
2563	11549	AI232174	Q, R		ESTs
2564	21242	AI232230	E, XX, YY		ESTs, Weakly similar to T27032 hypothetical protein Y49A3A.1 - Caenorhabditis elegans [C.elegans]
2565	14030	AI232248	T		ESTs
2566	349	AI232256	I, J	cytochrome b5, outer mitochondrial membrane isoform	cytochrome b5, outer mitochondrial membrane isoform
2568	2913	AI232272	PPP, QQQ		ESTs, Weakly similar to T25417 hypothetical protein T28D6.9 - Caenorhabditis elegans [C.elegans]

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2569	11720	AI232273	BB, CC, OO, PP, NNN		ESTs, Highly similar to RTC2_HUMAN PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE 2 (RNA-3'-PHOSPHATE CYCLASE 2) (RNA CYCLASE 2) [H.sapiens]
2570	15955	AI232294	QQ, TT, DDD, GGG, General Core Tox Markers		ESTs
2571	6594	AI232296	GG		ESTs
2573	6430	AI232319	J		ESTs, Highly similar to JC5221 stomatin - mouse [M.musculus]
2575	14502	AI232339	III, JJJ, General Alternate		ESTs
2576	14521	AI232350	General Core Tox Markers, General Alternate		ESTs, Moderately similar to POL3_MOUSE Retrovirus-related POL polypeptide (Endonuclease) [M.musculus]
2577	3435	AI232354	MM, TTT		ESTs
2579	14390	AI232385	LLL		ESTs
2580	3143	AI232408	TT, General Alternate		ESTs
2581	14264	AI232409	BBB, UUU		ESTs, Weakly similar to serine hydrolase protein [Mus musculus] [M.musculus]
2582	18910	AI232419	General Core Tox Markers		ESTs, Weakly similar to YLC4_CAEEL Hypothetical 81.0 kDa protein C35D10.4 in chromosome III [C.elegans]
2583	17703	AI232498	M, General Core Tox Markers, General Alternate		ESTs
2586	14056	AI232529	V		ESTs
2588	20350	AI232552	A, B, N, WW		EST
2590	4440	AI232643	FFF, GGG, General Core Tox Markers		ESTs
2594	14278	AI232722	V		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2595	14073	AI232723	General Alternate		ESTs
2596	3885	AI232776	MM, TTT		ESTs
2597	11190	AI232810	YY		ESTs
2598	21871	AI232841	CC, JJ, KK, HHH		ESTs
2600	3917	AI232970	F, T, U, W, MM, RR, TTT		ESTs
2601	23570	AI232979	PP, QQ		ESTs
2603	11815	AI232993	DDD		ESTs
2604	5355	AI233031	PPP, QQQ		ESTs
2607	6033	AI233081	JJJ, OOO, General Core Tox Markers		ESTs
2608	18794	AI233121	V		ESTs, Moderately similar to PS0139 H-2 class I histocompatibility antigen T18 - mouse (fragment) [M.musculus]
2610	14081	AI233164	BB, CC, NN		ESTs
2612	11561	AI233182	General Alternate		ESTs
2613	13598	AI233194	E		ESTs
2614	15107	AI233220	N, GG, PP, QQ, XX, YY		ESTs, Highly similar to RS18_HUMAN 40S ribosomal protein S18 (KE-3) (KE3) [R.norvegicus]
2617	15900	AI233262	G, H, FFF, General Core Tox Markers		ESTs
2621	14118	AI233367	H, P		EST
2622	7161	AI233407	R, General Alternate		ESTs, Weakly similar to S44853 K12H4.3 protein - Caenorhabditis elegans [C.elegans]
2623	19655	AI233460	ZZ, AAA		ESTs
2624	5794	AI233480	TT		ESTs
2625	14131	AI233493	LL, LLL, RRR, SSS, UUU		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2630	8549	AI233639	A, I, OOO, General Core Tox Markers		ESTs
2631	7837	AI233688	I, J		ESTs
2632	4670	AI233714	DD, MM, TTT, General Core Tox Markers		ESTs
2637	22686	AI233753	Q, R, S		ESTs
2639	2822	AI233763	General Core Tox Markers, General Alternate		ESTs
2640	14153	AI233787	A, B		ESTs
2641	2096	AI233801	C		ESTs
2643	15085	AI233829	U, FF, RRR	P11 protein	P11 protein
2644	4026	AI233835	E, BB, CC, NN, OO, PP		ESTs
2645	12655	AI233836	JJ		ESTs
2646	21260	AI233885	TT		ESTs
2647	21321	AI233902	UUU		ESTs
2648	4918	AI233941	T, GG		ESTs, Weakly similar to T19236 hypothetical protein C13C4.4 - <i>Caenorhabditis elegans</i> [C.elegans]
2649	10972	AI233956	PP, QQ		ESTs
2650	14167	AI233966	RR		ESTs
2652	21281	AI234090	BB, III	spinocerebellar ataxia 10 homolog (human)	spinocerebellar ataxia 10 homolog (human)
2653	22140	AI234098	W		ESTs
2654	6532	AI234105	D, V, BB, CC, NN, OO, PP, EEE, III, MMM		ESTs
2655	14181	AI234107	UUU		ESTs
2656	22233	AI234128	I, J		ESTs
2657	14187	AI234147	V		ESTs
2658	14190	AI234218	ZZ, AAA		ESTs
2661	2765	AI234283	O, P, VV		ESTs
2662	14197	AI234292	CCC		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2663	14202	AI234326	LLL, SSS, UUU		EST
2664	17664	AI234496	A, B, DD, EE, PP, III, NNN, General Alternate		ESTs
2666	7782	AI234515	D		ESTs
2668	26313	AI234599	SS		
2670	16960	AI234666	SS		ESTs
2671	18999	AI234677	R, W		ESTs
2672	23964	AI234748	II		ESTs
2673	9015	AI234810	General Alternate		ESTs
2674	23583	AI234819	W, III, JJJ		ESTs -
2676	2594	AI234843	Z		ESTs, Moderately similar to Yeast LPG22P protein like [Caenorhabditis elegans] [C.elegans]
2678	7282	AI234962	Z, AA		ESTs, Weakly similar to Human mRNA KIAA0066 predicted protein like [Caenorhabditis elegans] [C.elegans]
2679	8850	AI235059	Q, R, W		ESTs
2682	5316	AI235219	XX, YY		ESTs
2685	15181	AI235234	UUU		ESTs
2686	6632	AI235277	S		ESTs
2689	14725	AI235306	HH		ESTs
2692	22805	AI235403	S		ESTs, Highly similar to adaptor-related protein complex AP-3, delta subunit [Mus musculus] [M.musculus]
2693	21874	AI235405	SS		ESTs
2694	23228	AI235446	RRR		ESTs
2700	19052	AI235675	E		ESTs
2704	14766	AI235886	V, ZZ, AAA		ESTs
2705	14767	AI235895	EEE, MMM, OOO, General Core Tox Markers		ESTs, Weakly similar to RIKEN cDNA 2410005O16 [Mus musculus] [M.musculus]
2706	6512	AI235898	RRR, SSS, UUU		ESTs, Highly similar to RIKEN cDNA 2510027N19 [Mus musculus] [M.musculus]
2707	26330	AI235911	D		

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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2710	14776	AI235950	DD, III, JJJ, NNN, General Core Tox Markers		ESTs
2711	15836	AI235951	PP, QQ		ESTs, Moderately similar to N4BM_HUMAN NADH-ubiquinone oxidoreductase subunit B14.5b (Complex I-B14.5b) (CI-B14.5b) [H.sapiens]
2713	14312	AI236036	KKK, PPP, QQQ, General Core Tox Markers		ESTs
2715	19732	AI236066	G, GGG, HHH		ESTs
2718	15467	AI236106	QQ		ESTs, Moderately similar to S15785 heat-stable antigen-related hypothetical protein HSA-C - mouse [M.musculus]
2719	11431	AI236120	Q, R, PPP, QQQ		ESTs
2720	23230	AI236146	C, DD		ESTs
2721	14594	AI236152	II		ESTs
2722	14878	AI236188	M		EST
2723	9009	AI236223	General Alternate		ESTs, Highly similar to cullin 4A [Homo sapiens] [H.sapiens]
2724	12964	AI236227	XX, YY		ESTs
2725	14887	AI236243	N, PP, QQ, XX		EST, Moderately similar to 0806162D protein COII [Mus musculus] [M.musculus]
2727	15465	AI236280	G, H	protein S	protein S
2729	18610	AI236307	G, H		ESTs
2732	26335	AI236460	DD, EE		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds
2733	19075	AI236473	Q, II		ESTs
2737	17950	AI236590	E, DD, EE		ESTs
2738	18259	AI236601	Q, T		ESTs
2739	6567	AI236608	ZZ, AAA		ESTs
2741	17248	AI236635	M, X, Y		ESTs, Highly similar to 2120310B RNA polymerase II elongation factor [Mus musculus] [M.musculus]

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2742	13462	AI236683	C		ESTs, Moderately similar to RHG4_HUMAN Rho-GTPase-activating protein 4 (Rho-GAP hematopoietic protein C1) (P115) [H.sapiens]
2744	18783	AI236746	C, DD, MM, TTT		ESTs
2745	16609	AI236748	Z, AA		ESTs, Moderately similar to CENB_MOUSE MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) [M.musculus]
2746	16859	AI236753	DD, NNN		ESTs
2747	22443	AI236761	Q		ESTs
2748	24388	AI236772	R		ESTs
2749	23855	AI236773	PP, QQ		ESTs
2751	23081	AI236778	ZZ, AAA		ESTs
2752	14232	AI236794	N		ESTs
2754	17455	AI236818	AA, SS		ESTs, Highly similar to FKBX_MOUSE 65 kDa FK506-binding protein precursor (FKBP65) (FKBPRP) (Peptidyl-prolyl cis-trans isomerase) (PPiase) (Rotamase) (Immunophilin FKBP65) [M.musculus]
2755	23595	AI236834	Q, R		ESTs
2756	18303	AI236863	WW		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds.
2758	17323	AI236936	V		ESTs
2759	5059	AI236947	W, EEE, MMM		ESTs
2764	14811	AI237026	TT		ESTs
2765	22506	AI237047	AAA		ESTs
2767	13336	AI237070	Z, AA		ESTs
2769	4175	AI237092	UUU		ESTs
2770	14937	AI237159	XX, III, JJJ		ESTs, Weakly similar to T23655 hypothetical protein M01F1.3 - Caenorhabditis elegans [C.elegans]
2771	4937	AI237189	Z		ESTs
2772	14911	AI237403	L		ESTs
2774	22477	AI237525	Y		ESTs
2776	12956	AI237580	Z, LL		ESTs
2777	18267	AI237595	SS		ESTs
2778	22038	AI237609	General Core Tox Markers		ESTs

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2779	15170	AI237618	I, T, DD, III, JJJ, NNN, OOO, General Core Tox Markers		ESTs
2781	23860	AI237684	H		ESTs
2782	14840	AI237698	O, P, NN, OO, VV		ESTs
2783	14528	AI237718	General Alternate		ESTs
2784	14842	AI237724	C		ESTs
2785	14844	AI237782	S, Z, AA		
2787	14656	AI237820	P		ESTs
2789	5046	AI237855	A, B, SSS		ESTs
2790	14850	AI237880	RR		ESTs
2791	6127	AI638960	K, JJ, KK		ESTs
2791	6128	AI638960	JJ, KK		ESTs
2793	25855	AI639002	D, L		
2795	7176	AI639029	D, W, GG		ESTs
2796	24205	AI639045	UU		ESTs
2797	10071	AI639058	NN, OO, EEE, MMM		ESTs, Highly similar to Nedd4 WW binding# protein 4; Nedd4 WW-binding protein 4 [Mus musculus] [M.musculus]
2798	25883	AI639076	T, TT, NNN		
2799	19900	AI639079	D		EST
2800	16514	AI639093	RR		ESTs
2801	7170	AI639102	JJ, KK		ESTs
2802	19952	AI639108	F, III, JJJ, KKK, OOO, General Core Tox Markers		ESTs
2803	5545	AI639117	E, Y, MM, WW, BBB, CCC, TTT		ESTs, Highly similar to CFAB_MOUSE Complement factor B precursor (C3/C5 convertase) [M.musculus]
2804	13882	AI639120	LL		ESTs
2805	25907	AI639167	Q		ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2806	20615	AI639176	D		ESTs
2807	25915	AI639195	K		
2808	19795	AI639197	RR		EST
2809	19749	AI639203	ZZ, AAA		ESTs
2810	25928	AI639236	K		
2811	25930	AI639245	D		
2812	20614	AI639246	LLL		ESTs
2813	19962	AI639248	X, Y		
2814	17082	AI639255	TT		ESTs
2814	17083	AI639255	C, N, O, P		ESTs
2815	25934	AI639257	Q, R, WW		
2816	25938	AI639281	D		ESTs
2817	3787	AI639324	ZZ, AAA		ESTs
2817	3788	AI639324	Y, ZZ, AAA		ESTs
2819	25964	AI639352	Y		
2820	20026	AI639354	GG		EST
2821	25971	AI639365	K		
2822	18295	AI639381	LLL		ESTs
2823	25983	AI639390	K		
2825	10097	AI639425	K		ESTs
2825	10098	AI639425	D		ESTs
2826	799	AI639441	UU	eukaryotic translation initiation factor 2B, subunit 3 (gamma, 58kD)	eukaryotic translation initiation factor 2B, subunit 3 (gamma, 58kD)
2827	19870	AI639462	V		ESTs
2829	20402	AI639489	AA, BBB, CCC		ESTs, Moderately similar to Y039_HUMAN HYPOTHETICAL PROTEIN KIAA0039 [H.sapiens]
2830	5998	AI639501	LLL		ESTs
2831	20056	AI639504	A, B, GGG, HHH, General Alternate		ESTs, Weakly similar to T13607 hypothetical protein 87B1.3 - fruit fly (Drosophila melanogaster) [D.melanogaster]
2847	25257	D13623	G, H, O, T, OO		
2851	20384	D17349	TT, DDD		
2854	25270	D26498	D		
2856	25276	D28966	CC		
2863	25287	D38069	K, X, Y		
2874	970	D86580	JJ, KK, HHH	nuclear receptor subfamily 0, group B, member 2	nuclear receptor subfamily 0, group B, member 2
2875	19420	D86711	X, Y		ESTs
2878	25313	D87991	OO, EEE, MMM		

TABLE 1					
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Seq ID	GLGC ID No.	Genbank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2882	25805	E01050	Z, AA, MM, SS, TTT		
2889	22543	H31117	D		
2890	21863	H31128	D		ESTs
2892	4333	H31351	ZZ, AAA		ESTs
2893	20514	H31489	P		ESTs
2894	14933	H31588	III, JJJ, KKK, OOO		ESTs, Highly similar to Ral-A exchange factor RalGPS2 [Mus musculus] [M.musculus]
2895	12613	H31620	H, X, Y, HHH		ESTs, Highly similar to ORN_HUMAN Oligoribonuclease, mitochondrial precursor (Small fragment nuclease) (CGI-114) [H.sapiens]
2896	4349	H31648	UU		EST
2898	16588	H31711	BBB, CCC		ESTs, Weakly similar to S28312 hypothetical protein F02A9.4 - Caenorhabditis elegans [C.elegans]
2901	4364	H31887	BBB, CCC		ESTs
2902	10530	H31897	DD, EE		ESTs
2904	12485	H31964	C		ESTs
2906	20684	H32977	PPP		ESTs
2907	4395	H33149	K, FF		ESTs, Weakly similar to F38A5.1.p [Caenorhabditis elegans] [C.elegans]
2908	16524	H33219	ZZ, AAA		ESTs
2909	4397	H33255	E		ESTs, Weakly similar to END3_CAEEL Probable endonuclease III homolog (DNA-(Apyrimidic or apyrimidic site) lyase) [C.elegans]
2910	10184	H33426	KKK, OOO, General Core Tox Markers, General Alternate		ESTs
2910	10185	H33426	General Alternate		ESTs
2911	4407	H33528	F, Q, R, U, HH, UU, DDD, LLL		ESTs
2912	4414	H33629	ZZ, AAA		ESTs
2913	4421	H33723	T		EST

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
2914	9597	H33832	XX, YY		
2914	9598	H33832	U		
2918	12974	H34243	SS		ESTs
			K, L, X, HH, II, TT, DDD, LLL		
2919	12155	J00728	LLL		
2920	25050	J01435	HH, NNN		
2920	25319	J01435	FF		
			S, HH, NNN		
2921	25051	J01436	NNN		
			K, X, TT, DDD, LLL, RRR, UUU	cytochrome P450, 2b19	cytochrome P450, 2b19
2935	12156	K00996	UUU		
			K, L, X, FF, TT, DDD, LLL, UUU	cytochrome P450, 2b19	cytochrome P450, 2b19
2936	12157	K01721	UUU		
			S, GG, SS		
2939	25325	K03045	SS		
2939	25326	K03045	GG		
			X, TT, DDD, RRR		
2942	12158	L00320	RRR		
2943	25327	L00686	DDD		
			E, GG, III, JJJ, General Alternate		
2946	15378	L05541	General Alternate		
			Z, AA, General Alternate		
2947	25343	L07407	General Alternate		
				Phosphorylase, glycogen; muscle (McArdle syndrome)	
2948	25350	L10669	D		
2951	25363	L13235	UUU		
2954	25366	L14003	UU		
			I, J, T, PP, III, KKK, NNN, OOO, General Core Tox Markers, General Alternate		
2958	25370	L16995	General Alternate		
2959	25371	L17077	D, RR		

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
2962	25052	L22190	A, E, W, BB, EEE, JJJ, MMM		
2963	43	L23413	D, M, T, NN, UU, III, JJJ, UUU	sulfate anion transporter	sulfate anion transporter
2977	20170	L46593	V		
2981	25055	M11251	A, B, X, TT, DDD, LLL, RRR		
2985	17086	M13011	V, FFF		
2986	18480	M13100	RR		ESTs
2986	20625	M13100	RR		
2986	20626	M13100	RR, SS		
2986	20630	M13100	RR		
2987	25399	M13101	RR		
2988	25056	M13234	K, X, Z, TT, DDD, LLL		
2991	25400	M14776	K, N, TT, DDD		
2996	25412	M18530	XX		
2997	25413	M18531	X, Y		
2998	17274	M18854	PP, QQ		Rat T-cell receptor active beta-chain C-region mRNA, partial cds, clone TRB4
2999	20464	M20406	N, QQ, UU, HHH, PPP, QQQ, General Alternate		Rat cytochrome P450IIB3 (P450IIB subfamily) mRNA, complete cds
3002	20481	M22631	II, XX, YY	Propionyl Coenzyme A carboxylase, alpha polypeptide	
3003	1476	M22756	RR	24-kDa subunit of mitochondrial NADH dehydrogenase	24-kDa subunit of mitochondrial NADH dehydrogenase
3013	16305	M33312	E, M, GG	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene
3020	25439	M35826	S, SS		
3032	17130	M62992	O, P		
3037	1223	M75281	SS, III, JJJ		
3041	19730	M81183	LL, LLL		ESTs

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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3063	25049	NM_012507	GG	ATPase, Na+K+ transporting, beta polypeptide 2 (Atp1b2), mRNA. 4/2002 Length = 1764	
3079	16895	NM_012558	T, XX, YY, DDD	fructose-1,6-bisphosphatase 1 (Fbp1), mRNA. 10/2002 Length = 1357	Fructose-1,6- biphosphatase
3080	25317	NM_012559	E, CC, DD, EE, III, JJJ, NNN	Fibrinogen, gamma polypeptide (Fgg), mRNA. 11/2000 Length = 1358	
3092	25204	NM_012599	G, H, I, J, XX	Mannose binding protein A, serum (Mbpa), mRNA. 11/2000 Length = 717	
3096	23524	NM_012615	OOO, General Alternate	Ornithine decarboxylase (Odc1), mRNA. 11/2000 Length = 2442	
3101	18619	NM_012645	T, II	RT1 class Ib gene (RT1Aw2), mRNA. 11/2002 Length = 1540	RT1 class I gene
3101	18725	NM_012645	F, LL, LLL, RRR, UUU, General Alternate	RT1 class Ib gene (RT1Aw2), mRNA. 11/2002 Length = 1540	
3102	18637	NM_012646	QQ, XX	RT1 class Ib gene, H2-TL-like, grc region (RT1-N1), mRNA. 11/2000 Length = 1179	RT1 class I gene
3112	24589	NM_012674	NN, EEE, MMM	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic (Spink1), mRNA. 11/2000 Length = 2338	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic

TABLE 1					
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Seq ID	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3116	16306	NM_012692	JJ, KK, FFF, HHH, PPP, QQQ, General Alternate	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene (Cyp2a1), mRNA. 11/2000 Length = 1687	Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene, Cytochrome P450 IIA2
3117	24707	NM_012693	JJ, VV, XX, YY, HHH, PPP, QQQ, General Alternate	Cytochrome P450 IIA2 (Cyp2a2), mRNA. 11/2000 Length = 2259	Cytochrome P450 IIA2
3119	10622	NM_012695	N, YY	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Sulfotransferase hydroxysteroid gene 2
3119	10624	NM_012695	N, UUU	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Sulfotransferase hydroxysteroid gene 2
3119	10625	NM_012695	N	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Sulfotransferase hydroxysteroid gene 2
3119	10626	NM_012695	N, II, UUU	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Sulfotransferase hydroxysteroid gene 2
3119	18717	NM_012695	N	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rat senescence marker protein 2A gene, exons 1 and 2
3119	18719	NM_012695	M, N, UUU	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rat senescence marker protein 2A gene, exons 1 and 2

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3119	18860	NM_012695	X	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
3119	18861	NM_012695	N	Rat senescence marker protein 2A gene, exons 1 and 2 (Smp2a), mRNA. 11/2000 Length = 1000	Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
3122	26032	NM_012703	FF	Thyroid hormone responsive protein (spot14) (Thrsp), mRNA. 4/2002 Length = 453	
3133	20354	NM_012741	E, BB, CC, DD, NN, OO, PP, EEE, III, KKK, LLL, MMM, NNN, UUU	K-kininogen, differential splicing leads to HMW Kngk (Kng_v1), mRNA. 11/2002 Length = 2100	
3154	11136	NM_012839	MM, FFF, TTT	cytochrome c, somatic (Cyts), mRNA. 11/2002 Length = 318	
3158	25336	NM_012850	RR	Growth hormone - releasing receptor (Ghrhr), mRNA. 11/2000 Length = 1629	
3159	18960	NM_012851	General Core Tox Markers	Hydroxysteroid dehydrogenase 17 beta, type 1 (Hsd17b1), mRNA. 11/2000 Length = 1432	ESTs
3167	25284	NM_012888	C, K, GG, HH	Thyroid stimulating hormone receptor (Tshr), mRNA. 11/2002 Length = 5270	

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3177	6107	NM_012915	G, H, O, P, XX, YY, PPP, QQQ	ATPase inhibitor (rat mitochondrial IF1 protein) (Atpi), mRNA. 11/2000 Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein)
3177	6108	NM_012915	G, H, Y, General Alternate	ATPase inhibitor (rat mitochondrial IF1 protein) (Atpi), mRNA. 11/2000 Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein)
3177	6109	NM_012915	F, J, M, S, EE, HH, SS, NNN	ATPase inhibitor (rat mitochondrial IF1 protein) (Atpi), mRNA. 11/2000 Length = 833	ATPase inhibitor (rat mitochondrial IF1 protein)
3179	19302	NM_012930	BBB, CCC	Carnitine palmitoyltransferase 2 (Cpt2), mRNA. 11/2002 Length = 2296	EST, Moderately similar to CPT2_RAT CARNITINE O-PALMITOYLTRANSFERASE II, MITOCHONDRIAL PRECURSOR (CPT II)
3186	956	NM_012976	L, MM, RR, TTT	Lectin, galactose binding, soluble 5 (Galectin-5) (Lgals5), mRNA. 11/2000 Length = 872	Lectin, galactose binding, soluble 9 (Galectin-9)
3208	14997	NM_013059	W, DD, MM, III, JJJ, KKK, NNN, TTT	alkaline phosphatase, tissue-nonspecific (Alpl), mRNA. 11/2002 Length = 2415	Tissue-nonspecific ALP alkaline phosphatase
3212	16924	NM_013069	Z, AA	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. 11/2000 Length = 1150	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)
3212	16926	NM_013069	M	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. 11/2000 Length = 1150	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3212	25676	NM_013069	X, Y, QQ	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated) (Cd74), mRNA. 11/2000 Length = 1150	
3217	26047	NM_013096	TT	Hemoglobin, alpha 1 (Hba1), mRNA. 11/2000 Length = 556	
3217	26150	NM_013096	M, T	Hemoglobin, alpha 1 (Hba1), mRNA. 11/2000 Length = 556	
3229	25567	NM_013156	A, B, C, E, Q, W, MM, OOO, TTT	Cathepsin L (Ctsl), mRNA. 11/2002 Length = 1386	
3238	20728	NM_013217	UU, PPP, QQQ	afadin (AF-6), mRNA. 11/2000 Length = 5957	afadin
3238	20729	NM_013217	KK	afadin (AF-6), mRNA. 11/2000 Length = 5957	afadin
3254	25546	NM_017023	RR, SS	Potassium inwardly-rectifying channel, subfamily J, member 1 (Kcnj1), mRNA. 11/2002 Length = 2069	
3264	18973	NM_017060	T	Hras-revertant gene 107 (Hrev107), mRNA. 10/2002 Length = 966	ESTs, Moderately similar to S14234 hypothetical protein - mouse [M.musculus]
3271	1261	NM_017077	Q, R, MM, TTT	Hepatocyte nuclear factor 3 gamma (Hnf3g), mRNA. 11/2000 Length = 1497	
3310	6071	NM_017220	L, W	6-pyruvoyl-tetrahydropterin synthase (Pts), mRNA. 11/2002 Length = 1176	ESTs, Weakly similar to T20360 hypothetical protein D2030.9b - Caenorhabditis elegans [C.elegans]

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3310	21903	NM_017220	K, N, TT	6-pyruvoyl-tetrahydropterin synthase (Pts), mRNA. 11/2002 Length = 1176	cytochrome P450, 2c37
3311	18967	NM_017222	RR	solute carrier family 10, member 2 (Slc10a2), mRNA. 11/2002 Length = 4269	ESTs
3322	20913	NM_017272	M, TT, LLL, SSS, UUU	aldehyde dehydrogenase family 1, subfamily A4 (Aldh1a4), mRNA. 11/2002 Length = 2024	aldehyde dehydrogenase family 1, subfamily A4
3322	20914	NM_017272	A, B, L, TT, DDD, LLL, SSS, UUU	aldehyde dehydrogenase family 1, subfamily A4 (Aldh1a4), mRNA. 11/2002 Length = 2024	aldehyde dehydrogenase family 1, subfamily A4
3335	26109	NM_017306	U, FF, XX, YY, BBB, RRR, SSS	dodecenoyl-coenzyme A delta isomerase (Dci), mRNA. 11/2002 Length = 987	EST
3338	20564	NM_017315	JJ, KK	sodium-coupled ascorbic acid transporter 1 (SVCT1), mRNA. 11/2000 Length = 2472	ESTs
3344	355	NM_017334	C, DD, FF, MM, SSS, TTT, UUU, General Alternate	CAMP responsive element modulator (Crem), mRNA. 10/2002 Length = 436	CAMP responsive element modulator
3344	356	NM_017334	L, DD, FFF, GGG, HHH, General Alternate	CAMP responsive element modulator (Crem), mRNA. 10/2002 Length = 436	CAMP responsive element modulator
3345	16148	NM_017340	U, FF, LL, VV	acyl-coA oxidase (RATACOA1), mRNA. 11/2000 Length = 3741	acyl-coA oxidase

TABLE 1					
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Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3345	16150	NM_017340	J, U, DD, EE, FF, II, LL, RRR	acyl-coA oxidase (RATACOA1), mRNA. 11/2000 Length = 3741	acyl-coA oxidase
3350	26379	NM_019129	Z, AA	Insulin (Ins1), mRNA. 11/2000 Length = 333	
3351	25322	NM_019130	AA	Insulin 2 (Ins2), mRNA. 11/2000 Length = 333	
3364	1173	NM_019184	T, V, CC, OO, GGG, PPP, QQQ	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase) (Cyp2c), mRNA. 11/2002 Length = 1856	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
3364	1174	NM_019184	DD, TT	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase) (Cyp2c), mRNA. 11/2002 Length = 1856	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
3392	20750	NM_019301	C	Complement receptor related protein (Cr1), mRNA. 11/2000 Length = 1811	Complement receptor related protein
3423	26349	NM_021576	SS	5 nucleotidase (Nt5), mRNA. 11/2002 Length = 3152	
3434	25579	NM_021750	T	cysteine-sulfinic acid decarboxylase (Csad), mRNA. 11/2000 Length = 2413	
3440	20182	NM_021840	M, II	histone 2a (H2a), mRNA. 1/2001 Length = 393	
3453	18216	NM_022241	RR	prostaglandin D2 receptor (Ptgdr2), mRNA. 12/2000 Length = 1315	prostaglandin D2 receptor
3458	10369	NM_022271	Z, AA, WW	sertolin (LOC64038), mRNA. 12/2000 Length = 853	sertolin

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	UniGene Sequence Cluster Title
3496	20935	NM_022595	UU	kinase substrate HASPP28 (Haspp28), mRNA. 1/2001 Length = 1220	kinase substrate HASPP28
3500	21204	NM_022606	D	protein phosphatase 2C (AF095927), mRNA. 1/2001 Length = 1318	protein phosphatase 2C
3511	25303	NM_022699	V	ribosomal protein L30 (Rpl30), mRNA. 11/2002 Length = 392	
3515	17500	NM_022866	NN	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (Slc13a3), mRNA. 11/2002 Length = 3239	sodium-dependent high-affinity dicarboxylate transporter 3
3516	23606	NM_022867	C, I, DD, UU, WW, General Alternate	microtubule-associated proteins 1A/1B light chain 3 (MPL3), mRNA. 1/2001 Length = 861	microtubule-associated proteins 1A/1B light chain 3
3516	23608	NM_022867	C, DD, EE, HH, KKK, General Core Tox Markers, General Alternate	microtubule-associated proteins 1A/1B light chain 3 (MPL3), mRNA. 1/2001 Length = 861	microtubule-associated proteins 1A/1B light chain 3
3518	18630	NM_022921	O, P, XX, YY	RT1 class Ib gene, locus M3 (RT1-M3), mRNA. 11/2002 Length = 1341	RT1 class Ib gene, locus M3
3530	17487	NM_023092	X, Y	unconventional myosin Myr2 I heavy chain (Myr2), mRNA. 2/2001 Length = 3810	unconventional myosin Myr2 I heavy chain
3533	14468	NM_024002	HH	SECIS binding protein 2 (Sbp2), mRNA. 2/2001 Length = 3240	SECIS binding protein 2

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3562	348	NM_030586	Y	cytochrome b5, outer mitochondrial membrane isoform (omb5), mRNA. 3/2001 Length = 845	cytochrome b5, outer mitochondrial membrane isoform
3565	15120	NM_030833	LLL	interferon-inducible protein 16 (LOC80875), mRNA. 4/2001 Length = 630	interferon-inducible protein 16
3565	15121	NM_030833	P	interferon-inducible protein 16 (LOC80875), mRNA. 4/2001 Length = 630	interferon-inducible protein 16
3573	7872	NM_030985	F, H, LL, LLL, OOO, SSS, General Alternate	angiotensin receptor 1a (Agtr1a), mRNA. 11/2002 Length = 1450	ESTs
3573	25453	NM_030985	F, LLL, SSS, General Alternate	angiotensin receptor 1a (Agtr1a), mRNA. 11/2002 Length = 1450	
3592	17269	NM_031057	General Alternate	methylmalonate semialdehyde dehydrogenase gene (Mmsdh), mRNA. 4/2001 Length = 2059	methylmalonate semialdehyde dehydrogenase gene
3598	1404	NM_031087	DD, EE	presenilin-2 (Psen2), mRNA. 4/2001 Length = 2088	presenilin-2
3599	1175	NM_031093	F, T, V, BB, TT, DDD, FFF, PPP, QQQ	#NAME? (Rala), mRNA. 11/2002 Length = 952	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
3619	21623	NM_031144	M, N	cytoplasmic beta-actin (Actx), mRNA. 4/2001 Length = 1128	
3630	15359	NM_031335	ZZ, AAA	polymerase II (LOC83503), mRNA. 4/2001 Length = 470	polymerase II

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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3634	634	NM_031509	K, V, NN, TT, DDD, EEE, MMM	Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	Glutathione-S-transferase, alpha type (Ya)
3634	635	NM_031509	M, NN, TT, DDD, EEE, MMM	Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	Glutathione-S-transferase, alpha type (Ya)
3634	25069	NM_031509	G, K, Y, TT, LLL, UUU	Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	
3634	25525	NM_031509	N, V, NN, TT, DDD, EEE, MMM	Glutathione-S-transferase, alpha type (Ya) (Gsta1), mRNA. 5/2001 Length = 1178	Glutathione-S-transferase, alpha type (Ya)
3640	25058	NM_031533	D, RR	Androsterone UDP-glucuronosyltransferase (Ugt2b2), mRNA. 5/2001 Length = 1593	
3654	15803	NM_031593	T, PP, QQ	synaptic vesicle protein 2C (Sv2c), mRNA. 8/2001 Length = 2622	synaptic vesicle protein 2C
3688	21646	NM_031781	V	amyloid beta (A4) precursor protein-binding, family A, member 3 (X11-like 2) (Apba3), mRNA. 5/2001 Length = 1939	amyloid beta (A4) precursor protein-binding, family A, member 3 (X11-like 2)
3695	15759	NM_031815	PP, QQ	activin beta E (Inhbe), mRNA. 5/2001 Length = 2600	activin beta E
3703	8384	NM_031836	RR	vascular endothelial growth factor (Vegf), mRNA. 11/2002 Length = 645	vascular endothelial growth factor
3703	8386	NM_031836	RR	vascular endothelial growth factor (Vegf), mRNA. 11/2002 Length = 645	vascular endothelial growth factor

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3713	8661	NM_031971	C, K, Q, GG, HH	Heat shock protein 70-1 (Hspa1a), mRNA. 5/2001 Length = 2455	Heat shock protein 70-1
3717	25611	NM_031978	UU	26S proteasome, subunit p112 (PSMD1), mRNA. 5/2001 Length = 3089	
3732	21103	NM_033021	D, JJ, KK	vesicle associated protein (VAP1), mRNA. 7/2001 Length = 4422	vesicle associated protein
3732	21104	NM_033021	Z, AA	vesicle associated protein (VAP1), mRNA. 7/2001 Length = 4422	vesicle associated protein
3734	25469	NM_033234	M, T, HH, XX, YY	Hemoglobin, beta (Hbb), mRNA. 12/2001 Length = 620	
3757	9214	NM_053374	EEE, MMM	interferon gamma inducing factor binding protein (Igfbp), mRNA. 11/2002 Length = 626	interferon gamma inducing factor binding protein
3757	9215	NM_053374	EEE, MMM	interferon gamma inducing factor binding protein (Igfbp), mRNA. 11/2002 Length = 626	interferon gamma inducing factor binding protein
3758	11092	NM_053381	RR	ATPase, (Na ⁺)/K ⁺ transporting, beta 4 polypeptide (Atp1b4), mRNA. 11/2002 Length = 4174	ESTs, Weakly similar to I54060 Na ⁺ ,K ⁺ -ATPase beta2 subunit - rat (fragment) [R.norvegicus]
3764	14621	NM_053437	L, BBB, CCC	diacylglycerol O-acyltransferase 1 (Dgat1), mRNA. 11/2002 Length = 1751	diacylglycerol acyltransferase
3786	20708	NM_053543	Q, R, W, PPP	neurochondrin (Ncdn-pending), mRNA. 11/2001 Length = 3730	neurochondrin

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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3810	18644	NM_053648	E, LL, NNN	beta-carotene 15, 15'-dioxygenase (Bcd0), mRNA. 11/2002 Length = 2207	beta-carotene 15, 15'-dioxygenase
3832	15103	NM_053814	DD, EE, NNN	Rho interacting protein 3 (Rhoip3), mRNA. 11/2001 Length = 3286	Rho interacting protein 3
3841	25073	NM_053854	T	N-Acetyltransferase-2 (Nat2), mRNA. 10/2002 Length = 1385	
3849	17090	NM_053906	G, K, L, X	glutathione reductase (Gsr), mRNA. 11/2001 Length = 1428	glutathione reductase
3849	17091	NM_053906	G, K, L, X, TT, DDD, UUU	glutathione reductase (Gsr), mRNA. 11/2001 Length = 1428	glutathione reductase
3849	17092	NM_053906	G, H, K, S, X, TT, DDD	glutathione reductase (Gsr), mRNA. 11/2001 Length = 1428	glutathione reductase
3855	19772	NM_053961	HH	endoplasmic reticulum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	
3855	26264	NM_053961	RR	endoplasmic reticulum protein 29 (Erp29), mRNA. 11/2001 Length = 4529	ESTs
3873	26267	NM_054010	SS	neuraminidase 3 (Neu3), mRNA. 11/2001 Length = 2307	
3884	968	NM_057133	JJ, KK, HHH	nuclear receptor subfamily 0, group B, member 2 (Nr0b2), mRNA. 11/2001 Length = 1111	nuclear receptor subfamily 0, group B, member 2
3884	969	NM_057133	JJ, KK, HHH	nuclear receptor subfamily 0, group B, member 2 (Nr0b2), mRNA. 11/2001 Length = 1111	nuclear receptor subfamily 0, group B, member 2

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3892	17391	NM_057207	YY	synaptic vesicle glycoprotein 2 b (Sv2b), mRNA. 4/2002 Length = 6004	synaptic vesicle glycoprotein 2 b
3900	18779	NM_080581	T	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (Abcc3), mRNA. 11/2002 Length = 5174	ESTs
3908	7595	NM_080787	ZZ, AAA	diacylglycerol kinase, alpha (80 kDa) (Dgka), mRNA. 11/2002 Length = 3043	diacylglycerol kinase, alpha (80kD)
3918	18764	NM_130409	NNN	complement component factor h (Cfh), mRNA. 1/2002 Length = 4256	ESTs, Weakly similar to G35070 apolipoprotein H-related protein 13G1 - mouse [M.musculus]
3930	23348	NM_130894	DD, EE	mitofusin 2 (Mfn2), mRNA. 11/2002 Length = 4160	mitofusin 2
3930	23349	NM_130894	DD, EE, NNN	mitofusin 2 (Mfn2), mRNA. 11/2002 Length = 4160	mitofusin 2
3936	4956	NM_133315	JJ, KK, XX, YY	solute carrier family 39 (iron-regulated transporter), member 1 (Slc39a1), mRNA. 11/2002 Length = 2129	solute carrier family 39 (iron-regulated transporter), member 1
3936	4957	NM_133315	JJ, KK, HHH	solute carrier family 39 (iron-regulated transporter), member 1 (Slc39a1), mRNA. 11/2002 Length = 2129	solute carrier family 39 (iron-regulated transporter), member 1
3938	22501	NM_133394	A, B	putative zinc finger protein SERZ-1 (Serz-1), mRNA. 3/2002 Length = 2677	putative zinc finger protein SERZ-1
3939	21576	NM_133398	PPP, QQQ	LYRIC (Lyric), mRNA. 3/2002 Length = 2234	LYRIC

TABLE 1				Attorney Docket 44921-5038-01WO Document No. 1935823.1	
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3939	21577	NM_133398	HH	LYRIC (Lyric), mRNA. 3/2002 Length = 2234	LYRIC
3947	11483	NM_133546	Q, W	myeloid differentiation primary response gene 116 (Myd116), mRNA. 3/2002 Length = 2225	myeloid differentiation primary response gene 116
3947	18043	NM_133546	Q	myeloid differentiation primary response gene 116 (Myd116), mRNA. 3/2002 Length = 2225	myeloid differentiation primary response gene 116
3949	17886	NM_133561	U, RRR, SSS, General Alternate	brain protein 44-like (Brp44l), mRNA. 11/2002 Length = 901	brain protein 44-like
3949	17887	NM_133561	GGG, HHH, RRR, UUU, General Core Tox Markers, General Alternate	brain protein 44-like (Brp44l), mRNA. 11/2002 Length = 901	brain protein 44-like
3959	19384	NM_134326	QQ, YY	Albumin (Alb), mRNA. 3/2002 Length = 1956	EST
3963	17337	NM_134351	Q, WW	methionine adenosyltransferase II, alpha (Mat2a), mRNA. 3/2002 Length = 1337	ESTs
3967	2367	NM_134410	CC, DD, EE, NNN	Mg87 protein (Mg87), mRNA. 3/2002 Length = 1330	Mg87 protein
3967	2368	NM_134410	U, CC, DD, NNN	Mg87 protein (Mg87), mRNA. 3/2002 Length = 1330	Mg87 protein
3971	6397	NM_134458	D	nuclear receptor coactivator GT198 (Gt198), mRNA. 3/2002 Length = 721	nuclear receptor coactivator GT198

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
3978	48	NM_138547	LL, RRR, UUU	3-alpha-hydroxysteroid dehydrogenase (LOC191574), mRNA. 4/2002 Length = 2466	3-alpha-hydroxysteroid dehydrogenase
3978	25475	NM_138547	WW	3-alpha-hydroxysteroid dehydrogenase (LOC191574), mRNA. 4/2002 Length = 2466	3-alpha-hydroxysteroid dehydrogenase
3983	16401	NM_138828	S, DD, EE, SS	apolipoprotein E (ApoE), mRNA. 11/2002 Length = 936	
3997	17573	NM_139039	PP, QQ	membrane and microfilament-associated protein p58 (LOC207121), mRNA. 5/2002 Length = 2003	ESTs
4009	10018	NM_139186	MM, TTT, General Alternate	spermatogenesis-related protein (Srp) (LOC246042), mRNA. 5/2002 Length = 1016	spermatogenesis-related protein (Srp)
4009	10019	NM_139186	General Alternate	spermatogenesis-related protein (Srp) (LOC246042), mRNA. 5/2002 Length = 1016	spermatogenesis-related protein (Srp)
4011	16592	NM_139252	A, B, HHH	phosphatidic acid phosphatase type 2c (Ppap2c), mRNA. 5/2002 Length = 1603	phosphatidic acid phosphatase type 2c
4016	12450	NM_139337	F	LRP16 protein (Lrp16), mRNA. 11/2002 Length = 1030	Rattus norvegicus LRP16-like protein mRNA, complete cds
4024	6988	NM_145677	C, MM, TTT	peroxisomal Ca-dependent solute carrier-like protein (Pcscl), mRNA. 11/2002 Length = 3150	ESTs

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4030	20046	NM_145784	O, P	G protein-coupled receptor 37-like 1 (Gpr3711), mRNA. 11/2002 Length = 2451	ESTs
4030	20050	NM_145784	HH	G protein-coupled receptor 37-like 1 (Gpr3711), mRNA. 11/2002 Length = 2451	ESTs, Highly similar to T17310 hypothetical protein DKFZp434B168.1 - human (fragment) [H.sapiens]
4030	20698	NM_145784	E, V, W, BB, CC, PP, QQ, SS, UU, EEE, III, JJJ, KKK, LLL, MMM, NNN, SSS, UUU	G protein-coupled receptor 37-like 1 (Gpr3711), mRNA. 11/2002 Length = 2451	
4030	21355	NM_145784	U, FF, LL, CCC, RRR, SSS, UUU	G protein-coupled receptor 37-like 1 (Gpr3711), mRNA. 11/2002 Length = 2451	ESTs
4030	21904	NM_145784	K, N, HH, TT, DDD	G protein-coupled receptor 37-like 1 (Gpr3711), mRNA. 11/2002 Length = 2451	
4030	26320	NM_145784	BB	G protein-coupled receptor 37-like 1 (Gpr3711), mRNA. 11/2002 Length = 2451	
4031	11440	NM_145790	CCC	Lipogenin (Lipogenin), mRNA. 11/2002 Length = 1265	ESTs
4031	14664	NM_145790	Q, R	Lipogenin (Lipogenin), mRNA. 11/2002 Length = 1265	ESTs
4032	25644	NM_147136	XX, YY	rRNA promoter binding protein (LOC257642), mRNA. 11/2002 Length = 1038	

TABLE 1					
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Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4034	683	NM_147206	M	cytochrome P450 3A9 (CYP3A9), mRNA. 11/2002 Length = 2101	Rattus norvegicus cytochrome P450 3A9 mRNA, complete cds
4038	23070	NM_148891	GGG	N-myristoyltransferase 1 (Nmt1), mRNA. 11/2002 Length = 1491	ESTs, Highly similar to NMT1_MOUSE Glycylpeptide N-tetradecanoyltransferase 1 (Peptide N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase) [M.musculus]
4040	6274	NM_152242	SS	G protein-coupled receptor 56 (Gpr56), mRNA. 11/2002 Length = 2949	ESTs
4045	17995	NM_153312	QQ, TT, DDD, FFF	testosterone 6-beta-hydroxylase (CYP3A2), mRNA. 10/2002 Length = 1936	Rattus norvegicus Sprague Dawley testosterone 6-beta-hydroxylase, cytochrome P450/6-beta-A, (CYP3A2) mRNA, complete cds
4047	11755	NM_153314	TT	UDP-glucuronosyltransferase 2B3 precursor, microsomal (UDPGT), mRNA. 10/2002 Length = 1716	
4049	5920	NM_153622	G, EEE, MMM	Na/Pi cotransporter 4 (Rnpt4), mRNA. 10/2002 Length = 2316	ESTs
4051	25565	NM_153821	D	paired mesoderm homeobox 1 (Pmx1), mRNA. 10/2002 Length = 1375	
4058	25064	S45392	H, K, S, FF, PP, QQ, KKK		
4060	25481	S46798	F, HH, NNN		
4061	25495	S59892	ZZ, AAA		
4062	25496	S59893	R, ZZ, AAA, PPP, QQQ		
4064	25500	S63458	FF, RRR, SSS, UUU		

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4065	3244	S63519	A, B, General Alternate		ESTs
4066	25501	S63521	FF, LL		
4067	25507	S67316	Z, AA		
4068	15832	S68589	MM, TTT		ESTs, Moderately similar to N4BM_HUMAN NADH-ubiquinone oxidoreductase subunit B14.5b (Complex I-B14.5b) (CI-B14.5b) [H.sapiens]
4070	25513	S69315	D		
4072	25518	S70011	JJ, KK, HHH		
4073	7554	S70803	M		ESTs
4073	25520	S70803	E		
4075	25066	S75280	WW		
4078	25550	S79213	J, CC, II, OOO	protein phosphatase 1, regulatory (inhibitor) subunit 2	
4081	25559	S81025	M		
4083	25071	S83436	JJ, KK		
4090	357	U04835	C, K, MM, GGG, TTT	CAMP responsive element modulator	CAMP responsive element modulator
4092	15462	U06230	C, F, G, S, XX, YY, FFF	protein S	protein S
4098	17281	U10697	M, BB, NN	carboxylesterase 1	carboxylesterase 1
4103	9520	U17837	UU		ESTs
4108	90	U20796	T		Rattus norvegicus nuclear receptor Rev-ErbA-beta mRNA, partial cds
4109	25589	U21718	H, PPP, QQQ		
4110	22196	U21719	B, HHH, PPP, QQQ, General Alternate		ESTs
4111	25590	U21720	RR		
4112	25591	U21721	VV		
4116	17480	U31598	NN, OO, VV		R.norvegicus mRNA for RT1.Ma
4121	18301	U33500	M, DD, EE, WW		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4121	18302	U33500	N, DD, EE, WW		Rattus norvegicus retinol dehydrogenase type II mRNA, complete cds
4122	25078	U33540	QQQ, General Alternate		
4124	797	U38253	General Alternate	eukaryotic translation initiation factor 2B, subunit 3 (gamma, 58kD)	eukaryotic translation initiation factor 2B, subunit 3 (gamma, 58kD)
4133	772	U48288	PP, QQ, SS	A-kinase anchoring protein	A-kinase anchoring protein
4135	738	U49058	PP, QQ	CTD-binding SR-like protein rA4	
4142	25607	U53873	RR, SS, WW		
4152	25618	U64705	R		
4161	25629	U70270	PP, QQ		
4164	957	U72741	L, MM, WW, TTT	Lectin, galactose binding, soluble 9 (Galectin-9)	Lectin, galactose binding, soluble 9 (Galectin-9)
4164	958	U72741	F, MM, WW, TTT	Lectin, galactose binding, soluble 9 (Galectin-9)	Lectin, galactose binding, soluble 9 (Galectin-9)
4167	25632	U75405	II		
4172	25643	U77829	H, Q, R	growth arrest specific 5	
4175	25647	U83119	RR		
4180	22005	U96490	A, B	liver protein	liver protein
4180	22006	U96490	RR	liver protein	liver protein
4182	819	X02284	Y, SS		
4185	20168	X03347	E, DD, EE		
4189	25662	X05472	RR		
4189	25663	X05472	X, Y		
4191	25084	X06769	A, B, V, LL		
4193	25671	X07686	RR		
4197	25675	X14181	G, H, EEE, MMM		
4201	25678	X14848	V		
4202	25679	X15013	D, H, DDD		
4209	25087	X51615	WW, LLL, UUU		
4214	25689	X52815	A, B, T		

TABLE 1					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Known Gene Name	Unigene Sequence Cluster Title
4216	25691	X53504	BB, CC, DDD, III, JJJ, General Alternate		
4222	20308	X56327	RR, SS		
4224	15106	X57529	GG		ESTs, Highly similar to RS18_HUMAN 40S ribosomal protein S18 (KE-3) (KE3) [R.norvegicus]
4225	25701	X57986	S, CC, OOO, General Alternate	Protein kinase, cAMP dependent, catalytic, alpha	
4230	25705	X59375	F, I, K, II, TT, WW, FFF		
4232	25707	X59677	Z, AA		
4234	25717	X61296	RR		
4240	25723	X62327	X, Y		
4242	25725	X62660	X, GG, TT, XX, DDD		
4247	25091	X65190	D		
4262	16272	X76456	DDD, PPP, QQQ		
4267	25742	X80130	UU		
4268	25747	X81448	A, E, II, PP, QQ, VV, GGG	keratin complex 1, acidic, gene 18	
4274	25754	X89696	Z, AA		
4275	25756	X89698	RR, SS		
4276	25759	X89701	SS		
4279	25768	X94769	N, UU		
4283	25777	Y08355	V, FF, OO	oxidative stress induced	oxidative stress induced
4292	25797	Z68145	E		
4294	2387	AI029571	N		ESTs
4295	26099	AA963133	ZZ, AAA		

TABLE 2				
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Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3353	15977	NM_019132	S	Activation of Csk by cAMP-dependent Protein Kinase Inhibits Signaling through the T Cell Receptor, Activation of cAMP-dependent protein kinase, PKA, Attenuation of GPCR Signaling, CCR3 signaling in Eosinophils, ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling pathway, Phospholipase C-epsilon pathway, Signaling Pathway from G-Protein Families, Transcription factor CREB and its extracellular signals
3124	24545	NM_012713	D	Activation of PKC through G protein coupled receptor, Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Apoptotic Signaling in Response to DNA Damage, Attenuation of GPCR Signaling, BCR and Bioactive Peptide Induced Signaling Pathways, CCR3 signaling in Eosinophils, EGF, Growth Hormone, and CXCR4 Signaling Pathways, Effects of calcinurin in Keratinocyte Differentiation, Fc Epsilon Receptor I Signaling in Mast Cells, Ion Channel and Phorbol Esters Signaling Pathway, Links between Pyk2 and Map Kinases, PDGF and Phospholipase C Signaling Pathways, PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase, Pertussis toxin-insensitive CCR5 Signaling in Macrophage, Phospholipase C d1 in phospholipid associated cell signaling, Regulation of eIF4e and p70 S6 Kinase, Signaling Pathway from G-Protein Families, TPO Signaling Pathway, Thrombin signaling and protease-activated receptors, Transcription factor CREB and its extracellular signals, T Cell and Trka Receptor Signaling Pathways, egf, g-Secretase mediated
3185	2554	NM_012967	W	Adhesion Molecules on Lymphocyte, B Lymphocyte Cell Surface Molecules, CTL mediated immune response against target cells, Cells and Molecules involved in local acute inflammatory response, Monocyte and its Surface Molecules, Neutrophil and Its Surface Molecules, T Cytotoxic Cell Surface Molecules, T Helper Cell Surface Molecules
3185	2555	NM_012967	W, BB, CC, NN, OO, PP	Adhesion Molecules on Lymphocyte, B Lymphocyte Cell Surface Molecules, CTL mediated immune response against target cells, Cells and Molecules involved in local acute inflammatory response, Monocyte and its Surface Molecules, Neutrophil and Its Surface Molecules, T Cytotoxic Cell Surface Molecules, T Helper Cell Surface Molecules

TABLE 2				
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID.	Model Code	Pathways
2266	14989	AI177366	HHH	Adhesion Molecules on Lymphocyte, Cells and Molecules involved in local acute inflammatory response, Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Monocyte and its Surface Molecules, PTEN dependent cell cycle arrest and apoptosis, Ras-Independent pathway in NK cell-mediated cytotoxicity
4244	25089	X63594	I, J	AKT Signaling Pathway, ATM Signaling Pathway, Acetylation and Deacetylation of RelA in The Nucleus, Activation of PKC through G protein coupled receptor, CD40L Signaling Pathway, Double Stranded RNA Induced Gene Expression, Erythropoietin mediated neuroprotection through NF-kB, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors, Influence of Ras and Rho proteins on G1 to S Transition, NF-kB Signaling Pathway, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Signal transduction through IL1R, T Cell Receptor Signaling Pathway, TNF/Stress Related Signaling, TNFR2 Signaling Pathway, The 41BB-dependent immune response, Toll-Like Receptor Pathway, interact6-1
4244	25090	X63594	J	AKT Signaling Pathway, ATM Signaling Pathway, Acetylation and Deacetylation of RelA in The Nucleus, Activation of PKC through G protein coupled receptor, CD40L Signaling Pathway, Double Stranded RNA Induced Gene Expression, Erythropoietin mediated neuroprotection through NF-kB, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors, Influence of Ras and Rho proteins on G1 to S Transition, NF-kB Signaling Pathway, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Signal transduction through IL1R, T Cell Receptor Signaling Pathway, TNF/Stress Related Signaling, TNFR2 Signaling Pathway, The 41BB-dependent immune response, Toll-Like Receptor Pathway, interact6-1

TABLE 2				
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3205	16683	NM_013052	W, SS, HHH	AKT Signaling Pathway, Cell Cycle: G2/M Checkpoint, Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation, RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage, Regulation of BAD phosphorylation, Role of nicotinic acetylcholine receptors in the regulation of apoptosis, Signal Dependent Regulation of Myogenesis by Corepressor MITR, cdc25 and chk1 Regulatory Pathway in response to DNA damage
3205	16684	NM_013052	W, JJ, GGG, HHH	AKT Signaling Pathway, Cell Cycle: G2/M Checkpoint, Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation, RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage, Regulation of BAD phosphorylation, Role of nicotinic acetylcholine receptors in the regulation of apoptosis, Signal Dependent Regulation of Myogenesis by Corepressor MITR, cdc25 and chk1 Regulatory Pathway in response to DNA damage
1424	3203	AI012595	Q, R, General Alternate	AKT Signaling Pathway, ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling pathway, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Regulation of ck1/cdk5 by type 1 glutamate receptors, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, WNT Signaling Pathway, mTOR Signaling Pathway
3257	3202	NM_017039	B, Q, R, WW, General Alternate	AKT Signaling Pathway, ChREBP regulation by carbohydrates and cAMP, Erk1/Erk2 Mapk Signaling pathway, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Regulation of ck1/cdk5 by type 1 glutamate receptors, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, WNT Signaling Pathway, mTOR Signaling Pathway
1362	17524	AI010568	General Core Tox Markers	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase

TABLE 2				Attorney Docket 44921-5038-01WO
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3274	10886	NM_017094	B, H, S, LLL, PPP, QQQ, General Core Tox Markers, General Alternate	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase
3274	10887	NM_017094	A, B, T, FF, NN, OO, General Alternate	AKT Signaling Pathway, Growth Hormone Signaling Pathway, Regulation of eIF4e and p70 S6 Kinase
777	21010	AA925306	D, U, FF, BBB, RRR, SSS	Alanine and aspartate metabolism
3083	20744	NM_012571	C, I, J, X, EE, MM, UU, WW, KKK, TTT, General Alternate	Alanine and aspartate metabolism, Alkaloid biosynthesis I, Arginine and proline metabolism, Carbon fixation, Cysteine metabolism, Glutamate metabolism, Malate-aspartate shuttle, Phenylalanine metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis, Tyrosine metabolism
3230	17628	NM_013177	General Alternate	Alanine and aspartate metabolism, Alkaloid biosynthesis I, Arginine and proline metabolism, Carbon fixation, Cysteine metabolism, Glutamate metabolism, Phenylalanine metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis, Tyrosine metabolism
3429	23424	NM_021680	E	Alanine and aspartate metabolism, Aminoacyl-tRNA biosynthesis
4093	1583	U07201	E, GG, III, JJJ	Alanine and aspartate metabolism, Aminoacyl-tRNA biosynthesis, Nitrogen metabolism
3626	4234	NM_031330	A, B, I, L, Y, MM, HHH, KKK, OOO, TTT, General Alternate	Alanine and aspartate metabolism, Arginine and proline metabolism, Urea cycle and metabolism of amino groups
4194	20597	X12459	C, YY, BBB	Alanine and aspartate metabolism, Arginine and proline metabolism, Urea cycle and metabolism of amino groups
3424	18727	NM_021577	A, B, I, J, L, MM, WW, BBB, KKK, OOO, TTT, General Alternate	Alanine and aspartate metabolism, Arginine and proline metabolism, Urea cycle and metabolism of amino groups
3587	21094	NM_031039	HH, XX, General Alternate	Alanine and aspartate metabolism, Carbon fixation, Glutamate metabolism

TABLE 2					Attorney Docket 44921-5038-01WO Document No. 1935823.1
Seq ID No.	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3587	21096	NM_031039	M	Alanine and aspartate metabolism, Carbon fixation, Glutamate metabolism	
4118	1478	U32314	M, VV, DDD, GGG, LLL, UUU, General Core Tox Markers	Alanine and aspartate metabolism, Citrate cycle (TCA cycle), Pyruvate metabolism	
4118	1479	U32314	M, X, VV, DDD, GGG, LLL, UUU, General Core Tox Markers	Alanine and aspartate metabolism, Citrate cycle (TCA cycle), Pyruvate metabolism	
1944	24803	AI137065	MM, VV, TTT	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism	
2848	24797	D13667	MM, PP, QQ, RR, TTT	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism	
2882	24799	E01050	X, Y, MM, SS, TTT	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism	
3563	24798	NM_030656	F, N, MM, SS, BBB, CCC, TTT	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism	
3563	24800	NM_030656	MM, RR, SS, TTT	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism	
3563	24801	NM_030656	MM, VV, TTT	Alanine and aspartate metabolism, Glycine, serine and threonine metabolism	
1558	1431	AI044610	I, J, CC, II, General Alternate	Alkaloid biosynthesis I, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism	
3046	1430	M84648	TT, DDD, General Core Tox Markers, General Alternate	Alkaloid biosynthesis I, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism	
3109	24825	NM_012668	C, D, I, J, NNN	Alkaloid biosynthesis I, Phenylalanine metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis, Tyrosine metabolism	
3521	16184	NM_022935	Z, AA	Alkaloid biosynthesis II, Arginine and proline metabolism, Glycine, serine and threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism, beta-Alanine metabolism	
4163	25083	U72632	RR	Alkaloid biosynthesis II, Arginine and proline metabolism, Glycine, serine and threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism, beta-Alanine metabolism	

TABLE 2					Attorney Docket 44921-5038-01WO Document No. 1935828.1
Seq ID No.	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3096	23522	NM_012615	A	Alkaloid biosynthesis II, Arginine and proline metabolism, Urea cycle and metabolism of amino groups	
3096	23523	NM_012615	B, H, I, J	Alkaloid biosynthesis II, Arginine and proline metabolism, Urea cycle and metabolism of amino groups	
3246	1958	NM_016994	L, S, HH	Alternative Complement Pathway, Cells and Molecules involved in local acute inflammatory response, Classic Complement Pathway, Complement Pathway, Lectin Induced Complement Pathway	
4212	1959	X52477	S, HH, MM, SS, TTT	Alternative Complement Pathway, Cells and Molecules involved in local acute inflammatory response, Classic Complement Pathway, Complement Pathway, Lectin Induced Complement Pathway	
153	16756	AA818089	G, H	Aminoacyl-tRNA biosynthesis, Glycine, serine and threonine metabolism	
2300	6502	AI178283	XX	Aminoacyl-tRNA biosynthesis, Phenylalanine, tyrosine and tryptophan biosynthesis	
1684	2838	AI070511	G, H	Aminoacyl-tRNA biosynthesis, Valine, leucine and isoleucine biosynthesis	
3336	23130	NM_017307	V, FF	Aminophosphonate metabolism, Glycerolipid metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol	
3823	7927	NM_053765	I, U, X, Y, DDD, LLL	Aminosugars metabolism	
2842	1515	D10233	O, P	Aminosugars metabolism	
3130	1371	NM_012734	D, V, GG	Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Starch and sucrose metabolism	
3131	11839	NM_012735	Z, AA, NNN	Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism	
3445	17100	NM_022179	F	Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism	
3445	17101	NM_022179	JJ, KK, FFF, HHH	Aminosugars metabolism, Erythromycin biosynthesis, Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism	
3256	24861	NM_017033	T	Aminosugars metabolism, Erythromycin biosynthesis, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Starch and sucrose metabolism, Streptomycin biosynthesis	

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935623.1
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3256	24862	NM_017033	HH, UU	Aminosugars metabolism, Erythromycin biosynthesis, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Starch and sucrose metabolism, Streptomycin biosynthesis
3555	9929	NM_024392	U, EE, XX, YY, RRR, SSS	Androgen and estrogen metabolism
3555	9931	NM_024392	U, RRR, SSS	Androgen and estrogen metabolism
3555	25070	NM_024392	U, FF, LL, CCC, RRR, SSS	Androgen and estrogen metabolism
3107	21087	NM_012661	FFF	Androgen and estrogen metabolism
2930	20429	J05035	F, T, GG, GGG, LLL	Androgen and estrogen metabolism, Bile acid biosynthesis
2930	20430	J05035	F, T, GG, GGG, General Alternate	Androgen and estrogen metabolism, Bile acid biosynthesis
3086	17292	NM_012584	K, GGG	Androgen and estrogen metabolism, C21-Steroid hormone metabolism
3272	23660	NM_017080	T, U, RRR, SSS	Androgen and estrogen metabolism, C21-Steroid hormone metabolism, Visceral Fat Deposits and the Metabolic Syndrome
3879	5492	NM_057105	G, K, GG, HH, WW, DDD	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	5493	NM_057105	G, K, GG, HH, TT, WW, DDD	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	15124	NM_057105	J, K, L, N, S, U, FF, GG, HH, TT, LLL, UUU	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	15125	NM_057105	K, L, M, N, U, FF, GG, PP, QQ, TT, LLL, SSS, UUU	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3879	15126	NM_057105	I, J, K, L, M, N, U, X, Y, GG, HH, LLL, SSS, UUU	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3879	15127	NM_057105	I, J, K, L, M, S, U, X, GG, HH, TT, LLL, SSS, UUU	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	
3640	14633	NM_031533	K	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	
4047	14632	NM_153314	MM, TTT	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	
4047	11755	NM_153314	TT	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	
3165	4282	NM_012883	R, General Alternate	Androgen and estrogen metabolism, Sulfur metabolism	
3119	18718	NM_012695	X, Y	Androgen and estrogen metabolism, Sulfur metabolism	
3119	18717	NM_012695	N	Androgen and estrogen metabolism, Sulfur metabolism	
3119	18719	NM_012695	M, N, UUU	Androgen and estrogen metabolism, Sulfur metabolism	
3316	17562	NM_017245	VV	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	
3932	17560	NM_133283	N	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	
3932	17564	NM_133283	I, J, DD, EE	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935328.1
Seq ID No.	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3932	21848	NM_133283	I, J, RRR, UUU	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
3932	21849	NM_133283	U, RRR	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Anthrax Toxin Mechanism of Action, Bioactive Peptide Induced Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
3100	20798	NM_012639	V, X, Y	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, BCR, EGF, EPO, Erk1/Erk2 Mapk, IGF-1, and CXCR4 Signaling Pathways, Bioactive Peptide Induced Signaling Pathway, CCR3 signaling in Eosinophils, Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia, Fc Epsilon Receptor I Signaling in Mast Cells, Growth Hormone Signaling Pathway, IL-2, IL-3, and IL-6 signaling pathways, IL-2 Receptor B Protein Interaction Pathway, Influence of Ras and Rho proteins on G1 to S Transition, Inhibition of Cellular Proliferation by Gleevec, Insulin Signaling Pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway, Ras Signaling Pathway, Signaling Pathway from G-Protein Families, T Cell Receptor Signaling Pathway, TPO Signaling Pathway, egf, epo, igf-1, il2, il3, il6, insulin,

TABLE 2				
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3100	20799	NM_012639	I	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, BCR, CXCR4, EGF, insulin, Growth Hormone, TPO, and EPO Signaling Pathways, Bioactive Peptide Induced Signaling Pathway, CCR3 signaling in Eosinophils, Erk and PI-3 Kinase Are Necessary for Collagen Binding in Corneal Epithelia, Erk1/Erk2 Mapk Signaling pathway, Fc Epsilon Receptor I Signaling in Mast Cells, IGF-1 Signaling Pathway, IL-2, IL-3, and IL-6 signaling pathways, IL-2 Receptor B Protein Interaction Pathway, Influence of Ras and Rho proteins on G1 to S Transition, Inhibition of Cellular Proliferation by Gleevec, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway, Ras Signaling Pathway, Signaling Pathway from G-Protein Families, T Cell Receptor Signaling Pathway, egf, epo, igf-1, il2, il3, il6, insulin, interact6-
1846	2069	AI103616	VV	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, BCR Signaling Pathway, Influence of Ras and Rho proteins on G1 to S Transition, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Rac 1 cell motility signaling pathway, Ras Signaling Pathway, Ras-Independent pathway in NK cell-mediated cytotoxicity, Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration, T Cell Receptor Signaling Pathway, Transcription factor CREB and its extracellular signals, p38 MAPK Signaling Pathway
2983	21097	M12112	C, I, O, P, MM, NNN, TTT, General Core Tox Markers	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Bioactive Peptide Induced Signaling Pathway
3968	21098	NM_134432	C, L, DD, NNN	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, Bioactive Peptide Induced Signaling Pathway
694	17906	AA899762	NNN	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, EGF Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, egf
2615	17907	AI233224	U	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, EGF Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, egf

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935823.1
Seq ID No.	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3022	16604	M37394	K, LLL, UUU	Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, EGF Signaling Pathway, Erk1/Erk2 Mapk Signaling pathway, egf
3154	11137	NM_012839	D, MM, FFF, TTT	Apoptotic Signaling in Response to DNA Damage, Caspase Cascade in Apoptosis, D4-GDI Signaling Pathway, Electron -Transfer Reaction in Mitochondria, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors , Role of Mitochondria in Apoptotic Signaling
3154	11138	NM_012839	T, JJ, KK, LL	Apoptotic Signaling in Response to DNA Damage, Caspase Cascade in Apoptosis, D4-GDI Signaling Pathway, Electron -Transfer Reaction in Mitochondria, HIV-I Nef: negative effector of Fas and TNF, Induction of apoptosis through DR3 and DR4/5 Death Receptors , Role of Mitochondria in Apoptotic Signaling
3245	24897	NM_016993	QQ	Apoptotic Signaling in Response to DNA Damage, HIV-I Nef: negative effector of Fas and TNF, IL-2 Receptor B Protein Interaction Pathway, Induction of apoptosis through DR3 and DR4/5 Death Receptors , Inhibition of Cellular Proliferation by Gleevec, Regulation of BAD phosphorylation, Role of Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
4149	912	U59184	QQ, UU, General Core Tox Markers	Apoptotic Signaling in Response to DNA Damage, Hypoxia and p53 in the Cardiovascular system, Regulation of BAD phosphorylation, Role of Mitochondria in Apoptotic Signaling, p53 Signaling Pathway
905	22283	AA945172	LL	Arginine and proline metabolism
3581	15683	NM_031011	MM, TTT	Arginine and proline metabolism
1852	16884	AI103758	QQQ	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
1890	16885	AI105188	PP, General Core Tox Markers	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism

TABLE 2				
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3472	20915	NM_022407	F, U, LL, TT, BBB, CCC, EEE, LLL, MMM, RRR, SSS, UUU	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
3678	23884	NM_031731	U	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
1442	12300	AI013333	N	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
3728	12299	NM_032416	N, YY	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
3322	20913	NM_017272	M, TT, LLL, SSS, UUU	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
3322	20914	NM_017272	A, B, L, TT, DDD, LLL, SSS, UUU	Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Histidine metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935828.1
Seq ID No.	CLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3082	4573	NM_012570	XX, YY	Arginine and proline metabolism, Catabolic Pathways for Arginine, Histidine, Glutamate, Glutamine, and Proline, D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, Urea cycle and metabolism of amino groups
3082	4574	NM_012570	GG, OO, DDD	Arginine and proline metabolism, Catabolic Pathways for Arginine, Histidine, Glutamate, Glutamine, and Proline, D-Glutamine and D-glutamate metabolism, Glutamate metabolism, Nitrogen metabolism, Urea cycle and metabolism of amino groups
3283	24693	NM_017134	C, General Alternate	Arginine and proline metabolism, Catabolic Pathways for Arginine, Histidine, Glutamate, Glutamine, and Proline, Urea cycle and metabolism of amino groups
3807	1127	NM_053626	III, JJJ	Arginine and proline metabolism, D-Arginine and D-ornithine metabolism, Glycine, serine and threonine metabolism
3267	20649	NM_017072	L, WW	Arginine and proline metabolism, Glutamate metabolism, Nitrogen metabolism, Urea cycle and metabolism of amino groups
3233	21396	NM_013198	OO, OOO, General Core Tox Markers	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism
3142	16947	NM_012793	N, T, HHH, PPP, QQQ, General Alternate	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
3142	16948	NM_012793	PPP, QQQ	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups
3191	19391	NM_012998	U, FF, RRR	Arginine and proline metabolism, Hypoxia-Inducible Factor in the Cardiovascular System
3191	19392	NM_012998	D, BB	Arginine and proline metabolism, Hypoxia-Inducible Factor in the Cardiovascular System
3191	19393	NM_012998	FF	Arginine and proline metabolism, Hypoxia-Inducible Factor in the Cardiovascular System
3214	13282	NM_013078	WW, FFF, General Alternate	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
3214	13283	NM_013078	A, B, NN, OO	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
633	4242	AA893325	A, B, F, H, X, Y, LLL	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
3050	25467	M93297	A, B, II, WW	Arginine and proline metabolism, Urea cycle and metabolism of amino groups
3070	4467	NM_012529	ZZ, AAA	Arginine and proline metabolism, Urea cycle and metabolism of amino groups

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935823.1
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3450	20299	NM_022220	A, B, Y, FFF, GGG, HHH, LLL, PPP, QQQ, General Core Tox Markers	Ascorbate and aldarate metabolism
3438	22352	NM_021835	I, J, II	ATM, BCR, D4-GDI, EGF, and EPO Signaling Pathways, Angiotensin II mediated activation of JNK Pathway via Pyk2 dependent signaling, FAS signaling pathway (CD95), Fc Epsilon Receptor I Signaling in Mast Cells, Hypoxia-Inducible Factor in the Cardiovascular System, IGF-1 Signaling Pathway, IL 2 signaling pathway, IL 6 signaling pathway, Inhibition of Cellular Proliferation by Gleevec, Insulin Signaling Pathway, Integrin Signaling Pathway, Links between Pyk2 and Map Kinases, MAPKinase Signaling Pathway, Nerve growth factor pathway (NGF), PDGF Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage, Repression of Pain Sensation by the Transcriptional Regulator DREAM, Signal transduction through IL1R, Signaling Pathway from G-Protein Families, T Cell Receptor Signaling Pathway, TNF/Stress Related Signaling, TNFR1 Signaling Pathway, TPO Signaling Pathway, TSP-1 Induced Apoptosis in Microvascular Endothelial Cell , The 41BB-dependent immune response, Toll-Like Receptor Pathway, egf, epo, igf-1, il2, il6, insulin, ngf, pdgf, tpo
3576	17377	NM_030989	CC, NN, OO	ATM Signaling Pathway, Cell Cycle: G1/S Check Point , Cell Cycle: G2/M Checkpoint, Double Stranded RNA Induced Gene Expression, Hypoxia and p53 in the Cardiovascular system, Overview of telomerase protein component gene hTert Transcriptional Regulation , RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage, p53 Signaling Pathway
3535	351	NM_024127	C	ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
3535	353	NM_024127	C, HH, PP, QQ	ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
3535	354	NM_024127	C, FF, II, PP, NNN	ATM Signaling Pathway, Cell Cycle: G2/M Checkpoint, Hypoxia and p53 in the Cardiovascular system, p53 Signaling Pathway
3846	20939	NM_053884	FFF	ATP Synthesis, Oxidative phosphorylation
3948	15524	NM_133556	V	ATP Synthesis, Oxidative phosphorylation
4002	17203	NM_139099	RRR	ATP Synthesis, Oxidative phosphorylation
1828	17400	AI103097	KKK	ATP Synthesis, Oxidative phosphorylation

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3689	16178	NM_031785	T, V, JJ, KK	ATP Synthesis, Oxidative phosphorylation	
3409	18141	NM_019383	Y, JJ	ATP Synthesis, Oxidative phosphorylation	
3409	22727	NM_019383	GG	ATP Synthesis, Oxidative phosphorylation	
528	2106	AA892006	SS	ATP Synthesis, Oxidative phosphorylation	
528	2107	AA892006	O, P, ZZ, AAA	ATP Synthesis, Oxidative phosphorylation	
1498	2108	AI029960	ZZ, AAA	ATP Synthesis, Oxidative phosphorylation	
3802	20725	NM_053602	Q, R	ATP Synthesis, Oxidative phosphorylation, Purine metabolism	
3802	20726	NM_053602	LL	ATP Synthesis, Oxidative phosphorylation, Purine metabolism	
3270	18956	NM_017075	BBB	Benzoate degradation, Bile acid biosynthesis, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies, Tryptophan metabolism	
3270	18957	NM_017075	D, U, GG, XX, YY, BBB, CCC	Benzoate degradation, Bile acid biosynthesis, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies, Tryptophan metabolism	
3270	18958	NM_017075	U, FF, XX, BBB, CCC, RRR, SSS	Benzoate degradation, Bile acid biosynthesis, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies, Tryptophan metabolism	
3897	21562	NM_078623	S	Benzoate degradation, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism	
3667	15175	NM_031682	A, B, P, U, BBB, CCC, RRR, SSS, General Alternate	Benzoate degradation, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Tryptophan metabolism, Valine, leucine and isoleucine degradation	
3889	6613	NM_057186	A, U	Benzoate degradation, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Tryptophan metabolism, Valine, leucine and isoleucine degradation	
1897	23596	AI105435	VV	Benzoate degradation, Fatty acid metabolism, Lysine degradation, Tryptophan metabolism	

TABLE 2				Attorney Docket 449241-5038-01WO
				Document No. 1935323.1
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3058	23698	NM_012489	U, FF, HH, LL, XX, BBB, CCC, DDD, RRR, SSS, UUU	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Valine, leucine and isoleucine degradation
3058	23699	NM_012489	U, FF, GG, HH, LL, DDD	Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Valine, leucine and isoleucine degradation
4277	420	X90710	U, RRR, SSS	Bile acid biosynthesis, Fatty acid metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Tyrosine metabolism
3129	10260	NM_012732	T, GG, HH, LL	Bile acid biosynthesis, Glycerolipid metabolism
3129	25563	NM_012732	DD, EE	Bile acid biosynthesis, Glycerolipid metabolism
2866	1531	D43964	OO, PP, QQ, PPP, QQQ	Bile acid biosynthesis, Taurine and hypotaurine metabolism
3519	24838	NM_022924	PPP, QQQ	Bioactive Peptide Induced Signaling Pathway, Thrombin signaling and protease-activated receptors, Transcriptional activation of dbpb from mRNA
3148	835	NM_012813	SS	Blood group glycolipid biosynthesis - neolact series, Globoside metabolism, Sphingoglycolipid metabolism
3474	2236	NM_022512	BBB, CCC	Butanoate metabolism, Fatty acid metabolism, Valine, leucine and isoleucine degradation
4287	20426	Z12158	SS, WW	Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol, Valine, leucine and isoleucine biosynthesis
594	11997	AA892828	MM, DDD, TTT	Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism, Valine, leucine and isoleucine biosynthesis
594	11998	AA892828	MM, TTT	Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism, Valine, leucine and isoleucine biosynthesis
1028	12000	AA957319	MM, TTT	Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism, Valine, leucine and isoleucine biosynthesis
2187	5876	AI176117	UU	Butanoate metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism, Valine, leucine and isoleucine biosynthesis
3321	20600	NM_017268	G, H, FF, JJ, KK, FFF, General Alternate	Butanoate metabolism, SREBP and controls lipid synthesis, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation

TABLE 2				Attorney Docket 44921-5038-01WO
				Document No. 1935828.1
Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
			G, H, J, JJ, KK, FFF, KKK, OOO, General Alternate	Butanoate metabolism, SREBP and controls lipid synthesis, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
3321	20601	NM_017268	General Alternate	Butanoate metabolism, Synthesis and degradation of ketone bodies
3867	17739	NM_053995	General Alternate	Butanoate metabolism, Synthesis and degradation of ketone bodies
				Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
897	2813	AA945052	RRR	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
			FF, BBB, CCC, RRR, SSS	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
2079	2811	AI171090	SSS	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
				Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
2079	2812	AI171090	BBB, CCC	Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation
				C5-Branched dibasic acid metabolism, Citrate cycle (TCA cycle), Propanoate metabolism, Reductive carboxylate cycle (CO2 fixation)
727	22847	AA923982	BBB, CCC	C5-Branched dibasic acid metabolism, Citrate cycle (TCA cycle), Propanoate metabolism, Reductive carboxylate cycle (CO2 fixation)
				Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
1360	163	AI010480	X, Y	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
				Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
1360	164	AI010480	I	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
				Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
3476	162	NM_022516	VV	Carbon fixation, Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism, Reductive carboxylate cycle (CO2 fixation)
				Carbon fixation, Fructose and mannose metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Inositol metabolism
1870	18277	AI104399	T, HHH	Carbon fixation, Fructose and mannose metabolism, Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Inositol metabolism
			B, PPP, QQQ	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Pentose phosphate pathway
562	820	AA892395	QQQ	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Pentose phosphate pathway
				Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Pentose phosphate pathway
4183	818	X02291	HH, SS	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Glycolysis Pathway, Pentose phosphate pathway
				Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
3060	7062	NM_012495	VV	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
				Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
3060	7063	NM_012495	O, P, PP, QQ, UU, VV	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway

TABLE 2				
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Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3060	7064	NM_012495	II, VV, PPP, General Core Tox Markers	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
3079	16895	NM_012558	T, XX, YY, DDD	Carbon fixation, Fructose and mannose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway
3012	1312	M31788	I, J, LLL	Carbon fixation, Glycolysis / Gluconeogenesis, Glycolysis Pathway
3745	5175	NM_053297	O, P, NN, OO, VV, EEE, MMM	Carbon fixation, Glycolysis / Gluconeogenesis, Purine metabolism, Pyruvate metabolism
3494	20802	NM_022592	J, Y, FF	Carbon fixation, Pentose phosphate pathway
3494	20803	NM_022592	J, X, BB, CC, HH	Carbon fixation, Pentose phosphate pathway
3494	20804	NM_022592	X	Carbon fixation, Pentose phosphate pathway
1265	17353	AI008020	BBB, CCC	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3093	18746	NM_012600	BBB	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3093	18747	NM_012600	T, X, Y, BBB, LLL, RRR, SSS, UUU	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3093	18749	NM_012600	X, Y, BBB, LLL, RRR, SSS, UUU	Carbon fixation, Pyruvate metabolism, Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3048	291	M88347	JJ	Catabolic Pathways for Methionine, Isoleucine, Threonine and Valin, Glycine, serine and threonine metabolism, Methionine metabolism, Selenoamino acid metabolism
3289	15365	NM_017147	VV, FFF, General Alternate	CCR3 signaling in Eosinophils, Rac 1 cell motility signaling pathway, Rho cell motility signaling pathway
3825	15995	NM_053769	I, J, Q, R	CD40L Signaling Pathway, Phosphatidylinositol signaling system, TNFR2 Signaling Pathway
3825	15996	NM_053769	C, I, J, R, LLL	CD40L Signaling Pathway, Phosphatidylinositol signaling system, TNFR2 Signaling Pathway
3825	15997	NM_053769	I, J, R	CD40L Signaling Pathway, Phosphatidylinositol signaling system, TNFR2 Signaling Pathway
1480	2866	AI029058	Z, AA	Cell Cycle: G1/S Check Point, Cyclins and Cell Cycle Regulation, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S Transition, WNT Signaling Pathway, p53 Signaling Pathway

TABLE 2					Attorney Docket 44921-5033-01WO Document No. 1935823.1
Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
2849	25041	D14014	E, HH	Cell Cycle: G1/S Check Point , Cyclins and Cell Cycle Regulation, Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages, Influence of Ras and Rho proteins on G1 to S Transition, WNT Signaling Pathway, p53 Signaling Pathway	
4155	871	U66479	BB, CC	Cell Cycle: G1/S Check Point , TGF beta signaling pathway	
4096	1392	U10188	V	Cell Cycle: G2/M Checkpoint	
65	13683	AA799788	General Alternate	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction Pathway, E2F1 Destruction Pathway	
187	13684	AA818770	H	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction Pathway, E2F1 Destruction Pathway	
2973	13682	L38482	MM, FFF, TTT, General Alternate	Cell Cycle: G2/M Checkpoint, Cyclin E Destruction Pathway, E2F1 Destruction Pathway	
3605	17300	NM_031107	KKK	Cell Cycle: G2/M Checkpoint, Erk1/Erk2 Mapk Signaling pathway, Growth Hormone Signaling Pathway, Transcription factor CREB and its extracellular signals	
3809	15090	NM_053638	B, HHH	Citrate cycle (TCA cycle)	
3809	23305	NM_053638	KK, WW, HHH	Citrate cycle (TCA cycle)	
3635	17427	NM_031510	Q, R, GG, PPP, QQQ, General Alternate	Citrate cycle (TCA cycle), Glutathione metabolism, Reductive carboxylate cycle (CO2 fixation)	
1578	5697	AI045119	WW	Citrate cycle (TCA cycle), Glycine, serine and threonine metabolism, Glycolysis / Gluconeogenesis, Pyruvate metabolism	
3557	19992	NM_024398	L, Z, AA, WW, LLL, RRR, SSS, UUU	Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Reductive carboxylate cycle (CO2 fixation)	
3557	19993	NM_024398	Z, AA, GGG	Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Reductive carboxylate cycle (CO2 fixation)	
3557	19994	NM_024398	WW	Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Reductive carboxylate cycle (CO2 fixation)	
3340	17516	NM_017321	T, LL, YY, RRR, SSS	Citrate cycle (TCA cycle), Glyoxylate and dicarboxylate metabolism, Reductive carboxylate cycle (CO2 fixation)	
791	17514	AA925554	VV, General Alternate	Citrate cycle (TCA cycle), Oxidative phosphorylation	
3921	17512	NM_130428	S, General Alternate	Citrate cycle (TCA cycle), Oxidative phosphorylation	
3819	18174	NM_053752	BBB, CCC	Citrate cycle (TCA cycle), Propanoate metabolism	

TABLE 2				
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Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3819	18175	NM_053752	L, U, BBB, CCC, RRR	Citrate cycle (TCA cycle), Propanoate metabolism
3248	15621	NM_017005	MM, XX, YY, TTT	Citrate cycle (TCA cycle), Reductive carboxylate cycle (CO2 fixation)
3241	15610	NM_016987	Z, AA	Citrate cycle (TCA cycle), Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3241	15612	NM_016987	BB, CC, JJJ, OOO	Citrate cycle (TCA cycle), Shuttle for transfer of acetyl groups from mitochondria to the cytosol
3241	15613	NM_016987	E, J, WW, OOO, General Core Tox Markers, General Alternate	Citrate cycle (TCA cycle), Shuttle for transfer of acetyl groups from mitochondria to the cytosol
4130	15851	U42719	BBB, CCC	Classic Complement Pathway, Complement Pathway, Lectin Induced Complement Pathway
3513	24434	NM_022704	H, S, HH, FFF, GGG, General Core Tox Markers	Complement Pathway, Lectin Induced Complement Pathway
3739	25431	NM_052807	D, SS	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Erk1/Erk2 Mapk Signaling pathway, IGF-1 Signaling Pathway, Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation, Regulation of BAD phosphorylation, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, igf-1
2839	21051	D00698	D, G, H, GG, DDD	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Erythrocyte Differentiation Pathway, IGF-1 Signaling Pathway, Regulation of BAD phosphorylation, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, igf-1
2993	21052	M15481	H, S, GGG, PPP, QQQ, General Alternate	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Erythrocyte Differentiation Pathway, IGF-1 Signaling Pathway, Regulation of BAD phosphorylation, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, igf-1
2993	21053	M15481	G, H, PPP, QQQ	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Erythrocyte Differentiation Pathway, IGF-1 Signaling Pathway, Regulation of BAD phosphorylation, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, igf-1

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
4190	21054	X06107	G, H, M, S, GGG	Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK), Erythrocyte Differentiation Pathway, IGF-1 Signaling Pathway, Regulation of BAD phosphorylation, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, igf-1
3444	24321	NM_022177	G, J, S, WW, OOO, PPP, QQQ, General Core Tox Markers	CXCR4 Signaling Pathway, Pertussis toxin-insensitive CCR5 Signaling in Macrophage
3741	12577	NM_052981	A, D, V, BB, III, JJJ	Cyclins and Cell Cycle Regulation
3856	24778	NM_053962	C, MM, FFF, TTT	Cysteine metabolism, Glycine, serine and threonine metabolism
3856	24779	NM_053962	C, MM, TTT	Cysteine metabolism, Glycine, serine and threonine metabolism
3856	25321	NM_053962	MM, FFF, TTT	Cysteine metabolism, Glycine, serine and threonine metabolism
3255	17807	NM_017025	C, U, FF, HH, YY	Cysteine metabolism, Glycolysis / Gluconeogenesis, Hypoxia-Inducible Factor in the Cardiovascular System, Propanoate metabolism, Pyruvate metabolism
3269	18452	NM_017074	L, OO, UU	Cysteine metabolism, Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism
3269	18453	NM_017074	L, NN, OO, III, JJJ, OOO	Cysteine metabolism, Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism
3740	15028	NM_052809	A, B, T, LLL	Cysteine metabolism, Taurine and hypotaurine metabolism
3740	25024	NM_052809	A, YY	Cysteine metabolism, Taurine and hypotaurine metabolism
4171	1520	U77777	V	Cytokine Network, IL 18 Signaling Pathway, Ras-Independent pathway in NK cell-mediated cytotoxicity, Th1/Th2 Differentiation
3638	12996	NM_031528	C, RR	Degradation of the RAR and RXR by the proteasome, Nuclear receptors coordinate the activities of chromatin remodeling complexes and coactivators to facilitate initiation of transcription carcinoma cells, Transcription Regulation by Methyltransferase of CARM1
3286	24107	NM_017141	PP, QQ	DNA polymerase, Purine metabolism, Pyrimidine metabolism
3155	20885	NM_012842	II	EGF Signaling Pathway, egf

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935828.1
Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
				EGF Signaling Pathway, IFN alpha signaling pathway, IFN gamma signaling pathway , IL 2 signaling pathway, IL 4 signaling pathway, IL-2 Receptor B Protein Interaction Pathway, PDGF Signaling Pathway, egf, ifn_alpha, ifn_gamma, il2, il4, il6, interact6-1, pdgf
2834	25233	AJ000556	T	
3462	1914	NM_022380	M, Z, AA	egf, epo, il2, il3, tpo
1586	6697	AI045340	MM, TTT	epo, il2, il3, il6, insulin, interact6-1, ngf, pdgf, tpo
				Erk1/Erk2 Mapk Signaling pathway, IL-2 Receptor B Protein Interaction Pathway, Inhibition of Cellular Proliferation by Gleevec, Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells, Overview of telomerase protein component gene hTert Transcriptional Regulation , WNT Signaling Pathway, p38 MAPK Signaling Pathway
3094	2629	NM_012603	W	
				Erk1/Erk2 Mapk Signaling pathway, Nerve growth factor pathway (NGF), Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway, ngf
3095	1299	NM_012610	V	
				Erk1/Erk2 Mapk Signaling pathway, PDGF Signaling Pathway, Rac 1 cell motility signaling pathway, Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration, pdgf
2578	19287	AI232379	LLL, UUU	
2703	21414	AI235842	W, NN	Erythropoietin mediated neuroprotection through NF-kB
3262	682	NM_017051	EEE, MMM	Erythropoietin mediated neuroprotection through NF-kB
				Erythropoietin mediated neuroprotection through NF-kB, Hypoxia and p53 in the Cardiovascular system, Hypoxia-Inducible Factor in the Cardiovascular System
4284	1146	Y09507	WW	
1309	24249	AI009273	I, J, BB, CC	Fatty acid biosynthesis (path 1)
3343	24247	NM_017332	V	Fatty acid biosynthesis (path 1)
			B, I, J, U, FF, LL, XX, YY	
2840	18686	D00729		Fatty acid metabolism
2858	3743	D30666	BBB	Fatty acid metabolism
3150	6780	NM_012819	U, RRR	Fatty acid metabolism
3150	6781	NM_012819	HH	Fatty acid metabolism
			A, B, E, I, J, U, FF, LL, XX, YY	
3335	18687	NM_017306		Fatty acid metabolism
3803	15925	NM_053607	B	Fatty acid metabolism
			I, J, General Alternate	
3803	15926	NM_053607		Fatty acid metabolism

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Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Modal Code	Pathways
628	20985	AA893242	H, BBB, CCC, RRR, General Alternate	Fatty acid metabolism
628	20986	AA893242	A, B, BBB, CCC, FFF, General Alternate	Fatty acid metabolism
1566	20983	AI044900	A, FF, JJ, KK, LL, FFF, HHH, SSS, General Core Tox Markers, General Alternate	Fatty acid metabolism
2881	20984	D90109	U, FF, FFF, HHH, General Alternate	Fatty acid metabolism
3806	13005	NM_053623	LL, BBB, CCC, RRR	Fatty acid metabolism
3345	16148	NM_017340	U, FF, LL, VV	Fatty acid metabolism
3345	16150	NM_017340	J, U, DD, EE, FF, II, LL, RRR	Fatty acid metabolism
3234	20854	NM_013200	Z, AA	Fatty acid metabolism, Glycerolipid metabolism
3234	20855	NM_013200	BBB	Fatty acid metabolism, Glycerolipid metabolism
2932	1977	J05470	U, BBB, CCC, RRR, SSS	Fatty acid metabolism, Glycerolipid metabolism, Mitochondrial Carnitine Palmitoyltransferase (CPT) System
3646	15411	NM_031559	J	Fatty acid metabolism, Glycerolipid metabolism, Mitochondrial Carnitine Palmitoyltransferase (CPT) System, Reversal of Insulin Resistance by Leptin
3240	21078	NM_016986	T, U, X, TT, XX, YY, III, JJJ, RRR	Fatty acid metabolism, Propanoate metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism
738	20711	AA924267	U, FF, LL, XX, BBB, CCC, RRR, SSS	Fatty acid metabolism, Tryptophan metabolism
1151	20712	AA997806	FFF	Fatty acid metabolism, Tryptophan metabolism
2992	20714	M14972	I, J, U, FF, LL, XX, YY	Fatty acid metabolism, Tryptophan metabolism
3025	20713	M57718	U, EE, FF, LL, RRR	Fatty acid metabolism, Tryptophan metabolism

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3073	488	NM_012540	A, C, L, GG, HH, DDD	Fatty acid metabolism, Tryptophan metabolism	
3073	489	NM_012540	C, L, GG, HH	Fatty acid metabolism, Tryptophan metabolism	
3073	20705	NM_012540	C, K, L, U, GG, HH, II, DDD, RRR	Fatty acid metabolism, Tryptophan metabolism	
3074	20703	NM_012541	C, K, L, M, U, Y, GG, HH, II, RRR, SSS	Fatty acid metabolism, Tryptophan metabolism	
3074	20704	NM_012541	C, K, L, T, GG, HH, DDD	Fatty acid metabolism, Tryptophan metabolism	
3181	191	NM_012940	GG	Fatty acid metabolism, Tryptophan metabolism	
3182	20928	NM_012941	T	Fatty acid metabolism, Tryptophan metabolism	
3182	20931	NM_012941	G, H, I, J, FF, General Alternate	Fatty acid metabolism, Tryptophan metabolism	
4192	20715	X07259	J, U, DD, FF, LL, XX, QQQ, RRR, SSS	Fatty acid metabolism, Tryptophan metabolism	
3128	18730	NM_012730	N, TT	Fatty acid metabolism, Tryptophan metabolism	
3294	2967	NM_017158	HH	Fatty acid metabolism, Tryptophan metabolism	
3294	2968	NM_017158	MM, TTT	Fatty acid metabolism, Tryptophan metabolism	
3294	2969	NM_017158	N, TT	Fatty acid metabolism, Tryptophan metabolism	
3294	2970	NM_017158	N, HH, SS	Fatty acid metabolism, Tryptophan metabolism	
3411	20716	NM_019623	N, EEE, HHH, MMM, PPP, QQQ, General Alternate	Fatty acid metabolism, Tryptophan metabolism	
3650	15024	NM_031572	GG	Fatty acid metabolism, Tryptophan metabolism	
3393	1099	NM_019303	W, CC, General Core Tox Markers	Fatty acid metabolism, Tryptophan metabolism	
3643	4010	NM_031543	EE, MM, TTT	Fatty acid metabolism, Tryptophan metabolism	
3643	4011	NM_031543	K, O, P, FF, II, NN, OO, QQ, EEE, MMM	Fatty acid metabolism, Tryptophan metabolism	
3643	4012	NM_031543	T, EE, FF, MM, EEE, MMM, TTT	Fatty acid metabolism, Tryptophan metabolism	
168	12160	AA818412	O, P, X, TT, DDD	Fatty acid metabolism, Tryptophan metabolism	

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
2935	12156	K00996	K, X, TT, DDD, LLL, RRR, UUU	Fatty acid metabolism, Tryptophan metabolism	
2936	12157	K01721	K, L, X, FF, TT, DDD, LLL, UUU	Fatty acid metabolism, Tryptophan metabolism	
3013	16305	M33312	E, M, GG	Fatty acid metabolism, Tryptophan metabolism	
3116	16306	NM_012692	JJ, KK, FFF, HHH, PPP, QQQ, General Alternate	Fatty acid metabolism, Tryptophan metabolism	
3117	24707	NM_012693	JJ, VV, XX, YY, HHH, PPP, QQQ, General Alternate	Fatty acid metabolism, Tryptophan metabolism	
3364	1173	NM_019184	T, V, CC, OO, GGG, PPP, QQQ	Fatty acid metabolism, Tryptophan metabolism	
3364	1174	NM_019184	DD, TT	Fatty acid metabolism, Tryptophan metabolism	
3599	1175	NM_031093	F, T, V, BB, TT, DDD, FFF, PPP, QQQ	Fatty acid metabolism, Tryptophan metabolism	
4034	683	NM_147206	M	Fatty acid metabolism, Tryptophan metabolism	
3793	19252	NM_053576	G, H, L, N, HH	Flavonoids, stilbene and lignin biosynthesis, Methane metabolism, Phenylalanine metabolism	
3793	19253	NM_053576	G, H	Flavonoids, stilbene and lignin biosynthesis, Methane metabolism, Phenylalanine metabolism	
3793	19254	NM_053576	G, H, L	Flavonoids, stilbene and lignin biosynthesis, Methane metabolism, Phenylalanine metabolism	
3549	15350	NM_024356	L	Folate biosynthesis	
4125	368	U38379	XX, YY	Folate biosynthesis	
3466	13479	NM_022390	III, JJJ, KKK	Folate biosynthesis	
3466	13480	NM_022390	E, XX, YY, III, JJJ, General Alternate	Folate biosynthesis	
3208	14997	NM_013059	W, DD, MM, III, JJJ, KKK, NNN, TTT	Folate biosynthesis, Glycerolipid metabolism	
2934	1549	J05519	MM, TTT	Folate biosynthesis, Glyoxylate and dicarboxylate metabolism, One carbon pool by folate	
3261	20876	NM_017050	N, UUU	Free Radical Induced Apoptosis	
3261	20877	NM_017050	M	Free Radical Induced Apoptosis	
2974	6405	L38615	G, H, JJ, KK, GGG	Free Radical Induced Apoptosis, Glutamate metabolism, Glutathione metabolism	

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
2974	6406	L38615	GGG	Free Radical Induced Apoptosis, Glutamate metabolism, Glutathione metabolism	
3564	1853	NM_030826	MM, TT, TTT	Free Radical Induced Apoptosis, Glutathione metabolism	
3959	17109	NM_134326	M, S, DD, EE, SS, TT	Free Radical Induced Apoptosis, Glutathione metabolism	
3959	17112	NM_134326	S, HH	Free Radical Induced Apoptosis, Glutathione metabolism	
3293	21975	NM_017154	E, FF, LLL, RRR, SSS, UUU, General Alternate	Free Radical Induced Apoptosis, Purine metabolism	
1507	1876	AI030175	C, K, T, W, DD, EE, KKK, General Alternate	Fructose and mannose metabolism	
3710	16726	NM_031855	A, B, BB, CC, HH, OO, EEE, GGG, III, JJJ, MMM, General Core Tox Markers	Fructose and mannose metabolism	
4260	1877	X74593	W, DD, EE, SS, WW, XX, YY, General Core Tox Markers	Fructose and mannose metabolism	
2928	174	J04197	JJ, KK, SS	Fructose and mannose metabolism	
3099	172	NM_012621	JJ, KK, WW, YY	Fructose and mannose metabolism	
4204	173	X15580	L, Z, AA, JJ, KK, WW	Fructose and mannose metabolism	
2636	13023	AI233740	VV	Fructose and mannose metabolism, Galactose metabolism, Glycerolipid metabolism, Pentose and glucuronate interconversions, Pyruvate metabolism	
4113	1340	U25651	SS	Fructose and mannose metabolism, Galactose metabolism, Glycolysis / Gluconeogenesis, Pentose phosphate pathway	

TABLE 2				Attorney Docket 44921-5038-01WO
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3433	19712	NM_021745	A, B, General Core Tox Markers, General Alternate	FXR and LXR Regulation of Cholesterol Metabolism
4099	1639	U11685	W, DD, EE, KKK, NNN, General Alternate	FXR and LXR Regulation of Cholesterol Metabolism
1083	1322	AA964628	W	Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism
3218	1321	NM_013098	L	Galactose metabolism, Glycolysis / Gluconeogenesis, Starch and sucrose metabolism
2066	17027	AI170679	BBB, CCC, RRR	Galactose metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism
220	10157	AA819527	XX, YY	Generation of amyloid b-peptide by PS1
1018	10155	AA956735	V	Generation of amyloid b-peptide by PS1
3363	20256	NM_019163	JJ, KK	Generation of amyloid b-peptide by PS1, HIV-I Nef: negative effector of Fas and TNF, Presenilin action in Notch and Wnt signaling, Proteolysis and Signaling Pathway of Notch , g-Secretase mediated ErbB4 Signaling Pathway
2931	1247	J05181	Q, R, S	Glutamate metabolism, Glutathione metabolism
3334	14003	NM_017305	Q, R, S, X, Y, NN, OO, General Alternate	Glutamate metabolism, Glutathione metabolism
3334	14004	NM_017305	Q, R, T, KKK	Glutamate metabolism, Glutathione metabolism
3268	11150	NM_017073	II, RR, TT, DDD	Glutamate metabolism, Nitrogen metabolism
3268	11151	NM_017073	N, TT	Glutamate metabolism, Nitrogen metabolism
3268	11152	NM_017073	II, LL, TT, UU, DDD, LLL, UUU	Glutamate metabolism, Nitrogen metabolism
3268	11153	NM_017073	G, K, II, TT, DDD, GGG, LLL	Glutamate metabolism, Nitrogen metabolism
1196	3082	AA999172	C, UU, General Alternate	Glutamate metabolism, Purine metabolism
1968	961	AI138143	II	Glutathione metabolism
3143	960	NM_012796	V, DD, EE, UU, III, JJJ, General Alternate	Glutathione metabolism

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3744	1524	NM_053293	V, General Alternate	Glutathione metabolism
2667	16781	AI234527	M, GG, TT	Glutathione metabolism
			A, B, GGG, HHH, General Alternate	
3620	20862	NM_031154	Alternate	Glutathione metabolism
3848	15934	NM_053904	W	Glutathione metabolism
4242	16780	X62660	X, GG, II, XX, YY	Glutathione metabolism
			F, K, M, N, GG, HH, TT, DDD, EEE, LLL, MMM, UUU	
3250	18989	NM_017013	MMM, UUU	Glutathione metabolism
3296	17686	NM_017165	I, J, LL	Glutathione metabolism
			G, K, TT, SSS	
3634	18990	NM_031509	SSS	Glutathione metabolism
1423	20817	AI012589	G	Glutathione metabolism
4184	20818	X02904	G	Glutathione metabolism
			F, PP, QQ, TT, DDD	
2905	21011	H32189	TT, DDD	Glutathione metabolism
			GG, NN, OO, EEE, LLL, MMM	
2922	21012	J02592	LLL, MMM	Glutathione metabolism
			N, BB, CC, NN	
2926	21014	J03914	NN	Glutathione metabolism
			F, N, DD, EE, TT, DDD	
3251	21013	NM_017014	DDD	Glutathione metabolism
			F, K, N, TT, DDD	
3251	21015	NM_017014	DDD	Glutathione metabolism
3250	18988	NM_017013	V, NN, OO	Glutathione metabolism
			M, S, DD, EE, NNN	
3962	15017	NM_134349	EE, NNN	Glutathione metabolism
			K, V, NN, TT, DDD, EEE, MMM	
3634	634	NM_031509	EEE, MMM	Glutathione metabolism
			M, NN, TT, DDD, EEE, MMM	
3634	635	NM_031509	MMM	Glutathione metabolism
			N, V, NN, TT, DDD, EEE, MMM	
3634	25525	NM_031509	EEE, MMM	Glutathione metabolism
3249	1399	NM_017006	G, FF	Glutathione metabolism, Pentose phosphate pathway
				Glutathione metabolism, Styrene degradation, Tyrosine metabolism
1996	17812	AI169075	PPP, QQQ	
2843	1306	D10262	GG	Glycerolipid metabolism

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
2995	2505	M16235	B, F, G, NN, OO, GGG, LLL, General Core Tox Markers	Glycerolipid metabolism
3554	20380	NM_024381	HHH, General Core Tox Markers, General Alternate	Glycerolipid metabolism
1166	14149	AA998172	GG	Glycerolipid metabolism
3763	6774	NM_053410	CC	Glycerolipid metabolism
1205	3512	AB006607	BBB, CCC, RRR	Glycerolipid metabolism
1205	3513	AB006607	BBB, RRR, SSS	Glycerolipid metabolism
3764	14621	NM_053437	L, BBB, CCC	Glycerolipid metabolism
3580	23109	NM_031000	G, H	Glycerolipid metabolism, Glycolysis / Gluconeogenesis, Pentose and glucuronate interconversions
3370	20435	NM_019202	UU	Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and leukotriene metabolism
4207	1893	X51529	NN, EEE, MMM	Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and leukotriene metabolism
3091	18385	NM_012598	O, P, EEE, MMM	Glycerolipid metabolism, Visceral Fat Deposits and the Metabolic Syndrome
624	1552	AA893219	O, P, X, Y, WW	Glycine, serine and threonine metabolism
1384	21040	AI011734	K, L	Glycine, serine and threonine metabolism
3273	1550	NM_017084	F, N, O, P, X, Y, EEE, GGG, MMM	Glycine, serine and threonine metabolism
3273	1551	NM_017084	F, O, P, X, GGG, LLL, UUU	Glycine, serine and threonine metabolism
3561	21038	NM_024484	TT	Glycine, serine and threonine metabolism
3561	21039	NM_024484	K, QQ, TT	Glycine, serine and threonine metabolism
3194	24718	NM_013003	EE, JJ, KK	Glycine, serine and threonine metabolism
3658	21586	NM_031620	G	Glycine, serine and threonine metabolism
3232	16448	NM_013197	M, T	Glycine, serine and threonine metabolism
1233	1995	AF038870	C, NN, OO, DDD	Glycine, serine and threonine metabolism, Methionine metabolism

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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
2018	4091	AI169417	X, Y, FFF, GGG, General Core Tox Markers, General Alternate	Glycolysis / Gluconeogenesis, Glycolysis Pathway
2437	4092	AI228723	K, DDD	Glycolysis / Gluconeogenesis, Glycolysis Pathway
2552	4093	AI232001	S, GGG, LLL	Glycolysis / Gluconeogenesis, Glycolysis Pathway
3743	4090	NM_053290	JJ, KK, GGG, HHH	Glycolysis / Gluconeogenesis, Glycolysis Pathway
3743	25499	NM_053290	G, H, X, Y	Glycolysis / Gluconeogenesis, Glycolysis Pathway
3076	19407	NM_012554	G, H, VV	Glycolysis / Gluconeogenesis, Glycolysis Pathway, Phenylalanine, tyrosine and tryptophan biosynthesis
3714	24644	NM_031972	GG	Glycolysis / Gluconeogenesis, Histidine metabolism, Phenylalanine metabolism, Tyrosine metabolism
1497	1114	AI029917	E, DD, KKK, NNN	Glycolysis / Gluconeogenesis, Phenylalanine, tyrosine and tryptophan biosynthesis
3252	17815	NM_017015	NNN	Glycosaminoglycan degradation, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism
3412	574	NM_019905	O, VV, EEE, MMM	Glyoxylate and dicarboxylate metabolism
2558	573	AI232087	A, B, M, OOO, UUU, General Core Tox Markers	Glyoxylate and dicarboxylate metabolism
592	22537	AA892799	S	Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism
592	22538	AA892799	M	Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism
2557	22542	AI232066	QQ, XX, YY	Glyoxylate and dicarboxylate metabolism, Pyruvate metabolism
3266	24719	NM_017071	RR	Growth Hormone Signaling Pathway, Insulin Signaling Pathway, insulin
3110	24427	NM_012669	UU	Growth Hormone Signaling Pathway, Presenilin action in Notch and Wnt signaling, WNT Signaling Pathway
3027	70	M58308	K, GG, OO, General Alternate	Histidine metabolism, Nitrogen metabolism
3791	9267	NM_053567	OO, PP, TT	Histidine metabolism, One carbon pool by folate
3088	15097	NM_012588	Z	Hypoxia and p53 in the Cardiovascular system
3088	15098	NM_012588	GG, II	Hypoxia and p53 in the Cardiovascular system
3247	1698	NM_017000	K, S, GG, HH, GGG	Hypoxia and p53 in the Cardiovascular system, Sterol biosynthesis
2688	2746	AI235291	Z, AA	Hypoxia and p53 in the Cardiovascular system, WNT Signaling Pathway

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Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3804	20243	NM_053615	VV	Hypoxia and p53 in the Cardiovascular system, WNT Signaling Pathway
4101	1424	U14746	W	Hypoxia-Inducible Factor in the Cardiovascular System
3937	656	NM_133380	Y	IL 4 signaling pathway, Selective expression of chemokine receptors during T-cell polarization, Th1/Th2 Differentiation, il4
3636	24710	NM_031512	W	IL 5 Signaling Pathway, Msp/Ron Receptor Signaling Pathway, Signal transduction through IL1R, interact6-1
3253	6598	NM_017020	DD, EE, SS, WW, UUU	IL 6 signaling pathway, il6, interact6-1
3534	21238	NM_024125	I, J, MM, TTT	IL 6 signaling pathway, il6, interact6-1
3534	21239	NM_024125	MM, TTT, General Alternate	IL 6 signaling pathway, il6, interact6-1
3278	4391	NM_017101	II	IL-2 Receptor B Protein Interaction Pathway
3278	4392	NM_017101	XX, YY	IL-2 Receptor B Protein Interaction Pathway
3309	20529	NM_017208	A, D, E, V, W, BB, NN, EEE, III, JJJ, MMM	Inactivation of Gsk3 by AKT causes accumulation of b catenin in Alveolar Macrophages
3422	21336	NM_021266	UUU	Inactivation of Gsk3 by AKT causes accumulation of b catenin in Alveolar Macrophages, Presenilin action in Notch and Wnt signaling, WNT Signaling Pathway
1790	19373	AI102044	LL, NNN	Inactivation of Gsk3 by AKT causes accumulation of b catenin in Alveolar Macrophages, Presenilin action in Notch and Wnt signaling, WNT Signaling Pathway
3443	243	NM_021989	EE	Inhibition of Matrix Metalloproteinases
1814	17234	AI102741	RR	Inhibition of Matrix Metalloproteinases, p53 Signaling Pathway
3592	17269	NM_031057	General Alternate	Inositol metabolism, Propanoate metabolism, Valine, leucine and isoleucine degradation
4026	9096	NM_145771	RRR	Inositol phosphate metabolism
3852	4588	NM_053923	II, General Alternate	Inositol phosphate metabolism
3523	19669	NM_022944	ZZ	Inositol phosphate metabolism, Phosphatidylinositol signaling system, Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway
409	23336	AA859981	U, GG, HH, BBB, CCC, RRR	Inositol phosphate metabolism, Phosphatidylinositol signaling system, Streptomycin biosynthesis
3723	18640	NM_032057	C, I, J, TT, OOO	Inositol phosphate metabolism, Phosphatidylinositol signaling system, Streptomycin biosynthesis
794	21821	AA925664	LL	Integrin Signaling Pathway
3360	20863	NM_019152	D	Integrin Signaling Pathway
3067	15740	NM_012520	LL	Methane metabolism, Tryptophan metabolism
3067	15741	NM_012520	EEE, MMM	Methane metabolism, Tryptophan metabolism

TABLE 2					Attorney Docket 44921-5038-01WO Document No. 1935828.1
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
203	576	AA819118	C, YY	Methionine metabolism, Selenoamino acid metabolism	
3307	20779	NM_017201	I, J, HH	Methionine metabolism, Selenoamino acid metabolism	
4205	575	X15734	F, L, T, RR, SS, WW, SSS, UUU	Methionine metabolism, Selenoamino acid metabolism	
3639	20448	NM_031530	W, II, EEE, MMM	Msp/Ron Receptor Signaling Pathway, Pertussis toxin insensitive CCR5 Signaling in Macrophage	
3639	20449	NM_031530	W, II, QQ	Msp/Ron Receptor Signaling Pathway, Pertussis toxin insensitive CCR5 Signaling in Macrophage	
2193	6782	AI176170	FFF	mTOR Signaling Pathway	
3220	15295	NM_013102	P, HH, JJ	mTOR Signaling Pathway	
3220	15296	NM_013102	O, P, HH	mTOR Signaling Pathway	
3081	17237	NM_012562	XX, YY	N-Glycan degradation	
1161	16625	AA998062	A, B, N	N-Glycans biosynthesis	
3670	21575	NM_031698	V, FF	N-Glycans biosynthesis	
3211	19335	NM_013067	FF	N-Glycans biosynthesis	
3572	15186	NM_030861	DD, EE	N-Glycans biosynthesis	
3572	15187	NM_030861	FF, TT, NNN	N-Glycans biosynthesis	
3572	15188	NM_030861	DD, EE, GG, OOO	N-Glycans biosynthesis	
2857	2005	D29646	NN, OO, VV	Nicotinate and nicotinamide metabolism	
204	6018	AA819140	BB, CC, PPP, QQQ	Nitrogen metabolism	
3389	6017	NM_019292	A, B, S, X, Y, GGG, HHH, General Core Tox Markers	Nitrogen metabolism	
3388	15057	NM_019291	JJ	Nitrogen metabolism	
3390	24883	NM_019293	OO, General Core Tox Markers	Nitrogen metabolism	
3625	18597	NM_031325	E, S, WW, DDD	Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism	
3490	12606	NM_022547	O, P, NN, OO, VV, EEE, III, JJJ, MMM, General Alternate	One carbon pool by folate	
2880	1414	D89514	VV	One carbon pool by folate, Purine metabolism	
438	4339	AA875121	UU	Overview of telomerase RNA component gene hTerc Transcriptional Regulation	

TABLE 2				Attorney Docket 44921-5038-01WO
				Document No. 1935828.1
Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3204	20535	NM_013049	I, J	OX40 Signaling Pathway
1266	22056	AI008066	F	Oxidative phosphorylation
3308	14696	NM_017202	LL	Oxidative phosphorylation
3771	21866	NM_053472	V, RR, UU	Oxidative phosphorylation
3795	21424	NM_053586	XX, YY	Oxidative phosphorylation
4029	1448	NM_145783	U	Oxidative phosphorylation
3147	20605	NM_012812	BB, CC	Oxidative phosphorylation
1872	23574	AI104520	LL	Oxidative phosphorylation
4257	23576	X72757	HH, LL	Oxidative phosphorylation
20	16901	AA799479	FF	Oxidative phosphorylation, Ubiquinone biosynthesis
2090	4428	AI171362	CCC	Oxidative phosphorylation, Ubiquinone biosynthesis
2471	3099	AI229680	RRR	Oxidative phosphorylation, Ubiquinone biosynthesis
3375	20938	NM_019223	V, EE	Oxidative phosphorylation, Ubiquinone biosynthesis
			KK, GGG, HHH, General Alternate	
22	15654	AA799501		Oxidative phosphorylation, Ubiquinone biosynthesis
			N, PPP, QQQ	
2479	17672	AI230074		Oxidative phosphorylation, Ubiquinone biosynthesis
3187	20943	NM_012985	MM, TTT	Oxidative phosphorylation, Ubiquinone biosynthesis
4198	15653	X14210	CC, II	Oxidative phosphorylation, Ubiquinone biosynthesis
1676	4437	AI070308	Q, R	Oxidative phosphorylation, Ubiquinone biosynthesis
			Q, R, EEE, MMM	
10	1600	AA686470		p38 MAPK Signaling Pathway
3463	11454	NM_022381	VV	p53 Signaling Pathway
			VV, General Alternate	
3463	11455	NM_022381		p53 Signaling Pathway
			B, L, III, JJJ, OOO, QQQ, General Core Tox Markers	
2871	811	D63704		Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism
			OOO, PPP, QQQ, General Core Tox Markers	
2871	812	D63704		Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism
3056	1508	M97662	M	Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism
3692	16039	NM_031811	J, FF	Pentose phosphate pathway
416	17742	AA866302	HH, WW	Phenylalanine metabolism, Tyrosine metabolism
			L, S, EE, TT, WW	
3314	17740	NM_017233		Phenylalanine metabolism, Tyrosine metabolism
			WW, LLL, RRR, SSS, UUU	
3098	6055	NM_012619		Phenylalanine, tyrosine and tryptophan biosynthesis
2269	14977	AI177386	JJ, KK	Phosphatidylinositol signaling system

TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3197	11904	NM_013016	E, BB, PP, EEE, III, MMM	Phosphatidylinositol signaling system	
3356	14971	NM_019140	JJ, KK	Phosphatidylinositol signaling system	
3356	14973	NM_019140	JJ, KK, General Alternate	Phosphatidylinositol signaling system	
3356	14974	NM_019140	T	Phosphatidylinositol signaling system	
3866	16809	NM_053990	B, W, BB, CC, DD, EE, JJ, NN, OO, PP, HHH, III, KKK, NNN, General Core Tox Markers, General Alternate	Phosphatidylinositol signaling system	
1928	1841	AI113289	O, P, Q, R, V, DD, NN, OO, PP, QQ, III, JJJ, General Alternate	Phosphatidylinositol signaling system	
3016	1843	M33962	DD, ZZ, AAA, III, JJJ, KKK	Phosphatidylinositol signaling system	
3016	1844	M33962	E, DD, ZZ, AAA, III, JJJ	Phosphatidylinositol signaling system	
3029	1973	M60103	I, J, Y, FF, KKK, LLL, OOO, RRR, SSS, General Core Tox Markers, General Alternate	Phosphatidylinositol signaling system	
2271	18095	AI177482	S	Phosphatidylinositol signaling system	
3030	64	M60655	C, I, L, W, XX, YY, LLL, OOO, General Alternate	Phospholipase C d1 in phospholipid associated cell signaling	
3075	23868	NM_012551	A, BB, CC, NNN	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway	

TABLE 2				
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3075	23869	NM_012551	A, BB, CC, NNN	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
3075	23871	NM_012551	W	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
3075	23872	NM_012551	A, OO, NNN	Phosphorylation of MEK1 by cdk5/p35 down regulates the MAP kinase pathway
2353	16081	AI179610	B, E, Q, PP, EEE, MMM	Porphyrin and chlorophyll metabolism
3085	16080	NM_012580	E, OO, PP, EEE, MMM	Porphyrin and chlorophyll metabolism
3171	18564	NM_012899	L, CC, DD, EE, III, JJJ, KKK, OOO, General Core Tox Markers, General Alternate	Porphyrin and chlorophyll metabolism
393	14138	AA859700	E, General Alternate	Porphyrin and chlorophyll metabolism
393	14139	AA859700	E, III, JJJ, NNN, General Alternate	Porphyrin and chlorophyll metabolism
3541	1161	NM_024153	D	Porphyrin and chlorophyll metabolism
1359	16521	AI010470	FF	Porphyrin and chlorophyll metabolism
3072	16519	NM_012532	BB, CC, NN, SSS, UUU	Porphyrin and chlorophyll metabolism
3072	16520	NM_012532	BB, CC	Porphyrin and chlorophyll metabolism
2872	1125	D82071	OOO	Prostaglandin and leukotriene metabolism
338	13523	AA858552	NN, OO	Prostaglandin and leukotriene metabolism
4084	13520	S87522	KK, PP, QQ	Prostaglandin and leukotriene metabolism
260	18673	AA849028	DDD	Proteasome
2021	3256	AI169479	H, K, LLL, SSS, UUU	Proteasome
3123	4002	NM_012708	KKK	Proteasome
3123	4003	NM_012708	I, J, KKK	Proteasome
3323	15141	NM_017278	A, D, GGG, PPP, QQQ	Proteasome
3324	5747	NM_017279	D, General Alternate	Proteasome
3324	5748	NM_017279	X, Y	Proteasome
3324	5749	NM_017279	D, LL, YY, GGG, PPP, QQQ	Proteasome
3325	3987	NM_017280	GGG, HHH	Proteasome

TABLE 2				Attorney Docket 44921-5038-01WO
				Document No. 1935323.1
Seq ID No.	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3326	1447	NM_017281	A, BBB, CCC, GGG, PPP, QQQ	Proteasome
3327	3253	NM_017282	ZZ, AAA	Proteasome
3327	3254	NM_017282	TT, GGG, PPP, QQQ	Proteasome
3329	8956	NM_017284	PPP, QQQ	Proteasome
3329	8957	NM_017284	PPP, QQQ	Proteasome
3660	20940	NM_031629	G, H, X, Y, SSS	Proteasome
3660	20942	NM_031629	UUU	Proteasome
3875	22849	NM_057099	G, H	Proteasome
3875	25253	NM_057099	B, G, H, PPP, QQQ	Proteasome
3906	25252	NM_080767	O, P, HH	Proteasome
3797	20842	NM_053590	X, Y, RR, UUU	Proteasome
2860	9029	D30804	A, B, RR, WW, SSS	Proteasome
2867	9135	D45247	N, RRR	Proteasome
3328	15535	NM_017283	S, GGG, PPP, QQQ	Proteasome
3328	15538	NM_017283	NNN	Proteasome
3330	12523	NM_017285	G, H, PPP, QQQ	Proteasome
3330	12524	NM_017285	G, H, S, X, Y, GGG, PPP, QQQ	Proteasome
3781	18401	NM_053532	K, X, Y, UUU	Proteasome
2860	25281	D30804	G, H, K, X, Y, LLL, SSS, UUU	Proteasome
2867	9134	D45247	G, H, K, BB, CC, GGG	Proteasome
57	14250	AA799729	W	Purine metabolism
2629	16709	AI233602	PP, QQ	Purine metabolism
3169	16708	NM_012895	UU, WW	Purine metabolism
3547	10980	NM_024349	Z, AA	Purine metabolism
3574	17050	NM_030986	UU	Purine metabolism
4288	442	Z22867	Z, AA	Purine metabolism
3024	1246	M57507	A, B, M, FFF, HHH, KKK, NNN, OOO, General Core Tox Markers	Purine metabolism
3687	14184	NM_031776	V, UU	Purine metabolism

TABLE 2					Attorney Docket 44921-5038-01WO Document No. 1935823.1
Seq ID No.	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3687	14185	NM_031776	V, NN	Purine metabolism	
3033	13547	M63983	EE	Purine metabolism	
3039	997	M80550	RR	Purine metabolism	
2251	14384	AI177096	JJ, KK, NN, OO, EEE, HHH, MMM	Purine metabolism	
2927	1869	J03959	M, GG, WW	Purine metabolism	
2927	1870	J03959	M	Purine metabolism	
3824	1868	NM_053768	M	Purine metabolism	
3219	24	NM_013101	Z, AA, RRR, SSS	Purine metabolism	
3701	11170	NM_031833	O, P, General Alternate	Purine metabolism, Pyrimidine metabolism	
3854	15857	NM_053948	ZZ, AAA	Purine metabolism, Pyrimidine metabolism, RNA polymerase	
2616	5778	AI233246	G, H	Purine metabolism, Pyrimidine metabolism, RNA polymerase	
3630	15359	NM_031335	ZZ, AAA	Purine metabolism, Pyrimidine metabolism, RNA polymerase	
595	17332	AA892829	K, ZZ, AAA	Purine metabolism, Selenoamino acid metabolism, Sulfur metabolism	
3657	24234	NM_031614	G, H, Q, II	Pyrimidine metabolism	
3657	24235	NM_031614	Q, HH, ZZ, AAA, HHH	Pyrimidine metabolism	
838	24262	AA943116	X, Y, UUU	Pyrimidine metabolism	
3239	20826	NM_013218	C, HH	Pyrimidine metabolism	
3798	20896	NM_053592	U, NNN	Pyrimidine metabolism	
1430	1409	AI012802	A, B, M, HH, SS, UU, III, JJJ, KKK, OOO, General Core Tox Markers	Pyruvate metabolism	
1600	24374	AI045973	E	Rac 1 cell motility signaling pathway	
3726	21809	NM_032067	ZZ, AAA	Rac 1 cell motility signaling pathway, Ras Signaling Pathway	
3726	21810	NM_032067	ZZ, AAA	Rac 1 cell motility signaling pathway, Ras Signaling Pathway	
785	22843	AA925473	VV	Ras Signaling Pathway, Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration, p38 MAPK Signaling Pathway	
2403	22845	AI227887	K	Ras Signaling Pathway, Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration, p38 MAPK Signaling Pathway	
3259	21580	NM_017041	ZZ, AAA	Regulation of ck1/cdk5 by type 1 glutamate receptors	

TABLE 2					Attorney Docket 44921-5038-01WO Document No. 1935323.1
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3637	9369	NM_031527	E	Regulation of ck1/cdk5 by type 1 glutamate receptors, Regulation of eIF2	
3637	9370	NM_031527	RR, SS	Regulation of ck1/cdk5 by type 1 glutamate receptors, Regulation of eIF2	
3414	18713	NM_020075	C, FFF	Regulation of eIF2	
3414	18715	NM_020075	R, UU, FFF	Regulation of eIF2	
3655	14295	NM_031599	ZZ, AAA, PPP, QQQ	Regulation of eIF2	
4097	1928	U10357	II, General Alternate	Regulation of eIF4e and p70 S6 Kinase	
2002	23152	AI169170	S	Regulation of eIF4e and p70 S6 Kinase, mTOR Signaling Pathway	
3358	17304	NM_019144	GG	Riboflavin metabolism	
3242	24649	NM_016988	GG, HH	Riboflavin metabolism	
3359	20373	NM_019145	D, Z, AA	Role of nicotinic acetylcholine receptors in the regulation of apoptosis	
53	2040	AA799700	MM, TTT	Selenoamino acid metabolism	
3295	17104	NM_017160	G, H, II, JJ, KK, DDD, FFF, HHH, General Alternate	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR Signaling Pathway	
3295	17105	NM_017160	H, II, General Alternate	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR Signaling Pathway	
3295	17107	NM_017160	XX, YY	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway, mTOR Signaling Pathway	
4055	18356	R47042	D	Small Leucine-rich Proteoglycan (SLRP) molecules	
2853	179	D17809	GG, WW	Sphingoglycolipid metabolism	
894	17471	AA944965	LL	Sphingoglycolipid metabolism	
2984	4254	M12450	M, S, NNN	Sphingoglycolipid metabolism	
2062	15393	AI170663	FFF, General Alternate	SREBP and controls lipid synthesis	
87	4832	AA800190	ZZ, AAA	Starch and sucrose metabolism	
1304	4833	AI009178	E	Starch and sucrose metabolism	
3457	10509	NM_022268	B, I, J, V, GGG, OOO, General Core Tox Markers	Starch and sucrose metabolism	
3457	25814	NM_022268	I, FF, General Alternate	Starch and sucrose metabolism	
3633	24645	NM_031502	GGG, OOO, General Core Tox Markers	Starch and sucrose metabolism	
2054	11585	AI170502	PP, QQ, YY	Starch and sucrose metabolism	

TABLE 2				Attorney Docket 44921-5038-01WO
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3226	650	NM_013134	Q	Sterol biosynthesis
3226	651	NM_013134	Q	Sterol biosynthesis
3226	652	NM_013134	Q, R	Sterol biosynthesis
			G, WW, General	
3885	8592	NM_057137	Alternate	Sterol biosynthesis
3284	16681	NM_017136	A, B	Sterol biosynthesis, Terpenoid biosynthesis
			SS, KKK, OOO, General	
3378	16449	NM_019238	Alternate	Sterol biosynthesis, Terpenoid biosynthesis
			C, I, J, FF, OOO, General	
3378	16450	NM_019238	Alternate	Sterol biosynthesis, Terpenoid biosynthesis
1217	1058	AF003835	B, XX, YY	Sterol biosynthesis, Terpenoid biosynthesis
2740	7691	AI236611	Y	Sterol biosynthesis, Terpenoid biosynthesis
			I, J, N, T, General	
3707	15069	NM_031840	Alternate	Sterol biosynthesis, Terpenoid biosynthesis
3707	15070	NM_031840	I, T	Sterol biosynthesis, Terpenoid biosynthesis
3707	25460	NM_031840	I, J, T	Sterol biosynthesis, Terpenoid biosynthesis
3302	23961	NM_017181	PPP, QQQ	Styrene degradation, Tyrosine metabolism
			A, G, II, GGG, PPP, QQQ, General	
3679	24810	NM_031732	Alternate	Sulfur metabolism
			A, B, G, S, VV, GGG, PPP, QQQ, General	
3679	24811	NM_031732	Alternate	Sulfur metabolism
			G, I, J, OOO, PPP, QQQ, General	
3613	14970	NM_031127	Alternate	Sulfur metabolism
3702	4748	NM_031834	GGG, SSS	Sulfur metabolism
3702	4749	NM_031834	Y	Sulfur metabolism
742	17116	AA924339	X, Y	T Cytotoxic Cell Surface Molecules, T Helper Cell Surface Molecules
3111	17117	NM_012673	K	T Cytotoxic Cell Surface Molecules, T Helper Cell Surface Molecules

TABLE 2				
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Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways
3434	19824	NM_021750	A, B, JJ, HHH, General Alternate	Taurine and hypotaurine metabolism
3434	19825	NM_021750	B, I, J, JJ, HHH, General Alternate	Taurine and hypotaurine metabolism
3156	17541	NM_012844	F, N, S, CC, II, NN, OO, PP, QQ, TT, DDD, EEE, LLL, MMM, SSS, UUU, General Alternate	Tetrachloroethene degradation
3367	15242	NM_019191	O, P, EE	TGF beta signaling pathway, tgf-beta
3648	16163	NM_031563	MM, TTT	Transcriptional activation of dbpb from mRNA
3648	16164	NM_031563	RR, VV	Transcriptional activation of dbpb from mRNA
3648	16165	NM_031563	D	Transcriptional activation of dbpb from mRNA
901	402	AA945143	C, E, DD, SS, WW, KKK, NNN	Tryptophan metabolism
3415	20493	NM_020076	W	Tryptophan metabolism
4158	794	U68168	B, G, M, GG, HH, NN, OO, FFF, GGG, III, JJJ, General Core Tox Markers	Tryptophan metabolism
3647	18315	NM_031561	A, B, FF, BBB, CCC, RRR, SSS	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
3647	18316	NM_031561	A, B, II, BBB, CCC, RRR	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
3647	18318	NM_031561	BBB, HHH, RRR	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
3647	18319	NM_031561	BBB, CCC	TSP-1 Induced Apoptosis in Microvascular Endothelial Cell
3071	11115	NM_012531	M	Tyrosine metabolism
3071	11116	NM_012531	M	Tyrosine metabolism
3090	4449	NM_012592	F, V, Z, AA, XX, YY, General Alternate	Valine, leucine and isoleucine degradation

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TABLE 2				Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID No.	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Pathways	
3090	4450	NM_012592	A, B, V, BB, CC, II, OOO, General Alternate	Valine, leucine and isoleucine degradation	
3090	4451	NM_012592	VV, General Alternate	Valine, leucine and isoleucine degradation	
3090	4452	NM_012592	VV, General Alternate	Valine, leucine and isoleucine degradation	
1459	21950	AI013861	G, General Alternate	Valine, leucine and isoleucine degradation	
1990	5232	AI168942	WW	Valine, leucine and isoleucine degradation	
2925	17284	J02827	VV, XX, YY, EEE, MMM	Valine, leucine and isoleucine degradation	
3369	18573	NM_019201	A, B, KK, HHH	WNT Signaling Pathway	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	GLCC ID No.	GenBank Accession RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence	Cluster Title		
923	1707	AA945698	OO	15 kDa selenoprotein, 15-kDa selenoprotein	15 kDa selenoprotein, 15-kDa selenoprotein			
3891	15408	NM_057197	M, U, FF, XX, YY, BBB, CCC	2, 4-dienoyl CoA reductase 1, mitochondrial	2, 4-dienoyl CoA reductase 1, mitochondrial			
3891	15409	NM_057197	J, U, FF, VV, SSS	2, 4-dienoyl CoA reductase 1, mitochondrial	2, 4-dienoyl CoA reductase 1, mitochondrial			
914	22604	AA945578	U, FF, KK, XX, RRR	2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	2, 4-dienoyl CoA reductase 1, mitochondrial, 2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, Mus musculus, Similar to hypothetical protein MGC4172, clone MGC:18716 IMAGE:4219994, mRNA, complete cds, carbonyl reductase 2, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase, peroxisomal trans-2-enoyl-CoA reductase			
1234	22602	AF044574	U, FF, BBB, CCC, RRR, SSS	2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	2, 4-dienoyl CoA reductase 1, mitochondrial, 2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, Mus musculus, Similar to hypothetical protein MGC4172, clone MGC:18716 IMAGE:4219994, mRNA, complete cds, carbonyl reductase 2, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase, peroxisomal trans-2-enoyl-CoA reductase			
1234	22603	AF044574	U, FF, LL, BBB, CCC, RRR, SSS	2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	2, 4-dienoyl CoA reductase 1, mitochondrial, 2, 4-dienoyl CoA reductase 2, peroxisomal, 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, Mus musculus, Similar to hypothetical protein MGC4172, clone MGC:18716 IMAGE:4219994, mRNA, complete cds, carbonyl reductase 2, peroxisomal trans 2-enoyl CoA reductase; putative short chain alcohol dehydrogenase, peroxisomal trans-2-enoyl-CoA reductase			

TABLE 3					
Seq ID	GLGC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3226	650	NM_013134	Q	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Mus musculus, Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, clone MGC:25828 IMAGE:4166540, mRNA, complete cds, SREBP CLEAVAGE-ACTIVATING PROTEIN
3226	651	NM_013134	Q	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Mus musculus, Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, clone MGC:25828 IMAGE:4166540, mRNA, complete cds, SREBP CLEAVAGE-ACTIVATING PROTEIN
3226	652	NM_013134	Q, R	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Mus musculus, Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase, clone MGC:25828 IMAGE:4166540, mRNA, complete cds, SREBP CLEAVAGE-ACTIVATING PROTEIN
3321	20600	NM_017268	G, H, FF, JJ, KK, FFF, General Alternate	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2, pre B-cell leukemia transcription factor 1
3321	20601	NM_017268	G, H, J, JJ, KK, FFF, KKK, OOO, General Alternate	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble), 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2, pre B-cell leukemia transcription factor 1

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TABLE 3						
Seq ID	GLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster title	Attorney Docket 44924-5033-01WO Document No. 1935928.1
3415	20493	NM_020076	W	3-hydroxyanthranilate 3, 4-dioxygenase	3-hydroxyanthranilate 3, 4-dioxygenase	
3407	15680	NM_019376	Q, R, PPP, QQQ	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide, tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide		
3658	21586	NM_031620	G	3-phosphoglycerate dehydrogenase, phosphoglycerate dehydrogenase	3-phosphoglycerate dehydrogenase, EST, Moderately similar to SERA MOUSE D-3- PHOSPHOGLYCERATE DEHYDROGENASE [M.musculus], ESTs, Weakly similar to 3-phosphoglycerate dehydrogenase [Rattus norvegicus] [R.norvegicus], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930404C15.3- phosphoglycerate dehydrogenase, full insert sequence, glyoxylate reductase/hydroxypyruvate reductase, phosphoglycerate dehydrogenase	
416	17742	AA866302	HH, WW	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvate dioxygenase	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvate dioxygenase	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	CLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3314	17740	NM_017233	L, S, EE, TT, WW	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase	4-hydroxyphenylpyruvate dioxygenase, 4-hydroxyphenylpyruvic acid dioxygenase			
2880	1414	D89514	VV	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase			
3087	20313	NM_012585	D, E	5-hydroxytryptamine (serotonin) receptor 1A	5-hydroxytryptamine (serotonin) receptor 1A			
3556	22282	NM_024394	Z, AA, MM, WW, TTT	5-hydroxytryptamine (serotonin) receptor 3A	5-hydroxytryptamine (serotonin) receptor 3A			
3551	767	NM_024365	UU	5-hydroxytryptamine (serotonin) receptor 6	5-hydroxytryptamine (serotonin) receptor 6			
2928	174	J04197	JJ, KK, SS	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 1				
3099	172	NM_012621	JJ, KK, WW, YY	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 1				
4204	173	X15580	L, Z, AA, JJ, KK, WW	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 1				

TABLE 3						
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Seq ID	CLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
4166	2153	U75404	W, BB, CC, ZZ, AAA	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein (gravin) 12, ESTs, Highly similar to gravin [H.sapiens]	
3270	18956	NM_017075	BBB	acetyl-Coenzyme A acetyltransferase 1, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	Homo sapiens, Similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), clone MGC:13582 IMAGE:4278329, mRNA, complete cds, Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacetyl-Coenzyme A thiolase)	
3270	18957	NM_017075	D, U, GG, XX, YY, BBB, CCC	acetyl-Coenzyme A acetyltransferase 1, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	Homo sapiens, Similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), clone MGC:13582 IMAGE:4278329, mRNA, complete cds, Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacetyl-Coenzyme A thiolase)	
3270	18958	NM_017075	U, FF, XX, BBB, CCC, RRR, SSS	acetyl-Coenzyme A acetyltransferase 1, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	Homo sapiens, Similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), clone MGC:13582 IMAGE:4278329, mRNA, complete cds, Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase), acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacetyl-Coenzyme A thiolase)	

TABLE 3						
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935828.1
3058	23698	NM_012489	U, FF, HH, LL, XX, BBB, CCC, DDD, RRR, SSS, UUU	acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase), acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase), acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	
3058	23699	NM_012489	U, FF, GG, HH, LL, DDD	acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase), acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	Mus musculus, Similar to Acetyl-Co A acetyltransferase 1, mitochondrial, clone MGC:39067 IMAGE:5365469, mRNA, complete cds, acetyl-Coenzyme A acyltransferase (peroxisomal 3-oxoacyl-Coenzyme A thiolase), acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	
3150	6780	NM_012819	U, RRR	acetyl-Coenzyme A dehydrogenase, long-chain, acyl-Coenzyme A dehydrogenase, long chain	acetyl-Coenzyme A dehydrogenase, long-chain, acyl-Coenzyme A dehydrogenase, long chain	

TABLE 3						
Seq ID	CLGG ID No.	Genbank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster title	Attorney Docket 44921-5038-01WO Document No. 1933828.1
3150	6781	NM_012819	HH	acetyl-Coenzyme A dehydrogenase, long-chain, acyl-Coenzyme A dehydrogenase, long chain	acetyl-Coenzyme A dehydrogenase, long-chain, acyl-Coenzyme A dehydrogenase, long chain	
3240	21078	NM_016986	T, U, X, TT, XX, YY, III, JJ, RRR	acetyl-Coenzyme A dehydrogenase, medium chain, acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	ESTs, Highly similar to ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR [M.musculus], acetyl-Coenzyme A dehydrogenase, medium chain, acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	
3242	24649	NM_016988	GG, HH	acid phosphatase 2, lysosomal	ESTs, Weakly similar to A33395 acid phosphatase (EC 3.1.3.2) precursor - rat [R.norvegicus], acid phosphatase 2, lysosomal, acid phosphatase, testicular	
3557	19992	NM_024398	L, Z, AA, WW, LLL, RRR, SSS, UUU	aconitase 2, mitochondrial	aconitase 2, mitochondrial	
3557	19993	NM_024398	Z, AA, GGG	aconitase 2, mitochondrial	aconitase 2, mitochondrial	
3557	19994	NM_024398	WW	aconitase 2, mitochondrial	aconitase 2, mitochondrial	
3175	24431	NM_012912	W, II	activating transcription factor 3	ESTs, Weakly similar to A39382 liver regeneration factor LRF1 - rat [R.norvegicus], ESTs, Weakly similar to A54025 transcription factor ATF3 [H.sapiens], activating transcription factor 3	

TABLE 3						
Seq ID	GLGG ID No.	GenBank Accor RefSeq ID	Modal Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935328.1
1008	16722	AA956311	CCC	acyl-Coenzyme A dehydrogenase, very long chain	EST, Moderately similar to ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC [M.musculus], EST, Weakly similar to ACDV_RAT Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial precursor (VLCAD) [R.norvegicus], EST, Weakly similar to S54183 acyl-CoA dehydrogenase [H.sapiens], ESTs, Weakly similar to ACDV_RAT Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial precursor (VLCAD) [R.norvegicus], RIKEN cDNA 2600017P15 gene, acyl-Coenzyme A dehydrogenase, very long chain	
3168	16721	NM_012891	U, XX, YY, BBB, CCC, RRR, SSS	acyl-Coenzyme A dehydrogenase, very long chain	EST, Moderately similar to ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC [M.musculus], EST, Weakly similar to ACDV_RAT Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial precursor (VLCAD) [R.norvegicus], EST, Weakly similar to S54183 acyl-CoA dehydrogenase [H.sapiens], ESTs, Weakly similar to ACDV_RAT Acyl-CoA dehydrogenase, very-long-chain specific, mitochondrial precursor (VLCAD) [R.norvegicus], RIKEN cDNA 2600017P15 gene, acyl-Coenzyme A dehydrogenase, very long chain	
3901	17956	NM_080583	JJ, KK, HHH	adaptor-related protein complex 2, beta 1 subunit	adaptor protein complex AP-1, beta 1 subunit, adaptor-related protein complex 2, beta 1 subunit	
2629	16709	A1233602	PP, QQ	adenosine kinase	adenosine kinase, expressed sequence A1987814	
3169	16708	NM_012895	UU, WW	adenosine kinase	adenosine kinase, expressed sequence A1987814	
997	M80550		RR	adenylate cyclase 2, adenylate cyclase 2 (brain)	EST, Moderately similar to B Chain B, Complex Of Gs-Alpha With The Catalytic Domains Of Mammalian Adenylyl Cyclase: Complex With Beta-L-2', 3'-Dideoxyatp And Mg [R.norvegicus], ESTs, Highly similar to ADENYLATE CYCLASE, TYPE VII [M.musculus], ESTs, Weakly similar to ADENYLATE CYCLASE, TYPE VII [M.musculus], adenylate cyclase 2 (brain), adenylate cyclase 4, adenylate cyclase 7	
				adenylate cyclase activating polypeptide 1, adenylate cyclase activating polypeptide 1 (pituitary)	adenylate cyclase activating polypeptide 1, adenylate cyclase activating polypeptide 1 (pituitary)	

TABLE 3							Attorney Docket 44921-5088-01WO Document No. 1935828.1	
Seq. ID	GLCG ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3547	10980	NM_024349	Z, AA	adenylate kinase 1	RIKEN cDNA 0610011D08 gene, adenylate kinase 1			
3574	17050	NM_030986	UU	adenylate kinase 2	Homo sapiens cDNA FLJ30976 fis, clone HHDP2000055, weakly similar to ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3), Mus musculus AK5 mRNA for adenylate kinase isozyme 5, complete cds, adenylate kinase 2			
1850	3764	AI103651	C	ADP-ribosylarginine hydrolase	ADP-ribosylarginine hydrolase, ESTs, Weakly similar to ADP-RIBOSYLARGININE HYDROLASE [M.musculus]			
3366	24019	NM_019186	Q, R, General Alternate	ADP-ribosylation factor-like 4, ADP-ribosylation-like 4	ADP-ribosylation factor 4-like, ADP-ribosylation factor-like 7, ADP-ribosylation-like 4, ESTs, Weakly similar to ADP-ribosylation-like 4 [Mus musculus], Mus musculus, Similar to ADP-ribosylation-like 4, clone MGC:5774 IMAGE:3599701, mRNA, complete cds, RIKEN cDNA 1110036H21 gene, epithelial protein lost in neoplasm beta			
3030	64	M60655	C, I, L, W, XX, YY, LLL, OOO, General Alternate	adrenergic receptor, alpha 1b, adrenergic, alpha-1B-, receptor				
3560	1835	NM_024483	HH	adrenergic receptor, alpha 1d, adrenergic, alpha-1D-, receptor	Mus musculus histamine H4 receptor mRNA, complete cds, adrenergic, alpha-1D-, receptor			
1944	24803	AI137065	MM, VV, TTT	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)				

TABLE 3						
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44924-5038-01WO Document No. 1935328.1
2848	24797	D13667	MM, PP, QQ, RR, TTT	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	
2882	24799	E01050	X, Y, MM, SS, TTT	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	
3563	24798	NM_030656	F, N, MM, SS, BBB, CCC, TTT	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935323.1	
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
				alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)				
3563	24800	NM_030656	MM, RR, SS, TTT		alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)			
				alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)				
3563	24801	NM_030656	MM, VV, TTT		alanine-glyoxylate aminotransferase, alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)			
3429	23424	NM_021680	E	alanyl-tRNA synthetase	alanyl-tRNA synthetase			
412	17110	AA860062	Z, AA	albumin, albumin 1	ESTs, Moderately similar to ALBU_RAT Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)] [R.norvegicus], albumin, albumin 1			
412	17111	AA860062	S, SS	albumin, albumin 1	ESTs, Moderately similar to ALBU_RAT Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)] [R.norvegicus], albumin, albumin 1			
3959	17109	NM_134326	M, S, DD, EE, SS, TT	albumin, albumin 1, glutathione peroxidase 1	ESTs, Moderately similar to ALBU_RAT Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)] [R.norvegicus], albumin, albumin 1			

TABLE 3					
Attorney Docket 44921-5033-01WO Document No. 1935328.1					
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3959	17112	NM_134326	S, HH	albumin, albumin 1, glutathione peroxidase 1	ESTs, Moderately similar to ALBU_RAT Serum albumin precursor [Contains: Neutensin-related peptide (NRP)] [R.norvegicus], ESTs, Weakly similar to GSHC_RAT Glutathione peroxidase (GSHPX-1) (Cellular glutathione peroxidase) [R.norvegicus], albumin, albumin 1, glutathione peroxidase 1, glutathione peroxidase 2, glutathione peroxidase 2 (gastrointestinal)
4277	420	X90710	U, RRR, SSS	alcohol dehydrogenase 4 (class II), pi polypeptide	alcohol dehydrogenase 4 (class II), pi polypeptide
3472	20915	NM_022407	F, U, LL, TT, BBB, CCC, EEE, LLL, MMM, RRR, SSS, UUU	aldehyde dehydrogenase 1 family, member A1, aldehyde dehydrogenase family 1, subfamily A1	Mus musculus, Similar to aldehyde dehydrogenase 8 family, member A1, clone IMAGE:4234742, mRNA, partial cds, aldehyde dehydrogenase 1 family, member A1, aldehyde dehydrogenase family 1, subfamily A1
1442	12300	A013333	N	aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial	ESTs, Moderately similar to DHAM_RAT ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (ALDH CLASS 2) (ALDH1) (ALDH-E2) [R.norvegicus], RIKEN cDNA 2410004H02 gene, aldehyde dehydrogenase 1 family, member B1, aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial

TABLE 3					Attorney Docket 44921-5033-01WO Document No. 1933328.1	
Seq ID	CLC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3728	12299	NM_032416	N, YY	aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial	ESTs, Moderately similar to DHAM_RAT ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (ALDH CLASS 2) (ALDH1) (ALDH-E2) [R.norvegicus], RIKEN cDNA 241004H02 gene, aldehyde dehydrogenase 1 family, member B1, aldehyde dehydrogenase 2 family (mitochondrial), aldehyde dehydrogenase 2, mitochondrial	
3678	23884	NM_031731	U	aldehyde dehydrogenase 3 family, member A2, aldehyde dehydrogenase family 3, subfamily A2	RIKEN cDNA 170001N19 gene, RIKEN cDNA 1700055N04 gene, aldehyde dehydrogenase 3 family, member A2, aldehyde dehydrogenase family 3, subfamily A2, expressed sequence A1848594	
1852	16884	AI103758	QQQ	aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	Mus musculus, Similar to aldehyde dehydrogenase 4 family, member A1, clone IMAGE:5102023, mRNA, partial cds, RIKEN cDNA 1110038I05 gene, aldehyde dehydrogenase 4 family, member A1, aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	
1890	16885	AI105188	PP, General Core Tox Markers	aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	Mus musculus, Similar to aldehyde dehydrogenase 4 family, member A1, clone IMAGE:5102023, mRNA, partial cds, RIKEN cDNA 1110038I05 gene, aldehyde dehydrogenase 4 family, member A1, aldehyde dehydrogenase 9 family, member A1, aldehyde dehydrogenase 9, subfamily A1	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1936828.1						
Seq ID	GLC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
4026	9096	NM_145771	RRR	aldehyde reductase (aldose reductase) like 6, aldehyde reductase (aldose reductase)-like 6		aldehyde reductase (aldose reductase) like 6
3060	7062	NM_012495	VV	aldolase 1, A isoform, aldolase A, fructose-bisphosphate		EST, Moderately similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], ESTs, Highly similar to I39435 fructose-bisphosphate aldolase [H.sapiens], ESTs, Moderately similar to aldolase A [M.musculus], ESTs, Weakly similar to ALFA_HUMAN FRUCTOSE-BISPHOSPHATE ALDOLASE A [H.sapiens], Mus musculus, clone MGC:25455 IMAGE:4241025, mRNA, complete cds, RIKEN cDNA 4933425L11 gene, aldolase 1, A isoform, aldolase 3, C isoform, aldolase A, fructose-bisphosphate
3060	7063	NM_012495	O, P, PP, QQ, UU, VV	aldolase 1, A isoform, aldolase A, fructose-bisphosphate		EST, Moderately similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], ESTs, Highly similar to I39435 fructose-bisphosphate aldolase [H.sapiens], ESTs, Moderately similar to aldolase A [M.musculus], ESTs, Weakly similar to ALFA_HUMAN FRUCTOSE-BISPHOSPHATE ALDOLASE A [H.sapiens], Mus musculus, clone MGC:25455 IMAGE:4241025, mRNA, complete cds, RIKEN cDNA 4933425L11 gene, aldolase 1, A isoform, aldolase 3, C isoform, aldolase A, fructose-bisphosphate
3060	7064	NM_012495	II, VV, PPP, General Core Tox Markers	aldolase 1, A isoform, aldolase A, fructose-bisphosphate		EST, Moderately similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], EST, Weakly similar to ADHUA fructose-bisphosphate aldolase [H.sapiens], ESTs, Highly similar to I39435 fructose-bisphosphate aldolase [H.sapiens], ESTs, Moderately similar to aldolase A [M.musculus], ESTs, Weakly similar to ALFA_HUMAN FRUCTOSE-BISPHOSPHATE ALDOLASE A [H.sapiens], Mus musculus, clone MGC:25455 IMAGE:4241025, mRNA, complete cds, RIKEN cDNA 4933425L11 gene, aldolase 1, A isoform, aldolase 3, C isoform, aldolase A, fructose-bisphosphate

TABLE 3						
Seq ID	CLCG ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44924-5038-01WO Document No. 1935828.1
562	820	AA892395	B, PPP, QQQ	aldolase 2, B isoform, aldolase B, fructose-bisphosphate	Mus musculus, clone MGC:25455 IMAGE:4241025, mRNA, complete cds, aldolase 1, A isoform, aldolase 3, C isoform, aldolase B, fructose-bisphosphate	
4183	818	X02291	HH, SS	aldolase 2, B isoform, aldolase B, fructose-bisphosphate	Mus musculus, clone MGC:25455 IMAGE:4241025, mRNA, complete cds, aldolase 1, A isoform, aldolase 3, C isoform, aldolase B, fructose-bisphosphate	
1161	16625	AA998062	A, B, N	Alg5, S. cerevisiae, homolog of	Alg5, S. cerevisiae, homolog of	
3305	16269	NM_017196	V, X, Y	allograft inflammatory factor 1	Mus musculus, clone MGC:30545 IMAGE:5044495, mRNA, complete cds, RIKEN cDNA 2600015J22 gene, allograft inflammatory factor 1, expressed sequence	
3172	7897	NM_012901	V, SS, NNN	alpha 1 microglobulin/bikunin, alpha-1-microglobulin/bikunin precursor	RIKEN cDNA 1700013L23 gene, WAP, FS, Ig, KU, and NTR-containing protein, alpha 1 microglobulin/bikunin, alpha-1-microglobulin/bikunin precursor, complement component 8, gamma polypeptide, serine protease inhibitor, Kunitz type 2	
3172	7898	NM_012901	NNN	alpha 1 microglobulin/bikunin, alpha-1-microglobulin/bikunin precursor	RIKEN cDNA 1700013L23 gene, WAP, FS, Ig, KU, and NTR-containing protein, alpha 1 microglobulin/bikunin, alpha-1-microglobulin/bikunin precursor, complement component 8, gamma polypeptide, serine protease inhibitor, Kunitz type 2	
3172	7899	NM_012901	UUU	alpha 1 microglobulin/bikunin, alpha-1-microglobulin/bikunin precursor	RIKEN cDNA 1700013L23 gene, WAP, FS, Ig, KU, and NTR-containing protein, alpha 1 microglobulin/bikunin, alpha-1-microglobulin/bikunin precursor, complement component 8, gamma polypeptide, serine protease inhibitor, Kunitz type 2	

TABLE 3							Attorney Docket 44921-5033-01WO Document No. 1935328.1	
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3059	23942	NM_012493	General Alternate	alpha fetoprotein, alpha-fetoprotein	ESTs, Weakly similar to FETA_RAT Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-fetoprotein) [R.norvegicus], alpha fetoprotein, alpha-fetoprotein			
3152	20587	NM_012826	O, P, W	alpha-2-glycoprotein 1, zinc	UL16 binding protein 1, UL16 binding protein 2, alpha-2-glycoprotein 1, zinc			
3170	16274	NM_012898	M, S, SS, TT	alpha-2-HS-glycoprotein	alpha-2-HS-glycoprotein			
3170	16275	NM_012898	S, FF, HH, SS, NNN	alpha-2-HS-glycoprotein	alpha-2-HS-glycoprotein			
3057	22512	NM_012488	BB, NN, EEE, MMM	alpha-2-macroglobulin	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin, murinoglobulin 1, pregnancy-zone protein			
3057	22513	NM_012488	A, E, W, BB, UU, EEE, MMM	alpha-2-macroglobulin	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin, murinoglobulin 1, pregnancy-zone protein			
3057	22514	NM_012488	BB, NN, UU	alpha-2-macroglobulin	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin, murinoglobulin 1, pregnancy-zone protein			
3057	22515	NM_012488	E, W, BB, NN, OO, EEE, III, JJJ, KKK, MMM	alpha-2-macroglobulin	ESTs, Highly similar to A2MG_RAT ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) [R.norvegicus], ESTs, Weakly similar to A2MG MOUSE ALPHA-2-MACROGLOBULIN PRECURSOR [M.musculus], alpha-2-macroglobulin, murinoglobulin 1, pregnancy-zone protein			
3081	17237	NM_012562	XX, YY	alpha-L-fucosidase, fucosidase, alpha-L-1, tissue				

TABLE 3						
Seq ID	CLCG ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-50338-01WO Document No. 1935323.1
3149	15032	NM_012816	X, Y	alpha-methylacyl-CoA racemase	alpha-methylacyl-CoA racemase, cDNA sequence AF397014, chromosome 7 open reading frame 10	
4052	1937	R46934	HH	amelogenin, amelogenin (X chromosome, amelogenesis imperfecta 1)		
3521	16184	NM_022935	Z, AA	amiloride binding protein 1 (amine oxidase (copper-containing)), amiloride binding protein 1 (amine oxidase, copper-containing)	EST, Moderately similar to amiloride binding protein 1 [Rattus norvegicus] [R.norvegicus], EST, Weakly similar to amiloride binding protein 1 [Rattus norvegicus] [R.norvegicus], EST, Weakly similar to amiloride binding protein 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to AOC3 MOUSE MEMBRANE COPPER AMINE OXIDASE [M.musculus], ESTs, Weakly similar to AOC3 MOUSE MEMBRANE COPPER AMINE OXIDASE [M.musculus], RIKEN cDNA 1600015110 gene, amiloride binding protein 1 (amine oxidase (copper-containing)), amiloride binding protein 1 (amine oxidase, copper-containing), amine oxidase, copper containing 3, androgen-responsive protein pSv-2	
4163	25083	U72632	RR	amine oxidase, copper containing 3, amine oxidase, copper containing 3 (vascular adhesion protein 1)		
3171	18564	NM_012899	L, CC, DD, EE, III, JJ, KKK, OOO, General Core Tox Markers, General Alternate	aminolevulinatase, delta-, dehydratase	aminolevulinatase, delta-, dehydratase	

TABLE 3						
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1384	21040	AI011734	K, L	aminolevulinatase, delta, synthase 1, aminolevulinic acid synthase 1	aminolevulinatase, delta-, synthase 1, aminolevulinic acid synthase 1, serine palmitoyltransferase, long chain base subunit 1, serine palmitoyltransferase, long chain base subunit 2	
3561	21038	NM_024484	TT	aminolevulinatase, delta, synthase 1, aminolevulinic acid synthase 1	aminolevulinatase, delta-, synthase 1, aminolevulinic acid synthase 1, serine palmitoyltransferase, long chain base subunit 1, serine palmitoyltransferase, long chain base subunit 2	
3561	21039	NM_024484	K, QQ, TT	aminolevulinatase, delta, synthase 1, aminolevulinic acid synthase 1	aminolevulinatase, delta-, synthase 1, aminolevulinic acid synthase 1, serine palmitoyltransferase, long chain base subunit 1, serine palmitoyltransferase, long chain base subunit 2	
3373	2078	NM_019220	S, V	amino-terminal enhancer of split	amino-terminal enhancer of split	
3373	2079	NM_019220	General Alternate	amino-terminal enhancer of split	amino-terminal enhancer of split	
3633	24645	NM_031502	GGG, OOO, General Core Tox Markers	amylase 1, salivary, amylase, alpha 1A; salivary	ESTs, Moderately similar to AMYP_HUMAN ALPHA-AMYLASE, PANCREATIC PRECURSOR [H.sapiens], amylase 1, salivary, amylase 2, pancreatic, amylase, alpha 1A; salivary, amylase, alpha 2A; pancreatic	
220	10157	AA819527	XX, YY	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	ESTs, Highly similar to I39451 amyloid-beta protein [H.sapiens], ESTs, Weakly similar to S23094 beta-amyloid protein precursor - rat [R.norvegicus], amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	
1018	10155	AA956735	V	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	ESTs, Highly similar to I39451 amyloid-beta protein [H.sapiens], ESTs, Weakly similar to S23094 beta-amyloid protein precursor - rat [R.norvegicus], amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	

TABLE 3					Attorney Docket 44921-5038-01WO Document No. 1995828.1	
Seq ID	GLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
4263	11260	X77934	WW	amyloid beta (A4) precursor-like protein 2	ESTs, Weakly similar to 2019243A amyloid precursor-like protein 2 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to EPPI_MOUSE Eppin precursor [M.musculus], amyloid beta (A4) precursor-like protein 1, amyloid beta (A4) precursor-like protein 2	
3299	8182	NM_017170	GG, LL, MM, CCC, GGG, RRR, TTT	amyloid P component, serum, amyloid P-component	EST, Weakly similar to S11473 serum amyloid P-component - rat [R.norvegicus], EST, Weakly similar to SAMP MOUSE SERUM AMYLOID P-COMPONENT PRECURSOR [M.musculus], ESTs, Weakly similar to SAMP_HUMAN SERUM AMYLOID P-COMPONENT PRECURSOR [H.sapiens], amyloid P component, serum	
2983	21097	M12112	C, I, O, P, MM, NNN, TTT, General Core Tox Markers	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsin), member 8)	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsin), member 8)	
3968	21098	NM_134432	C, L, DD, NNN	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsin), member 8)	angiotensinogen, angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsin), member 8)	
3173	7197	NM_012904	O, P, VW	annexin A1	annexin A1	

TABLE 3						
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	EST, Moderately similar to 0806162C protein COI [M.musculus], EST, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], EST, Weakly similar to 0806162C protein COI [M.musculus], ESTs, Highly similar to hydroxyacid oxidase 3 (medium-chain) [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to 0806162C protein COI [M.musculus], ESTs, Moderately similar to 810024C cytochrome oxidase I [H.sapiens], ESTs, Weakly similar to 0806162C protein COI [M.musculus], annexin A2, annexin A9, hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 1, liver
3412	574	NM_019905	MMM	annexin A2, hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 3 (medium-chain)		ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ESTs, Weakly similar to ZAP 36/annexin IV [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to annexin A8, clone MGC:13875 IMAGE:4013266, mRNA, complete cds, annexin A13, annexin A4, annexin A8
2699	8440	A1235611	T	annexin A4		ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ESTs, Weakly similar to ZAP 36/annexin IV [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to annexin A8, clone MGC:13875 IMAGE:4013266, mRNA, complete cds, annexin A13, annexin A4, annexin A8
3542	8439	NM_024155	O, P	annexin A4		ESTs, Moderately similar to ANX4 MOUSE ANNEXIN IV [M.musculus], ESTs, Weakly similar to ZAP 36/annexin IV [Rattus norvegicus] [R.norvegicus], Mus musculus, Similar to annexin A8, clone MGC:13875 IMAGE:4013266, mRNA, complete cds, annexin A13, annexin A4, annexin A8
3920	21391	NM_130416	X, Y	annexin A7		annexin A11, annexin A13, annexin A7
3793	19252	NM_053576	HH	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5		ESTs, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus], ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5

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TABLE 3						
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935328.1
3793	19253	NM_053576	G, H	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	ESTs, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus], ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	
3793	19254	NM_053576	G, H, L	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5 APEX nuclease (multifunctional DNA repair enzyme), apurinic/apyrimidinic endonuclease	ESTs, Moderately similar to AOP2 MOUSE ANTIOXIDANT PROTEIN 2 [M.musculus], ESTs, Moderately similar to AOP2_HUMAN ANTIOXIDANT PROTEIN 2 [H.sapiens], anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2), peroxiredoxin 5	
3537	20801	NM_024148	FFF, QQQ	apurinic/apyrimidinic endonuclease	APEX nuclease (multifunctional DNA repair enzyme), Mus musculus ape2 mRNA for AP endonuclease 2, complete cds, apurinic/apyrimidinic endonuclease	
2979	427	M00001	CCC	apolipoprotein A-I	ESTs, Weakly similar to apolipoprotein A-I [Rattus norvegicus]	
3132	5318	NM_012737	PP, QQ	apolipoprotein A-IV	apolipoprotein A-I	
3132	18236	NM_012737	V	apolipoprotein A-IV	apolipoprotein A-IV, desmoplakin (DPI, DPII)	
3132	5317	NM_012737	BBB, CCC	apolipoprotein A-IV	apolipoprotein A-IV, desmoplakin (DPI, DPII)	
3151	23670	NM_012824	S, V	apolipoprotein C-I	EST, Moderately similar to LPHUC1 apolipoprotein C-I precursor [H.sapiens], RIKEN cDNA 4932417P04 gene, apolipoprotein C-I, apolipoprotein C-I	
3061	17785	NM_012501	M, V	apolipoprotein C-III	apolipoprotein C-III, apolipoprotein CIII	
3061	17787	NM_012501	S, DD, EE, HH, XX, YY	apolipoprotein C-III	apolipoprotein C-III, apolipoprotein CIII	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3983	16400	NM_138828	S	apolipoprotein E	apolipoprotein E			
3362	21090	NM_019158	KKK	aquaporin 8	aquaporin 8			
			C, U, X, DD, EE, DDD, LLL, OOO, RRR, SSS, UUU					
3528	15755	NM_022960	UUU	aquaporin 9				
3283	24693	NM_017134	C, General Alternate	arginase 1, liver, arginase, liver	arginase 1, liver, arginase, liver			
1238	145	AF064541	N	arginine vasopressin receptor 1B	arginine vasopressin receptor 1B			
				arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)				
3244	24869	NM_016992	Z, AA	argininosuccinate synthetase, argininosuccinate synthetase 1	arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)			
4194	20597	X12459	C, YY, BBB	argininosuccinate synthetase, argininosuccinate synthetase 1	arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)			
				argininosuccinate synthetase, argininosuccinate synthetase 1	arginine vasopressin, arginine vasopressin (neurophysin II, antidiuretic hormone, diabetes insipidus, neurohypophyseal)			
2503	23013	A1230743	O, VV, HHH	ARP3 actin-related protein 3 homolog (yeast)	ARP3 actin-related protein 3 homolog (yeast), EST, Weakly similar to ARP3_HUMAN ACTIN-LIKE PROTEIN 3 [H.sapiens], EST, Weakly similar to ATRT actin, skeletal muscle - rat [R.norvegicus], ESTs, Moderately similar to ARP3_HUMAN ACTIN-LIKE PROTEIN 3 [H.sapiens], ESTs, Weakly similar to ATHU actin alpha 1, skeletal muscle [H.sapiens], Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955, actin-related protein 3-beta, hypothetical protein FLJ12785, mitochondrial ribosomal protein L47			

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	GLGC ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3303	24670	NM_017189	L	asialoglycoprotein receptor 2	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 6, C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 7, C-type lectin related f, RIKEN cDNA 1810029C22 gene, asialoglycoprotein receptor 2			
4093	1583	U07201	E, GG, III, JJJ	asparagine synthetase				
3241	15610	NM_016987	Z, AA	ATP citrate lyase	ATP citrate lyase, EST, Moderately similar to SUCA_MOUSE SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) [M.musculus], expressed sequence AW538652, succinate-CoA ligase, GDP-forming, alpha subunit			
3241	15612	NM_016987	BB, CC, JJJ, OOO	ATP citrate lyase	ATP citrate lyase, EST, Moderately similar to SUCA_MOUSE SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) [M.musculus], expressed sequence AW538652, succinate-CoA ligase, GDP-forming, alpha subunit			
3241	15613	NM_016987	E, J, VVW, OOO, General Core Tox Markers, General Alternate	ATP citrate lyase	ATP citrate lyase, EST, Moderately similar to SUCA_MOUSE SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) [M.musculus], expressed sequence AW538652, succinate-CoA ligase, GDP-forming, alpha subunit			
3802	20725	NM_053602	Q, R	ATP synthase, H+ transporting, mitochondrial F0 complex subunit F, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6				

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	CLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3802	20726	NM_053602	LL	ATP synthase, H+ transporting, mitochondrial F0 complex subunit F6	ATP synthase, H+ transporting, mitochondrial F0 complex subunit F, ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6			
3948	15524	NM_133556	V	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2			
4002	17203	NM_139099	RRR	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit, RIKEN cDNA 2410043G19 gene, expressed sequence AV000645			
3331	12350	NM_017290	PP, QQ	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2				
4173	1359	U78977	XX, YY	ATPase, Class II, type 9A	ATPase, Class II, type 9A, EST, Highly similar to AT2A_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIA [H.sapiens], ESTs, Moderately similar to AT2A_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIA [H.sapiens], ESTs, Weakly similar to AT2A_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIA [H.sapiens], Homo sapiens mRNA; cDNA DKFZp58610624 (from clone DKFZp58610624)			

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935823.1						
Seq ID	CLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2923	1577	J02649	D	ATPase, H+/K+ exchanging, alpha polypeptide, ATPase, H+/K+ transporting, alpha polypeptide		
3062	15675	NM_012504	H, DD, EE	ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATPase, Na+/K+ transporting, alpha 1 polypeptide, ATPase, alpha 4 polypeptide, Mus musculus, Similar to ATPase, Na+/K+ transporting, alpha 1a.1 polypeptide, clone IMAGE:3599053, mRNA, partial cds	
3062	15677	NM_012504	N, RR, WW	ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATPase, Na+/K+ transporting, alpha 1 polypeptide, ATPase, alpha 4 polypeptide, Mus musculus, Similar to ATPase, Na+/K+ transporting, alpha 1a.1 polypeptide, clone IMAGE:3599053, mRNA, partial cds	
3176	18119	NM_012913	VV	ATPase, Na+/K+ transporting, beta 3 polypeptide	ATPase, Na+/K+ transporting, beta 3 polypeptide, ESTs, Highly similar to ATND_HUMAN SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN [H.sapiens], expressed sequence AI664000	
3115	24453	NM_012690	A	ATP-binding cassette, sub-family B (MDR/TAP), member 4	ATP-binding cassette, sub-family B (MDR/TAP), member 4, ESTs, Highly similar to MDR3_HUMAN MULTIDRUG RESISTANCE PROTEIN 3 [H.sapiens], ESTs, Weakly similar to B54774 ATP binding cassette transporter ABC2 - human [M.musculus], Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810428N17:ATP-binding cassette, sub-family B (MDR/TAP), member 10, full insert sequence	

TABLE 3 Human Homologous Sequence Cluster Title						
Seq ID	GLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Human Homologous Sequence Cluster Title
4223	1037	X57523	II	ATP-binding cassette, sub-family B (MDR/TAP), member 2, transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	ATP-binding cassette, sub-family B (MDR/TAP), member 2, ESTs, Highly similar to S13426 multidrug resistance protein homolog - rat [R.norvegicus], transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	
4245	515	X63854	UU	ATP-binding cassette, sub-family B (MDR/TAP), member 3, transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	ATP-binding cassette, sub-family B (MDR/TAP), member 3, ATP-binding cassette, sub-family B (MDR/TAP)	
3153	373	NM_012833	NN, UU, KKK, NNN	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2, ATP-binding cassette, sub-family C (CFTR/MRP), member 4, expressed sequence A173996	
3582	15700	NM_031013	W, FFF, GGG, III, JJJ, KKK, OOO, General Core Tox Markers	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	

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TABLE 3						Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence (Cluster Title)		
1244	25211	AF087839	SSS, UUU	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to T42751 sulfonylurea receptor 2 - rat [R.norvegicus], Homo sapiens cDNA FLJ31957 fis, clone NT2RP7007381, highly similar to Sulfonylurea receptor 2A, Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-binding cassette, sub-family C (CFTR/MRP), member 9, full insert sequence		
3201	730	NM_013040	E, Z, AA, RR	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9, ESTs, Weakly similar to T42751 sulfonylurea receptor 2 - rat [R.norvegicus], Homo sapiens cDNA FLJ31957 fis, clone NT2RP7007381, highly similar to Sulfonylurea receptor 2A, Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330439B14:ATP-binding cassette, sub-family C (CFTR/MRP), member 9, full insert sequence		
3145	21729	NM_012804	WW, RRR, SSS	ATP-binding cassette, sub-family D (ALD), member 3	ATP-binding cassette, sub-family D (ALD), member 3, ATP-binding cassette, sub-family D (ALD), member 4, ESTs, Weakly similar to A35723 70K peroxisomal membrane protein - rat [R.norvegicus]		
3145	21730	NM_012804	K, U, FF	ATP-binding cassette, sub-family D (ALD), member 3	ATP-binding cassette, sub-family D (ALD), member 3, ATP-binding cassette, sub-family D (ALD), member 4, ESTs, Weakly similar to A35723 70K peroxisomal membrane protein - rat [R.norvegicus]		
2309	6287	A1178652	RR	BAI1-associated protein 2, brain-specific angiogenesis inhibitor 1-associated protein 2	BAI1-associated protein 2, ESTs, Weakly similar to brain-specific angiogenesis inhibitor 1-associated protein 2 [Mus musculus] [M.musculus], Mus musculus, Similar to KIAA0429 gene product, clone IMAGE:2811240, mRNA, partial cds, RIKEN cDNA 1300006M19 gene, brain-specific angiogenesis inhibitor 1-associated protein 2, hypothetical protein FLJ22582, insulin receptor tyrosine kinase substrate		
3139	11938	NM_012783	X, Y, EE	basigin, basigin (OK blood group)	ESTs, Weakly similar to A46506 leukocyte activation antigen M6 [H.sapiens], Mus musculus, Similar to spindle pole body protein, clone IMAGE:5324982, mRNA, partial cds, basigin, basigin (OK blood group), spindle pole body protein		
3245	24897	NM_016993	QQ	B-cell CLL/lymphoma 2, B-cell leukemia/lymphoma 2			

TABLE 3							Attorney Docket 49241-5088-01WO Document No. 1995828.1	
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
2968	19	L26268	N, BB, CC, DD, HH, III, JJ, KKK, NNN, General Alternate	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative, Homo sapiens cDNA FLJ30547 fis, clone BRAWH2001439, transducer of ERBB2, 1, transducer of ERBB2, 2, transducer of ErbB-2.1			
2968	20	L26268	BB, CC, DD, LL, UU, III, JJ, KKK, NNN, General Alternate	B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative, Homo sapiens cDNA FLJ30547 fis, clone BRAWH2001439, transducer of ERBB2, 1, transducer of ERBB2, 2, transducer of ErbB-2.1			
3319	15299	NM_017259	W, II, KKK, OOO, General Core Tox Markers	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]			
3319	15300	NM_017259	W, II	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]			
3319	15301	NM_017259	A, B, W, II	B-cell translocation gene 2, anti-proliferative, BTG family, member 2	B-cell translocation gene 2, anti-proliferative, B-cell translocation gene 4, BTG family, member 2, ESTs, Highly similar to BTG2_HUMAN BTG2 PROTEIN PRECURSOR [H.sapiens]			
4149	912	U59184	QQ, UU, General Core Tox Markers	BCL2-associated X protein, Bcl2-associated X protein				
3064	7427	NM_012515	O, P, NN, OO, VV, EEE, MMM	benzodiazepine receptor (peripheral), benzodiazepine receptor, peripheral	ESTs, Weakly similar to 138724 mitochondrial benzodiazepine receptor [H.sapiens], benzodiazepine receptor (peripheral), benzodiazepine receptor, peripheral			

TABLE 3

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Document No. 1935828.1

Seq ID	CLGG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3252	17815	NM_017015	NNN	beta-glucuronidase, glucuronidase, beta amino acid N-acyltransferase (glycine N-choyltransferase), bile acid-Coenzyme A: amino acid N-acyltransferase	ESTs, Highly similar to A26581 beta-glucuronidase [H.sapiens], SMA3, beta-glucuronidase structural, glucuronidase, beta
2866	1531	D43964	OO, PP, QQ, PPP, QQQ	bile acid Coenzyme A: amino acid N-acyltransferase	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens], Mus musculus, Similar to bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choyltransferase), clone MGC:19156 IMAGE:4220620, mRNA, complete cds, bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choyltransferase), bile acid-Coenzyme A: amino acid N-acyltransferase, expressed sequence A1118337
889	22504	AA944827	Q, R	bone morphogenetic protein 2	ESTs, Highly similar to BMP2_RAT Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A) [R.norvegicus], ESTs, Weakly similar to GDF3 MOUSE GROWTH/DIFFERENTIATION FACTOR 3 PRECURSOR [M.musculus], bone morphogenetic protein 2, growth differentiation factor 5 (cartilage-derived morphogenetic protein-1), nodal
3235	397	NM_013214	I, J, U, FF, BBB	brain acyl-CoA hydrolase	
3235	20851	NM_013214	BBB, CCC, RRR, SSS	brain acyl-CoA hydrolase	
4136	396	U49694	NNN	brain acyl-CoA hydrolase	

TABLE 3						
Attorney Docket 4321-5033-01WO Document No. 1935323.1						
Seq ID	GLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2925	17284	J02827	VV, XX, YY, EEE, MMM	branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disease), branched chain ketoacid dehydrogenase E1, alpha polypeptide		
1990	5232	A1168942	WW	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease), branched chain ketoacid dehydrogenase E1, beta polypeptide	EST, Highly similar to ODBB_RAT 2-OXOISVALERATE DEHYDROGENASE BETA SUBUNIT, MITOCHONDRIAL PRECURSOR (BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPONENT BETA CHAIN (E1)) (BCKDH E1-BETA) [R.norvegicus], branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease), branched chain ketoacid dehydrogenase E1, beta polypeptide	
4123	433	U37142	RR	brevican, chondroitin sulfate proteoglycan BEHAB/brevican		
2969	1632	L27487	GG	calcitonin receptor-like calcium/calmodulin-dependent protein kinase (CaM kinase) II beta, calcium/calmodulin-dependent protein kinase II, beta	calcitonin receptor-like	
3430	17976	NM_021739	Z, AA			

TABLE 3						Attorney Docket 449241-50338-01WO Document No. 1935823.1	
Seq ID	CLC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
3711	19191	NM_031969	O, P	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence AI327027, expressed sequence AL024000, troponin C, fast skeletal		
3711	25802	NM_031969	EEE, MMM	calmodulin 1, calmodulin 1 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence AI327027, expressed sequence AL024000, troponin C, fast skeletal		
3342	20809	NM_017326	K	calmodulin 2, calmodulin 2 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence AI327027, expressed sequence AL024000, troponin C, fast skeletal		
880	15476	AA944426	ZZ, AAA	calmodulin 3, calmodulin 3 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence AI327027, expressed sequence AL024000, troponin C, fast skeletal		
3066	20518	NM_012518	R	calmodulin 3, calmodulin 3 (phosphorylase kinase, delta)	RIKEN cDNA 2310068O22 gene, calmodulin 1, calmodulin 1 (phosphorylase kinase, delta), calmodulin 2, calmodulin 2 (phosphorylase kinase, delta), calmodulin 3, calmodulin-like 3, centrin 1, centrin, EF-hand protein, 1, expressed sequence AI327027, expressed sequence AL024000, troponin C, fast skeletal		
3360	20863	NM_019152	D	calpain 1, calpain 1, (mu/l) large subunit	ESTs, Weakly similar to CAN1_MOUSE CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE) [M.musculus], calpain 1, calpain 11, small optic lobes homolog (Drosophila)		
3281	21538	NM_017116	P	calpain 2, calpain 2, (m/II) large subunit	RIKEN cDNA 2600002E23 gene, calpain 12, calpain 2, calpain 2, (m/II) large subunit		
4176	1084	U89514	UU	calpain 9 (nCL-4)	EST, Moderately similar to CAN3_MOUSE CALPAIN P94, LARGE [M.musculus], ESTs, Highly similar to A56218 calpain [H.sapiens], RIKEN cDNA 2310005G05 gene, calpain 3, calpain 3, (p94), calpain 9 (nCL-4), expressed sequence AI323605, programmed cell death 6		

TABLE 3						
Attorney Docket 4921-5038-01WO Document No. 1935323.1						
Seq. ID	GLCC ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
593	17080	AA892814	M	calpain, small subunit 1	EST, Moderately similar to CAN3 MOUSE CALPAIN P94, LARGE [M.musculus], ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus], Mus musculus, Similar to grancalcin, EF-hand calcium binding protein, clone MGC:29240 IMAGE:5044040, mRNA, complete cds, RIKEN cDNA 2310005G05 gene, calpain 3, calpain, small subunit 1, expressed sequence AI323605, sorcin	
4141	17078	U53859	M	calpain, small subunit 1	EST, Moderately similar to CAN3 MOUSE CALPAIN P94, LARGE [M.musculus], ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus], Mus musculus, Similar to grancalcin, EF-hand calcium binding protein, clone MGC:29240 IMAGE:5044040, mRNA, complete cds, RIKEN cDNA 2310005G05 gene, calpain 3, calpain, small subunit 1, expressed sequence AI323605, sorcin	
4141	17079	U53859	M	calpain, small subunit 1	EST, Moderately similar to CAN3 MOUSE CALPAIN P94, LARGE [M.musculus], ESTs, Weakly similar to A55143 calpain (EC 3.4.22.17) light chain - rat (fragment) [R.norvegicus], Mus musculus, Similar to grancalcin, EF-hand calcium binding protein, clone MGC:29240 IMAGE:5044040, mRNA, complete cds, RIKEN cDNA 2310005G05 gene, calpain 3, calpain, small subunit 1, expressed sequence AI323605, sorcin	
3401	23491	NM_019359	C, E, DD, JJ, MM, HHH, TTT	calponin 3, acidic	ESTs, Moderately similar to CALPONIN H1, SMOOTH MUSCLE [M.musculus], calponin 1, calponin 2, calponin 3, acidic	
1583	169	A1045171	E	calsequestrin 2, calsequestrin 2 (cardiac muscle)	ESTs, Highly similar to CAQS MOUSE CALSEQUESTRIN, SKELETAL MUSCLE ISOFORM PRECURSOR [M.musculus], ESTs, Moderately similar to CAQC_RAT CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM PRECURSOR [R.norvegicus], calsequestrin 1, calsequestrin 1 (fast-twitch, skeletal muscle), calsequestrin 2, calsequestrin 2 (cardiac muscle)	

TABLE 3						Attorney Docket 44921-5038-01WO Document No. 1935328.1
Seq ID	CLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3267	20649	NM_017072	L, WW	carbamoyl-phosphate synthetase 1, carbamoyl-phosphate synthetase 1, mitochondrial	DNA segment, Chr 1, University of California at Los Angeles 3, ESTs, Moderately similar to JQ1348 carbamoyl-phosphate synthase [H.sapiens], ESTs, Weakly similar to CP5M RAT CARBAMOYL-PHOSPHATE SYNTHASE [R.norvegicus], Mus musculus, Similar to Propionyl Coenzyme A carboxylase, alpha polypeptide, clone MGC:11973 IMAGE:3601148, mRNA, complete cds, carbamoyl-phosphate synthetase 1, mitochondrial, carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase, pyruvate decarboxylase	
3388	15057	NM_019291	JJ	carbonic anhydrase 2, carbonic anhydrase II	EST, Weakly similar to CRMS2 carbonic dehydratase [M.musculus], ESTs, Weakly similar to CAH2_RAT Carbonic anhydrase II (Carbonate dehydratase II) (CA-II) [R.norvegicus], carbonic anhydrase 2, carbonic anhydrase I, carbonic anhydrase II, carbonic anhydrase VIII, carbonic anhydrase-like sequence 1	
204	6018	AA819140	BB, CC, PPP, QQQ	carbonic anhydrase 3, carbonic anhydrase III, muscle specific	ESTs, Moderately similar to 1205233A anhydrase, carbonic [H.sapiens], Mus musculus adult male xiphoid cartilage cDNA, RIKEN full-length enriched library, clone:5230400J22:carbonic anhydrase 3, full insert sequence, carbonic anhydrase 1, carbonic anhydrase 3, carbonic anhydrase III, muscle specific	
3389	6017	NM_019292	A, B, S, X, Y, GGG, HHH, General Core Tox Markers	carbonic anhydrase 3, carbonic anhydrase III, muscle specific	ESTs, Moderately similar to 1205233A anhydrase, carbonic [H.sapiens], Mus musculus adult male xiphoid cartilage cDNA, RIKEN full-length enriched library, clone:5230400J22:carbonic anhydrase 3, full insert sequence, carbonic anhydrase 1, carbonic anhydrase 3, carbonic anhydrase III, muscle specific	
3933	20879	NM_133295	D, V, NN, OO, FFF	carboxylesterase 3, carboxylesterase 3 (brain)	ESTs, Weakly similar to A41010 carboxylesterase [H.sapiens], Mus musculus, Similar to carboxylesterase 2 (intestine, liver), clone MGC:18908 IMAGE:4241028, mRNA, complete cds, Mus musculus, clone MGC:18894 IMAGE:4239756, mRNA, complete cds, RIKEN cDNA 2310039D24 gene, T-complex expressed gene 5, carboxylesterase 1, carboxylesterase 1 (monocyte/macrophage serine esterase 1), carboxylesterase 3, carboxylesterase 3 (brain), carboxylesterase-related protein esterase 22	

TABLE 3						
Seq. ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935323.1
3933	20880	NM_133295	LL	carboxylesterase 3, carboxylesterase 3 (brain)	ESTs, Weakly similar to A41010 carboxylesterase [H.sapiens], Mus musculus, Similar to carboxylesterase 2 (intestine, liver), clone MGC:18908 IMAGE:4241028, mRNA, complete cds, Mus musculus, clone MGC:18894 IMAGE:4239756, mRNA, complete cds, RIKEN cDNA 2310039D24 gene, T-complex expressed gene 5, carboxylesterase 1, carboxylesterase 1 (monocyte/macrophage serine esterase 1), carboxylesterase 3, carboxylesterase 3 (brain), carboxylesterase-related protein, esterase 22	
1188	3062	AA998857	H, T, GG, PPP, QQQ	carboxypeptidase B2 (plasma), carboxypeptidase B2 (plasma), carboxypeptidase U)	carboxypeptidase B2 (plasma), carboxypeptidase B2 (plasma, carboxypeptidase U)	
3722	20554	NM_031987	U, LL, BBB, CCC, RRR, SSS	carnitine O-octanoyltransferase	carnitine O-octanoyltransferase	
3722	20555	NM_031987	U, FF, BBB, CCC, RRR	carnitine O-octanoyltransferase	carnitine O-octanoyltransferase	
3646	15411	NM_031559	J	carnitine palmitoyltransferase 1, liver, carnitine palmitoyltransferase I, liver	ESTs, Weakly similar to CPT1 MOUSE CARNITINE O-PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM [M.musculus], carnitine palmitoyltransferase 1, liver, carnitine palmitoyltransferase I, liver	
3234	20854	NM_013200	Z, AA	carnitine palmitoyltransferase 1, muscle, carnitine palmitoyltransferase I, muscle	carnitine palmitoyltransferase 1, muscle, carnitine palmitoyltransferase I, muscle	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3234	20855	NM_013200	BBB	carnitine palmitoyltransferase 1, muscle, carnitine palmitoyltransferase I, muscle	carnitine palmitoyltransferase 1, muscle, carnitine palmitoyltransferase I, muscle			
2932	1977	J05470	U, BBB, CCC, RRR, SSS	carnitine palmitoyltransferase 2, carnitine palmitoyltransferase II	carnitine palmitoyltransferase 2, carnitine palmitoyltransferase II			
2688	2746	A1235291	Z, AA	casein kinase 1, alpha 1	ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, casein kinase 1, delta			
3804	20243	NM_053615	VV	casein kinase 1, alpha 1	ESTs, Weakly similar to casein kinase [M.musculus], RIKEN cDNA 2610208K14 gene, RIKEN cDNA 3300002K07 gene, casein kinase 1, alpha 1, casein kinase 1, delta			
3067	15740	NM_012520	LL	catalase, catalase 1	catalase, catalase 1			
3067	15741	NM_012520	EEE, MMM	catalase, catalase 1	catalase, catalase 1			
3071	11115	NM_012531	M	catechol-O-methyltransferase	RIKEN cDNA 6330414C15 gene, catechol-O-methyltransferase			
3071	11116	NM_012531	M	catechol-O-methyltransferase	RIKEN cDNA 6330414C15 gene, catechol-O-methyltransferase			
3276	2149	NM_017097	H, U, GGG, General Core Tox Markers, General Alternate	cathepsin C	RIKEN cDNA 4921537117 gene, cathepsin C			

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	CLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3276	2150	NM_017097	LL, FFF, GGG, OOO, RRR, SSS, UUU, General Core Tox Markers, General Alternate	cathepsin C	RIKEN cDNA 4921537117 gene, cathepsin C			
2218	3431	AI176595	C, D, W, BB, CC, FF, KKK, NNN, OOO, General Core Tox Markers, General Alternate	cathepsin L	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 4930486L24 gene, cathepsin L, expressed sequence AA408230			
3229	3430	NM_013156	C, Q, W, MM, OOO, TTT	cathepsin L	ESTs, Weakly similar to CATL MOUSE CATHEPSIN L PRECURSOR [M.musculus], RIKEN cDNA 4930486L24 gene, cathepsin L, expressed sequence AA408230			
3534	21238	NM_024125	I, J, MM, TTT	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), beta			
3534	21239	NM_024125	MM, TTT, General Alternate	CCAAT/enhancer binding protein (C/EBP), beta	CCAAT/enhancer binding protein (C/EBP), beta			
3228	21681	NM_013154	D, GG, HH	CCAAT/enhancer binding protein (C/EBP), delta	CCAAT/enhancer binding protein (C/EBP), delta			

TABLE 3						
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3693	17941	NM_031812	T, XX, YY, PPP, QQQ	CD164 antigen, CD164 antigen, sialomucin	CD164 antigen, CD164 antigen, pro-oncosis receptor inducing membrane injury gene	
3642	16048	NM_031541	NN, OO	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, scavenger receptor class B1	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1, scavenger receptor class B1	
3647	18315	NM_031561	A, B, FF, BBB, CCC, RRR, SSS	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	
3647	18316	NM_031561	A, B, II, BBB, CCC, RRR	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	
3647	18318	NM_031561	BBB, HHH, RRR	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	

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TABLE 3						
Seq ID	GLCG ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5088-01WO Document No. 1935828.1
3647	18319	NM_031561	BBB, CCC	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	CD36 antigen, CD36 antigen (collagen type I receptor, thrombospondin receptor)	
2857	2005	D29646	NN, OO, VV	CD38 antigen, CD38 antigen (p45)	CD38 antigen, CD38 antigen (p45)	
3368	22062	NM_019195	CCC	CD47 antigen (Rh-related antigen, integrin-associated signal transducer), integrin-associated protein	CD47 antigen (Rh-related antigen, integrin-associated signal transducer), RIKEN cDNA 1700026J12 gene, integrin-associated protein	
3368	22063	NM_019195	BBB, CCC	CD47 antigen (Rh-related antigen, integrin-associated signal transducer), integrin-associated protein	CD47 antigen (Rh-related antigen, integrin-associated signal transducer), RIKEN cDNA 1700026J12 gene, integrin-associated protein	
3068	16214	NM_012523	O, P	CD53 antigen	CD53 antigen, ESTs, Weakly similar to A39574 leukocyte antigen OX-44 - rat [R.norvegicus], ESTs, Weakly similar to CD53 MOUSE LEUKOCYTE SURFACE ANTIGEN CD53 [M.musculus], RIKEN cDNA 2610042G18 gene, RIKEN cDNA 9030418M05 gene, solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34 kDa), member 17, tetraspan transmembrane 4 super family, transmembrane 4 superfamily member 7	

TABLE 3					Attorney Docket 44921-5038-01WO Document No. 1995828.1	
Seq ID	GLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
147	2830	AA818025	XX, YY	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen		
147	2831	AA818025	L, XX, YY	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344), CD59a antigen		
1153	1437	AA997844	V	CD63 antigen (melanoma 1 antigen), Cd63 antigen	CD63 antigen (melanoma 1 antigen), Cd63 antigen, EST, Weakly similar to CD63 MOUSE CD63 ANTIGEN [M.musculus], ESTs, Weakly similar to CD63_RAT CD63 antigen (AD1 antigen) [R.norvegicus], Mus musculus, clone MGC:36554 IMAGE:4954874, mRNA, complete cds, RIKEN cDNA 1300010A20 gene, expressed sequence C75951, expressed sequence C80071, transmembrane 4 superfamily member 2	
4236	1435	X61654	O, P	CD63 antigen (melanoma 1 antigen), Cd63 antigen	CD63 antigen (melanoma 1 antigen), Cd63 antigen, EST, Weakly similar to CD63 MOUSE CD63 ANTIGEN [M.musculus], ESTs, Weakly similar to CD63_RAT CD63 antigen (AD1 antigen) [R.norvegicus], Mus musculus, clone MGC:36554 IMAGE:4954874, mRNA, complete cds, RIKEN cDNA 1300010A20 gene, expressed sequence C75951, expressed sequence C80071, transmembrane 4 superfamily member 2	

TABLE 3						Attorney Docket 44924-5088-01WO Document No. 1993828.1	
Seq. ID	GLCG ID No.	GenBank Accor. RefSeqID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
3805	1178	NM_053620	PP, QQ	CDC42 binding protein kinase beta (DMPK-like), Cdc42 binding protein kinase beta	CDC42 binding protein kinase beta (DMPK-like), DNA segment, Chr X, Immunex 40, expressed, ESTs, Highly similar to Cdc42-binding protein kinase beta [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to Cdc42-binding protein kinase beta [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 1190006F07 gene, dystrophin myotonia kinase, B15		
1216	2016	AF000578	PPP, QQQ	CDC5 cell division cycle 5-like (S. pombe), cell division cycle 5-like (S. pombe)	cell division cycle 5-like (S. pombe), myeloblastosis oncogene-like 1, myeloblastosis oncogene-like 2, v-myb myeloblastosis viral oncogene homolog (avian), v-myb myeloblastosis viral oncogene homolog (avian)-like 2		
3683	13185	NM_031755	GG, RR	CEA-related cell adhesion molecule 1, carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein), carcinoembryonic antigen-related cell adhesion molecule 5, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), carcinoembryonic antigen-related cell adhesion molecule 8, pregnancy specific beta-1-glycoprotein 2, pregnancy specific beta-1-glycoprotein 4		
3683	13186	NM_031755	LL, RR	CEA-related cell adhesion molecule 1, carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein), carcinoembryonic antigen-related cell adhesion molecule 5, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), carcinoembryonic antigen-related cell adhesion molecule 8, pregnancy specific beta-1-glycoprotein 2, pregnancy specific beta-1-glycoprotein 4		
3683	13187	NM_031755	GG, OO	CEA-related cell adhesion molecule 1, carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein), carcinoembryonic antigen-related cell adhesion molecule 5, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), carcinoembryonic antigen-related cell adhesion molecule 8, pregnancy specific beta-1-glycoprotein 2, pregnancy specific beta-1-glycoprotein 4		

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1995823.1						
Seq ID	GLCC ID No.	Genbank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
65	13683	AA799788	General Alternate	cell division cycle 34	ESTs, Highly similar to A41222 ubiquitin--protein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed sequence A1327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C	
187	13684	AA818770	H	cell division cycle 34	ESTs, Highly similar to A41222 ubiquitin--protein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed sequence A1327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C	
2973	13682	L38482	MM, FFF, TTT, General Alternate	cell division cycle 34	ESTs, Highly similar to A41222 ubiquitin--protein ligase [H.sapiens], ESTs, Weakly similar to UBC2_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD [M.musculus], RIKEN cDNA 2610301N02 gene, cell division cycle 34, expressed sequence A1327276, ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae), ubiquitin-conjugating enzyme E2C	
785	22843	AA925473	VV	cell division cycle 42 (GTP binding protein, 25kD), cell division cycle 42 homolog (S. cerevisiae)	RIKEN cDNA 4930544G11 gene, RIKEN cDNA 5830400A04 gene, cell division cycle 42 (GTP binding protein, 25kD), p135 ras-related homolog A2, ras homolog 9 (RhoC), ras homolog A2, ras homolog gene family, member C	
2403	22845	A1227887	K	cell division cycle 42 (GTP binding protein, 25kD), cell division cycle 42 homolog (S. cerevisiae)	RIKEN cDNA 4930544G11 gene, RIKEN cDNA 5830400A04 gene, cell division cycle 42 (GTP binding protein, 25kD), p135 ras-related homolog A2, ras homolog 9 (RhoC), ras homolog A2, ras homolog gene family, member C	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935323.1
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
1359	16521	AI010470	FF	ceruloplasmin, ceruloplasmin (ferroxidase)	DNA segment, Chr 3, ERATO Doi 555, expressed, EST, Highly similar to FA8_HUMAN COAGULATION FACTOR VIII PRECURSOR [H.sapiens], ESTs, Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs, Weakly similar to CERU_RAT CERULOPLASMIN PRECURSOR (FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase [H.sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII, procoagulant component (hemophilia A)		
3072	16519	NM_012532	BB, CC, NN, SSS, UUU	ceruloplasmin, ceruloplasmin (ferroxidase)	DNA segment, Chr 3, ERATO Doi 555, expressed, EST, Highly similar to FA8_HUMAN COAGULATION FACTOR VIII PRECURSOR [H.sapiens], ESTs, Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs, Weakly similar to CERU_RAT CERULOPLASMIN PRECURSOR (FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase [H.sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII, procoagulant component (hemophilia A)		
3072	16520	NM_012532	BB, CC	ceruloplasmin, ceruloplasmin (ferroxidase)	DNA segment, Chr 3, ERATO Doi 555, expressed, EST, Highly similar to FA8_HUMAN COAGULATION FACTOR VIII PRECURSOR [H.sapiens], ESTs, Weakly similar to CERU MOUSE CERULOPLASMIN PRECURSOR [M.musculus], ESTs, Weakly similar to CERU_RAT CERULOPLASMIN PRECURSOR (FERROXIDASE) [R.norvegicus], ESTs, Weakly similar to KUHU ferroxidase [H.sapiens], ceruloplasmin, ceruloplasmin (ferroxidase), coagulation factor VIII, procoagulant component (hemophilia A)		
3676	19048	NM_031719	RR, SS	chloride channel, nucleotide-sensitive, 1A	chloride channel, nucleotide-sensitive, 1A		
4266	447	X79208	RR	cholecystokinin B receptor	cholecystokinin B receptor		
2843	1306	D10262	GG	choline kinase	Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110043M12:choline kinase, full insert sequence, choline kinase, hypothetical protein FLJ10761		

TABLE 3						
Seq ID	GLGC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Human Homologous Sequence Cluster Title
1205	3512	AB006607	BBB, CCC, RRR	choline kinase-like	EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE [M.musculus], ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus], Homo sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA, complete cds, RIKEN cDNA 4930555L11 gene, choline kinase-like, ethanolamine kinase, expressed sequence A197444	EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE [M.musculus], ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus], Homo sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA, complete cds, RIKEN cDNA 4930555L11 gene, choline kinase-like, ethanolamine kinase, expressed sequence A197444
1205	3513	AB006607	BBB, RRR, SSS	choline kinase-like	EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE [M.musculus], ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus], Homo sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA, complete cds, RIKEN cDNA 4930555L11 gene, choline kinase-like, ethanolamine kinase, expressed sequence A197444	EST, Weakly similar to KICE MOUSE CHOLINE/ETHANOLAMINE KINASE [M.musculus], ESTs, Weakly similar to KICE_RAT Choline/ethanolamine kinase [Includes: Choline kinase (CK); Ethanolamine kinase (EK)] [R.norvegicus], Homo sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA, complete cds, RIKEN cDNA 4930555L11 gene, choline kinase-like, ethanolamine kinase, expressed sequence A197444
3069	24433	NM_012527	PP, QQ	cholinergic receptor, muscarinic 3, cholinergic receptor, muscarinic 3, cardiac	cholinergic receptor, muscarinic 3, cholinergic receptor, muscarinic 3, cardiac, cholinergic receptor, muscarinic 5	cholinergic receptor, muscarinic 3, cholinergic receptor, muscarinic 3, cardiac, cholinergic receptor, muscarinic 5
3359	20373	NM_019145	D, Z, AA	cholinergic receptor, nicotinic, gamma polypeptide	cholinergic receptor, nicotinic, gamma polypeptide	cholinergic receptor, nicotinic, gamma polypeptide
3671	13706	NM_031699	QQ	claudin 1	ESTs, Weakly similar to claudin 1 [Rattus norvegicus] [R.norvegicus], Homo sapiens, clone MGC:23949 IMAGE:4243903, mRNA, complete cds, Mus musculus claudin 19 mRNA, complete cds, claudin 1, claudin 18	ESTs, Weakly similar to claudin 1 [Rattus norvegicus] [R.norvegicus], Homo sapiens, clone MGC:23949 IMAGE:4243903, mRNA, complete cds, Mus musculus claudin 19 mRNA, complete cds, claudin 1, claudin 18
3672	20404	NM_031700	K, HH, TT	claudin 3	claudin 3	claudin 3
3519	24838	NM_022924	PPP, QQQ	coagulation factor II, coagulation factor II (thrombin)	coagulation factor II, coagulation factor II (thrombin)	coagulation factor II, coagulation factor II (thrombin)

TABLE 3						
Seq ID	CLGG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935828.1
3006	25430	M26247	N, WW, UUU	coagulation factor IX, coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)		
3287	10503	NM_017143	VV, FFF, GGG, General Alternate	coagulation factor X	ESTs, Weakly similar to 2209311A coagulation factor X [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to FA7 MOUSE COAGULATION FACTOR VII PRECURSOR [M.musculus], coagulation factor X, proline-rich Glu (G-carboxyglutamic acid) polypeptide 1, proline-rich Glu (G-carboxyglutamic acid) polypeptide 2	
3287	10504	NM_017143	S, GG, WV, PPP, QQQ	coagulation factor X	ESTs, Weakly similar to 2209311A coagulation factor X [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to FA7 MOUSE COAGULATION FACTOR VII PRECURSOR [M.musculus], coagulation factor X, proline-rich Glu (G-carboxyglutamic acid) polypeptide 1, proline-rich Glu (G-carboxyglutamic acid) polypeptide 2	
3677	12052	NM_031722	CC, WW	coated vesicle membrane protein	ESTs, Weakly similar to coated vesicle membrane protein [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to P24_MOUSE COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (P24A) [M.musculus], RIKEN cDNA 1110014C03 gene, RIKEN cDNA 1200002G13 gene, RIKEN cDNA 1810020N21 gene, RIKEN cDNA 3930401E15 gene, RIKEN cDNA 4432412D15 gene, coated vesicle membrane protein, integral type I protein, putative T1/ST2 receptor binding protein	
3907	19831	NM_080781	U	coatamer protein complex, subunit beta, coatamer protein complex, subunit beta 1	coatamer protein complex, subunit beta, coatamer protein complex, subunit beta 1	

TABLE 3						
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1995328.1
3289	15365	NM_017147	VV, FFF, General Alternate	cofilin 1 (non-muscle), cofilin 1, non-muscle	cofilin 1 (non-muscle), cofilin 1, non-muscle, cofilin 2 (muscle), expressed sequence AW987265	
2855	16610	D28557	D, PP, QQ, HHH, General Alternate	cold shock domain protein A	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:261020519:Y box protein 1, full insert sequence, Mus musculus Y-box binding protein (oxyR) mRNA, partial cds, cold shock domain protein A	
3007	15571	M27207	M, II	collagen, type I, alpha 1, procollagen, type I, alpha 1	EST, Weakly similar to CA11_HUMAN COLLAGEN ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to ALPHA 1(I) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR [M.musculus], F-box only protein 29, Mus musculus, Similar to RIKEN cDNA 170005112 gene, clone MGC:28741 IMAGE:4481590, mRNA, complete cds, collagen, type IV, alpha 3 (Goodpasture antigen), expressed sequence AW742721, procollagen, type I, alpha 1, procollagen, type IV, alpha 1, procollagen, type IV, alpha 4, procollagen, type IV, alpha 5, procollagen, type VI, alpha 1, putative emu1	
505	21674	AA891828	SSS	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
2160	21676	A1175101	SSS, UUU	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
3754	6155	NM_053356	G, M, II	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
3754	6156	NM_053356	M	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	

TABLE 3						
Seq ID	CLGG ID No	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01W0 Document No. 1935323.1
3754	6157	NM_053356	S	collagen, type I, alpha 2, procollagen, type I, alpha 2	F-box only protein 29, Mus musculus, clone IMAGE:5323568, mRNA, partial cds, collagen, type VI, alpha 3, procollagen, type I, alpha 2, prostate tumor over expressed gene 1, retinoblastoma binding protein 1	
3001	16427	M21354	M, II	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Moderately similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA13_MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus], EST, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to S41067 collagen alpha 1(III) chain - rat [R.norvegicus], Mus musculus, Similar to putative protein phosphatase 1 nuclear targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN cDNA 2010011D20 gene, cleavage and polyadenylation specific factor 6, 68kD subunit, collagen type V, alpha 2, collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	
4254	16426	X70369	M, II	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	EST, Highly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Moderately similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], EST, Weakly similar to CA13_MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus], EST, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens], ESTs, Weakly similar to S41067 collagen alpha 1(III) chain - rat [R.norvegicus], Mus musculus, Similar to putative protein phosphatase 1 nuclear targeting subunit, clone IMAGE:3157989, mRNA, partial cds, RIKEN cDNA 2010011D20 gene, cleavage and polyadenylation specific factor 6, 68kD subunit, collagen type V, alpha 2, collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant), procollagen, type III, alpha 1	

TABLE 3					
Seq ID	GenBank Accor ID No.	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Human Homologous Sequence Cluster Title
3970	25237	NM_134452	NNN	collagen, type V, alpha 1, procollagen, type V, alpha 1	EST, Weakly similar to CGHU1V collagen alpha 1(V) chain precursor [H.sapiens], Homo sapiens cDNA FLJ30442 fis, clone BRACE2009212, Homo sapiens proline-rich acidic protein mRNA, complete cds, Mus musculus, clone IMAGE:3490511, mRNA, partial cds, collagen, type V, alpha 1, collagen, type XI, alpha 1, endoplasmic reticulum chaperone SIL1, homolog of yeast, hypothetical protein MGC2705, procollagen, type V, alpha 1, procollagen, type V, alpha 3, procollagen, type XI, alpha 1
4079	9687	S79214	G, H	collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia), procollagen, type X, alpha 1	ESTs, Highly similar to 1917150A collagen:SUBUNIT=alpha1:ISOTYPE=VIII [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to CA18 MOUSE COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR [M.musculus], ESTs, Weakly similar to CGHU1D collagen alpha 1(X) chain precursor [H.sapiens], RIKEN cDNA 1810033K05 gene, collagen, type VIII, alpha 1, collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia), procollagen, type VIII, alpha 1, procollagen, type X, alpha 1
4138	1960	U52102	FF	collapsin response mediator protein 1	ESTs, Weakly similar to DPY1 MOUSE DIHYDROXYRIMIDINASE RELATED PROTEIN-1 [M.musculus], Ellis van Creveld syndrome, collapsin response mediator protein 1
3382	15259	NM_019259	QQ, General Alternate	complement component 1, q subcomponent binding protein	complement component 1, q subcomponent binding protein
3383	21443	NM_019262	NN	complement component 1, q subcomponent, beta polypeptide	complement component 1, q subcomponent binding protein
3246	1958	NM_016994	L, S, HH	complement component 3	EST, Weakly similar to CO3_RAT COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN] [R.norvegicus], complement component 3, complement component 4 (within H-2S), complement component 4A, complement component 4B, expressed sequence A1663842, hemolytic complement

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935328.1						
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
4212	1959	X52477	S, HH, MM, SS, TTT	complement component 3	EST, Weakly similar to CO3_RAT COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN] [R.norvegicus], complement component 3, complement component 4 (within H-2S), complement component 4A, complement component 4B, expressed sequence A1663842, hemolytic complement	
4130	15851	U42719	BBB, CCC	complement component 4 (within H-2S), complement component 4B	complement component 4 (within H-2S), complement component 4A	
4290	1561	Z50052	E, I, J, BB, JJ, EEE, GGG, III, JJJ, MMM, SSS	complement component 4 binding protein, beta, complement component 4 binding protein, pseudogene 1	complement component 4 binding protein, beta	
3065	563	NM_012516	BB, JJ, KK	complement component 4 binding protein, complement component 4 binding protein, alpha	ESTs, Moderately similar to NBHUC4 C4b-binding protein alpha chain precursor [H.sapiens], complement component (3d/Epstein Barr virus) receptor 2, complement component 4 binding protein, complement component 4 binding protein, alpha, complement receptor 2, decay-accelerating factor, expressed sequence A1195242, zona pellucida 3 receptor	
1203	926	AB003042	O, P, VV	complement component 5 receptor 1 (C5a ligand), complement component 5, receptor 1	ESTs, Weakly similar to GPRY_MOUSE PROBABLE G PROTEIN-COUPLED RECEPTOR GPR34 [M.musculus], complement component 5 receptor 1 (C5a ligand), complement component 5, receptor 1	

TABLE 3					Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1215	954	AF000114	D	contactin associated protein 1	EST, Weakly similar to T14158 neurexin IV - mouse [M.musculus], EST, Weakly similar to T31083 paranodin - rat [R.norvegicus], ESTs, Weakly similar to T14158 neurexin IV - mouse [M.musculus], ESTs, Weakly similar to T31083 paranodin - rat [R.norvegicus], contactin associated protein 1	
3374	15347	NM_019222	P, T	coronin, actin binding protein 1B, coronin, actin-binding protein, 1B	ESTs, Moderately similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus], coronin 6, coronin, actin binding protein 1B, coronin, actin binding protein 1C, coronin, actin binding protein, 1C, hypothetical protein DKFZp7621166	
3374	15348	NM_019222	X, Y	coronin, actin binding protein 1B, coronin, actin-binding protein, 1B	ESTs, Moderately similar to CO1B_RAT Coronin 1B (Coronin 2) [R.norvegicus], coronin 6, coronin, actin binding protein 1B, coronin, actin binding protein 1C, coronin, actin binding protein, 1C, hypothetical protein DKFZp7621166	
3275	6013	NM_017096	DD, KKK, NNN, PPP, QQQ	C-reactive protein, pentraxin-related, C-reactive protein, pentaxin related	C-reactive protein, pentaxin related, Homo sapiens, Similar to C-reactive protein, pentraxin-related, clone MGC:22631 IMAGE:4766715, mRNA, complete cds	
3070	4467	NM_012529	ZZ, AAA	creatine kinase, brain		
3369	18573	NM_019201	A, B, KK, HHH	C-terminal binding protein 1	C-terminal binding protein 1, Homo sapiens mRNA; cDNA DKFZp434B0914 (from clone DKFZp434B0914); partial cds	
1808	2057	A1102579	UUU	cyclic AMP phosphoprotein, 19 kDa		
1480	2866	A1029058	Z, AA	cyclin D1, cyclin D1 (PRAD1; parathyroid adenomatosis 1)	EST, Moderately similar to JC2342 cyclin D1 - rat [R.norvegicus], cyclin D1 (PRAD1; parathyroid adenomatosis 1)	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1995828.1	
Seq ID	GLCG ID No.	GenBank Accession RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
2849	25041	D14014	E, HH	cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis 1)	EST, Moderately similar to JC2342 cyclin D1 - rat [R.norvegicus], cyclin D1, cyclin D1 (PRAD1: parathyroid adenomatosis 1)			
3178	20755	NM_012923	F, R, II, VV, General Alternate	cyclin G, cyclin G1	ESTs, Weakly similar to CCG1_RAT Cyclin G1 (Cyclin G) [R.norvegicus], cyclin G, cyclin G2, cyclin I			
3178	20757	NM_012923	F, II, FFF, General Core Tox Markers	cyclin G, cyclin G1	ESTs, Weakly similar to CCG1_RAT Cyclin G1 (Cyclin G) [R.norvegicus], cyclin G, cyclin G2, cyclin I			
3741	12577	NM_052981	A, D, V, BB, III, JJJ	cyclin H	cyclin H			
3048	291	M88347	JJ	cystathionine beta-synthase, cystathionine-beta-synthase	cystathionine-beta-synthase, expressed sequence AU040765, serine dehydratase, serine racemase			
1287	2853	A1008888	B, O, BB, CC, GG, NN, OO	cystatin B, cystatin B (stefin B)	cystatin B, cystatin B (stefin B)			
1287	2854	A1008888	O	cystatin B, cystatin B (stefin B)	cystatin B, cystatin B (stefin B)			
2743	2855	A1236707	EEE, MMM	cystatin B, cystatin B (stefin B)	cystatin B, cystatin B (stefin B)			
2527	24326	A1231292	X, Y	cystatin C, cystatin C (amyloid angiopathy and cerebral hemorrhage)	ESTs, Moderately similar to CYTC MOUSE CYSTATIN C PRECURSOR [M.musculus], ESTs, Weakly similar to CYTC MOUSE CYSTATIN C PRECURSOR [M.musculus], RIKEN cDNA 1110017E11 gene, RIKEN cDNA 9230101F08 gene, cystatin C, cystatin C (amyloid angiopathy and cerebral hemorrhage), cystatin D, cystatin S, cystatin SA, cystatin SN			

TABLE 3						
Attorney/Docket 4921-5038-01W0 Document No. 1935828.1						
Seq. ID	GLCG ID No.	Genbank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2852	2515	D17512	E, GG, HH, GGG	cysteine and glycine-rich protein 2, cysteine-rich protein 2,	RIKEN cDNA 0610010123 gene, cysteine-rich protein 2, thymus LIM protein	
4131	19543	U44948	General Alternate	cysteine and glycine-rich protein 2, cysteine-rich protein 2,	RIKEN cDNA 0610010123 gene, cysteine-rich protein 2, thymus LIM protein	
3740	15028	NM_052809	A, B, T, LLL	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type I	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type I	
3740	25024	NM_052809	A, YY	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type I	cysteine dioxygenase 1, cytosolic, cysteine dioxygenase, type I	
3308	14696	NM_017202	LL	cytochrome c oxidase subunit IV isoform 1, cytochrome c oxidase, subunit IVa	EST, Weakly similar to COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR [H.sapiens], ESTs, Moderately similar to COX4_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR [H.sapiens], cytochrome c oxidase subunit IV isoform 1, cytochrome c oxidase, subunit IVa	
3771	21866	NM_053472	V, RR, UU	cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IVb	cytochrome c oxidase subunit IV isoform 2, cytochrome c oxidase, subunit IVb	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935323.1						
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1872	23574	AI104520	LL	cytochrome c oxidase subunit VIa polypeptide 1, cytochrome c oxidase, subunit VI a, polypeptide 1		
4257	23576	X72757	HH, LL	cytochrome c oxidase subunit VIa polypeptide 1, cytochrome c oxidase, subunit VI a, polypeptide 1		
3147	20605	NM_012812	BB, CC	cytochrome c oxidase subunit VIa polypeptide 2, cytochrome c oxidase, subunit VI a, polypeptide 2	EST, Moderately similar to COXD_RAT Cytochrome c oxidase polypeptide VIa-heart, mitochondrial precursor (COXVIAH) [R.norvegicus], ESTs, Weakly similar to COXD MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VIA-HEART PRECURSOR [M.musculus], cytochrome c oxidase subunit VIa polypeptide 2, cytochrome c oxidase, subunit VI a, polypeptide 2	
3154	11137	NM_012839	D, MM, FFF, TTT	cytochrome c, cytochrome c, somatic		
3154	11138	NM_012839	T, JJ, KK, LL	cytochrome c, cytochrome c, somatic		

TABLE 3						
Attorney Docket 44921-5033-01WO Document No. 1935323.1						
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence	Cluster Title
3073	488	NM_012540	A, C, L, GG, HH, DDD	cytochrome P450, 1a1, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1	cytochrome P450, 1a1, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1	
3073	489	NM_012540	C, L, GG, HH	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1	cytochrome P450, 1a1, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1	
3073	20705	NM_012540	C, K, L, U, GG, HH, II, DDD, RRR	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	
3074	20703	NM_012541	C, K, L, M, U, Y, GG, HH, II, RRR, SSS	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLGC ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3074	20704	NM_012541	C, K, L, T, GG, HH, DDD	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2	cytochrome P450, 1a2, aromatic compound inducible, cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2			
3181	191	NM_012940	GG	cytochrome P450, 1b1, benz[a]anthracene inducible, cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)	cytochrome P450, 1b1, benz[a]anthracene inducible, cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile)			
3643	4010	NM_031543	EE, MM, TTT	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)				
3643	4011	NM_031543	K, O, P, FF, II, NN, OO, QQ, EEE, MMM	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)				

TABLE 3						
Attorney Docket 44921-5033-01WO Document No. 1935323.1						
Seq ID	CLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3643	4012	NM_031543	T, EE, FF, MM, EEE, MMM, TTT	cytochrome P450, 2e1, ethanol inducible, cytochrome P450, subfamily IIE (ethanol-inducible)		
3182	20928	NM_012941	T	cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	
3182	20931	NM_012941	G, H, I, J, FF, General Alternate	cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	cytochrome P450, 51, cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	
3622	12313	NM_031241	JJ, KK, HHH	cytochrome P450, 8b1, sterol 12 alpha-hydroxylase, cytochrome P450, subfamily VIIIB (sterol 12-alpha-hydroxylase), polypeptide 1	cytochrome P450, 8b1, sterol 12 alpha-hydroxylase, cytochrome P450, subfamily VIIIB (sterol 12-alpha-hydroxylase), polypeptide 1	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935928.1						
Seq ID	CLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
738	20711	AA924267	U, FF, LL, XX, BBB, CCC, RRR, SSS	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	EST, Moderately similar to I65981 fatty acid omega-hydroxylase [H.sapiens], Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837, mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11, expressed sequence AI314743	
1151	20712	AA997806	FFF	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	EST, Moderately similar to I65981 fatty acid omega-hydroxylase [H.sapiens], Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837, mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11, expressed sequence AI314743	
2992	20714	M14972	I, J, U, FF, LL, XX, YY	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	EST, Moderately similar to I65981 fatty acid omega-hydroxylase [H.sapiens], Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837, mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11, expressed sequence AI314743	
3025	20713	M57718	U, EE, FF, LL, RRR	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	EST, Moderately similar to I65981 fatty acid omega-hydroxylase [H.sapiens], Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837, mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11, expressed sequence AI314743	

TABLE 3						
Seq ID	CLGG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01W0 Document No. 1935328.1
4192	20715	X07259	J, U, DD, FF, LL, XX, QQ, RRR, SSS	cytochrome P450, subfamily IV B, polypeptide 1, cytochrome P450, subfamily IVB, polypeptide 1	EST, Moderately similar to I65981 fatty acid omega-hydroxylase [H.sapiens], Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:18880 IMAGE:4237837, mRNA, complete cds, Mus musculus, Similar to cytochrome P450, 4a10, clone MGC:25972 IMAGE:4240359, mRNA, complete cds, RIKEN cDNA A230105L22 gene, cytochrome P450, 4a10, cytochrome P450, subfamily IVA, polypeptide 11, expressed sequence A1314743	
3994	1858	NM_138907	FF, LL	cytosolic acyl-CoA thioesterase 1, mitochondrial acyl-CoA thioesterase 1, CoA thioesterase 1, peroxisomal long-chain acyl-coA thioesterase	EST, Moderately similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to MTE1_RAT Acyl coenzyme A thioester hydrolase, mitochondrial precursor (Very-long-chain acyl-CoA thioesterase) (MTE-I) [R.norvegicus], ESTs, Weakly similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], Homo sapiens cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus peroxisomal long chain acyl-CoA thioesterase 1b (Pte1b) gene, Mus musculus, Similar to bile acid Coenzyme A: amino acid N-acyltransferase (glycine N-choloyltransferase), clone MGC:19156 IMAGE:4220620, mRNA, complete cds, cytosolic acyl-CoA thioesterase 1, mitochondrial acyl-CoA thioesterase 1, peroxisomal long-chain acyl-coA thioesterase	
3623	1857	NM_031315	FF, LL	cytosolic acyl-CoA thioesterase 1, peroxisomal long-chain acyl-coA thioesterase	EST, Moderately similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], ESTs, Weakly similar to PTE2_HUMAN PEROXISOMAL ACYL-COENZYME A THIOESTER HYDROLASE 2 (PEROXISOMAL LONG-CHAIN ACYL-COA THIOESTERASE 2) (ZAP128) [H.sapiens], Homo sapiens cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus peroxisomal long chain acyl-CoA thioesterase 1b (Pte1b) gene, cytosolic acyl-CoA thioesterase 1, peroxisomal long-chain acyl-coA thioesterase	
3536	17226	NM_024131	Q, R, Y	D-dopachrome tautomerase	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D-DOPACHROME TAUTOMERASE [H.sapiens]	

TABLE 3							Attorney Docket 44924-5038-01 WO Document No. 1935828.1	
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3536	17227	NM_024131	F, N	D-dopachrome tautomerase	D-dopachrome tautomerase, EST, Moderately similar to DOPD_HUMAN D-DOPACHROME TAUTOMERASE [H.sapiens]			
4055	18356	R47042	D	decorin	RIKEN cDNA 5530600M07 gene, decorin, expressed sequence C85409, extracellular matrix protein 2, female organ and adipocyte specific			
3748	23597	NM_053323	Y	degenerative spermatocyte homolog (Drosophila), degenerative spermatocyte homolog, lipid desaturase (Drosophila)	ESTs, Moderately similar to degenerative spermatocyte homolog (Drosophila) [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2210008A03 gene, degenerative spermatocyte homolog (Drosophila), degenerative spermatocyte homolog, lipid desaturase (Drosophila)			
3428	19679	NM_021653	S, U, RR, CCC, LLL, RRR, SSS, UUU	deiodinase, iodothyronine, type I	ESTs, Moderately similar to IOD1_RAT TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIO1) (TYPE 1 DI) (5DI) [R.norvegicus], deiodinase, iodothyronine, type I			
3709	16535	NM_031853	Q, R, U, YY	diazepam binding inhibitor, diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)				
2871	811	D63704	B, L, III, JJJ, OOO, QQQ, General Core Tox Markers	dihydropyrimidinase	ESTs, Weakly similar to DPY1 MOUSE DIHYDROPYRIMIDINASE RELATED PROTEIN 1 [M.musculus], dihydropyrimidinase			

TABLE 3						
Attorney Docket 44921-5038-01WQ Document No. 1935823.1						
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence	Cluster Title
2871	812	D63704	OOQ, PPP, QQQ, General Core Tox Markers	dihydropyrimidinase	ESTs, Weakly similar to DPY1 MOUSE DIHYDROPYRIMIDINASE RELATED PROTEIN 1 [M.musculus], dihydropyrimidinase	
673	6377	AA894273	UU	dimethylarginine dimethylaminohydrolyase 1	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolyase 1; NG,NG dimethylarginine dimethylaminohydrolyase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolyase 1, dimethylarginine dimethylaminohydrolyase 2	
854	19425	AA943842	N	dimethylarginine dimethylaminohydrolyase 1	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolyase 1; NG,NG dimethylarginine dimethylaminohydrolyase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolyase 1, dimethylarginine dimethylaminohydrolyase 2	
902	19421	AA945152	S, NNN	dimethylarginine dimethylaminohydrolyase 1	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolyase 1; NG,NG dimethylarginine dimethylaminohydrolyase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolyase 1, dimethylarginine dimethylaminohydrolyase 2	
2349	19427	A1179510	EE, PP, QQ, YY	dimethylarginine dimethylaminohydrolyase 1	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolyase 1; NG,NG dimethylarginine dimethylaminohydrolyase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolyase 1, dimethylarginine dimethylaminohydrolyase 2	
4054	19428	R47028	HH	dimethylarginine dimethylaminohydrolyase 1	ESTs, Highly similar to DDH1_HUMAN NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1 [H.sapiens], ESTs, Weakly similar to dimethylarginine dimethylaminohydrolyase 1; NG,NG dimethylarginine dimethylaminohydrolyase [Rattus norvegicus] [R.norvegicus], dimethylarginine dimethylaminohydrolyase 1, dimethylarginine dimethylaminohydrolyase 2	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1995828.1						
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3140	7784	NM_012789	BB, CC, II, OO	dipeptidylpeptidase 4, dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)	ESTs, Weakly similar to DPP4 MOUSE DIPEPTIDYL PEPTIDASE IV [M.musculus], ESTs, Weakly similar to DPP4_RAT Dipeptidyl peptidase IV (DPP IV) (GP110 glycoprotein) (Bile canaliculus domain-specific membrane glycoprotein) [R.norvegicus], dipeptidylpeptidase 4, dipeptidylpeptidase 8, fibroblast activation protein, alpha	
3286	24107	NM_017141	PP, QQ	DNA polymerase beta, polymerase (DNA directed), beta	Mus musculus, Similar to DNA polymerase beta, clone MGC:6386 IMAGE:3581916, mRNA, complete cds, polymerase (DNA directed), beta	
10	1600	AA686470	Q, R, EEE, MMM	DNA-damage inducible transcript 3, inducible transcript 3, DNA-damage-inducible transcript 3, ESTs, Highly similar to GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 [M.musculus], ESTs, Weakly similar to 1916411A TLS-CHOP protein [H.sapiens]	DNA-damage inducible transcript 3, DNA-damage-inducible transcript 3, ESTs, Highly similar to GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 [M.musculus], ESTs, Weakly similar to 1916411A TLS-CHOP protein [H.sapiens]	
3727	18492	NM_032079	HHH	DnaJ (Hsp40) homolog, subfamily A, member 2	DnaJ (Hsp40) homolog, subfamily A, member 2, DnaJ (Hsp40) homolog, subfamily B, member 11, DnaJ (Hsp40) homolog, subfamily B, member 1, ESTs, Weakly similar to DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2810451A06 gene, RIKEN cDNA 5730496F10 gene, expressed sequence AI506245	
3727	18494	NM_032079	PPP, QQQ	DnaJ (Hsp40) homolog, subfamily A, member 2	DnaJ (Hsp40) homolog, subfamily A, member 2, DnaJ (Hsp40) homolog, subfamily B, member 11, DnaJ (Hsp40) homolog, subfamily B, member 1, ESTs, Weakly similar to DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2810451A06 gene, RIKEN cDNA 5730496F10 gene, expressed sequence AI506245	
3121	15616	NM_012699	Q	DnaJ (Hsp40) homolog, subfamily B, member 9		

TABLE 3						
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1995828.1
2840	18686	D00729	B, I, J, U, FF, LL, XX, YY	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)	
3335	18687	NM_017306	A, B, E, I, J, U, FF, LL, XX, YY	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase), dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoil-Coenzyme A isomerase)	
1558	1431	A1044610	I, J, CC, II, General Alternate	dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)	EST, Highly similar to DDC_RAT Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], EST, Moderately similar to DDC_RAT Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610109O21:dopa decarboxylase, full insert sequence, dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)	

TABLE 3						
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935328.1
3046	1430	M84648	TT, DDD, General Core Tox Markers, General Alternate	dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)	EST, Highly similar to DDC_RAT Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], EST, Moderately similar to DDC_RAT Aromatic-L-amino-acid decarboxylase (AADC) (DOPA decarboxylase) (DDC) [R.norvegicus], Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610109O21:dopa decarboxylase, full insert sequence, dopa decarboxylase, dopa decarboxylase (aromatic L-amino acid decarboxylase)	
4218	492	X53944	RR	dopamine receptor 3, dopamine receptor D3		
4229	1719	X59267	Z, AA, SS	drebrin 1		
3631	19096	NM_031352	L	drebrin-like		
3825	15995	NM_053769	I, J, Q, R	dual specificity phosphatase 1, protein tyrosine phosphatase, non-receptor type 16	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-receptor type 16	
3825	15996	NM_053769	C, I, J, R, LLL	dual specificity phosphatase 1, protein tyrosine phosphatase, non-receptor type 16	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-receptor type 16	
3825	15997	NM_053769	I, J, R	dual specificity phosphatase 1, protein tyrosine phosphatase, non-receptor type 16	Mus musculus, clone MGC:11703 IMAGE:3964527, mRNA, complete cds, RIKEN cDNA 2310076D10 gene, RIKEN cDNA 4930527G07 gene, dual specificity phosphatase 1, expressed sequence BB104621, protein tyrosine phosphatase, non-receptor type 16	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3747	17473	NM_053319	GGG	dynein, cytoplasmic, light chain 1, dynein, cytoplasmic, light polypeptide	ESTs, Moderately similar to protein inhibitor of nitric oxide synthase [M.musculus], dynein, axon, light chain 4, dynein, axonemal, light polypeptide 4, dynein, cytoplasmic, light chain 1, dynein, cytoplasmic, light polypeptide			
3077	21836	NM_012555	O, P, PP, QQ	E26 avian leukemia oncogene 1, 5' domain, v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	E26 avian leukemia oncogene 1, 5' domain, ESTs, Moderately similar to A53988 transcription factor ets-1, splice form a - rat [R.norvegicus], Mus musculus ETS-domain transcription factor mRNA, complete cds, Rattus norvegicus ETS domain transcription factor Pet-1 mRNA, complete cds, v-ets erythroblastosis virus E26 oncogene homolog 1 (avian), v-ets erythroblastosis virus E26 oncogene like (avian)			
3075	23868	NM_012551	A, BB, CC, NNN	early growth response 1	early growth response 1, expressed sequence AI835008			
3075	23869	NM_012551	A, BB, CC, NNN	early growth response 1	early growth response 1, expressed sequence AI835008			
3075	23871	NM_012551	W	early growth response 1	early growth response 1, expressed sequence AI835008			
3075	23872	NM_012551	A, OO, NNN	early growth response 1	early growth response 1, expressed sequence AI835008			
3355	16227	NM_019137	SS, XX, YY	early growth response 4	RIKEN cDNA 4930563M09 gene, early growth response 4			
3878	9527	NM_057104	E, Y, CC, HH, General Alternate	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)			

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1
Seq ID	CLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
3878	9528	NM_057104	HH, General Alternate	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ectonucleotide pyrophosphatase/phosphodiesterase 2, ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)		
2940	20865	L00117	F, M, Y	elastase 1, pancreatic	elastase 1, pancreatic		
2019	24341	AI169421	GG	endosulfine alpha	endosulfine alpha		
3441	20114	NM_021842	BB, CC, PP, QQ	endosulfine alpha	endosulfine alpha		
850	19069	AA943737	Z, General Core Tox Markers	endothelial differentiation sphingolipid G-protein-coupled receptor 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	endothelial differentiation sphingolipid G-protein-coupled receptor 1, endothelial differentiation, G-protein-coupled receptor 6, endothelial differentiation, sphingolipid G-protein-coupled receptor, 1, endothelial differentiation, sphingolipid G-protein-coupled receptor, 3		
3076	19407	NM_012554	G, H, VV	enolase 1, (alpha), enolase 1, alpha non-neuron	EST, Moderately similar to ENOA_RAT Alpha enolase (2-phospho-D-glycerate hydrolyase) (NON-neural enolase) (NNE) (Enolase 1) [R.norvegicus], Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3230402G19:enolase 1, alpha non-neuron, full insert sequence, enolase 1, (alpha), enolase 1, alpha non-neuron, expressed sequence AL022784		

TABLE 3						
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
1497	1114	AI029917	E, DD, KKK, NNN	enolase 2, (gamma, neuronal), enolase 2, gamma neuronal	enolase 2, (gamma, neuronal), enolase 2, gamma neuronal	
3495	20925	NM_022594	U, FF, LL, CCC, RRR, SSS	enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal	EST, Moderately similar to Peroxisomal enoyl hydratase-like protein; enoyl hydratase-like protein, peroxisomal [Rattus norvegicus] [R.norvegicus], enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal	
3196	20926	NM_013013	PP, QQ	enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal, prosaposin, prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	EST, Moderately similar to Peroxisomal enoyl hydratase-like protein; enoyl hydratase-like protein, peroxisomal [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 2310020A21 gene, enoyl Coenzyme A hydratase 1, peroxisomal, enoyl coenzyme A hydratase 1, peroxisomal, prosaposin	
3897	21562	NM_078623	S	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	AU RNA binding protein/enoyl-Coenzyme A hydratase, AU RNA binding protein/enoyl-coenzyme A hydratase, Mus musculus, Similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase, clone MGC:31364 IMAGE:4238681, mRNA, complete cds, RIKEN cDNA 1300017C12 gene, RIKEN cDNA 1810022C23 gene, RIKEN cDNA 2310005D12 gene, enoyl Coenzyme A hydratase, short chain, 1, mitochondrial, hypothetical protein FLJ10948	

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Document No. 1935828.1

TABLE 3							Attorney Docket 44924-5038-01WO Document No. 1995828.1	
Seq. ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
694	17906	AA899762	NNN	epidermal growth factor receptor, epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR [H.sapiens], Homo sapiens truncated epidermal growth factor receptor (EGFR) mRNA, partial cds; alternatively spliced, epidermal growth factor receptor			
2615	17907	A1233224	U	epidermal growth factor receptor, epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR [H.sapiens], Homo sapiens truncated epidermal growth factor receptor (EGFR) mRNA, partial cds; alternatively spliced, epidermal growth factor receptor			
3022	16604	M37394	K, LLL, UUU	epidermal growth factor receptor, epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	EST, Moderately similar to EGFR_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR [H.sapiens], Homo sapiens truncated epidermal growth factor receptor (EGFR) mRNA, partial cds; alternatively spliced, epidermal growth factor receptor			
3155	20885	NM_012842	II	epidermal growth factor, epidermal growth factor (beta-urogastrone)	Homo sapiens mRNA; cDNA DKFZp667O055 (from clone DKFZp667O055), epidermal growth factor, epidermal growth factor (beta-urogastrone), nidogen 2			
2961	854	L20823	RR	epimorphin				

TABLE 3						
Seq ID	GLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935828.1
3156	17541	NM_012844	F, N, S, CC, II, NN, OO, PP, QQ, TT, DDD, EEE, LLL, MMM, SSS, UUU, General Alternate	epoxide hydrolase 1, microsomal, epoxide hydrolase 1, (xenobiotic)	epoxide hydrolase 1, microsomal, epoxide hydrolase 1, microsomal (xenobiotic)	
3738	24420	NM_033539	HH	eukaryotic translation elongation factor 1 alpha 2	EST, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain [R.norvegicus], ESTs, Highly similar to EFHU1 translation elongation factor eEF-1 alpha chain - rat [R.norvegicus], ESTs, Weakly similar to S21055 translation elongation factor eEF-1 alpha chain - rat [R.norvegicus], G1 to S phase transition 1, G1 to phase transition 2, eukaryotic translation elongation factor 1 alpha 1	
3316	17561	NM_017245	N, RR	eukaryotic translation elongation factor 2	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Mus musculus, Similar to elongation factor G2, clone MGC:28160 IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence A1451340	
3316	17563	NM_017245	E	eukaryotic translation elongation factor 2	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Mus musculus, Similar to elongation factor G2, clone MGC:28160 IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence A1451340	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence	Cluster Title		
3316	17562	NM_017245	VV	eukaryotic translation elongation factor 2, mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase 2	ESTs, Highly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], ESTs, Weakly similar to EF2_MOUSE Elongation factor 2 (EF-2) [M.musculus], ESTs, Weakly similar to EF2_RAT Elongation factor 2 (EF-2) [R.norvegicus], G elongation factor, Mus musculus, Similar to elongation factor G2, clone MGC:28160 IMAGE:3984129, mRNA, complete cds, U5 small nuclear ribonucleoprotein 116 kDa, U5 snRNP-specific protein, 116 kD, eukaryotic translation elongation factor 2, expressed sequence AI451340, mitogen activated protein kinase kinase 2			
3932	17560	NM_133283	N	eukaryotic translation elongation factor 2, mitogen activated protein kinase kinase 2				
3655	14295	NM_031599	ZZ, AAA, PPP, QQQ	eukaryotic translation initiation factor 2 alpha kinase 3	EST, Weakly similar to eukaryotic translation initiation factor 2 alpha kinase 3 [Rattus norvegicus] [R.norvegicus], eukaryotic translation initiation factor 2 alpha kinase 3, eukaryotic translation initiation factor 2 alpha kinase 4, eukaryotic translation initiation factor 2-alpha kinase 3			
2002	23152	AI169170	S	eukaryotic translation initiation factor 4A, isoform 2	ESTs, Weakly similar to EUKARYOTIC INITIATION FACTOR 4A-II [M.musculus], eukaryotic translation initiation factor 4A, isoform 2			
3414	18713	NM_020075	C, FFF	eukaryotic translation initiation factor 5	DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 5 [R.norvegicus], KIAA1856 protein, eukaryotic translation initiation factor 5			
3414	18715	NM_020075	R, UU, FFF	eukaryotic translation initiation factor 5	DNA segment, Chr 1, ERATO Doi 692, expressed, ESTs, Highly similar to EUKARYOTIC TRANSLATION INITIATION FACTOR 5 [R.norvegicus], KIAA1856 protein, eukaryotic translation initiation factor 5			

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 193523.1						
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3378	16449	NM_019238	SS, KKK, OOO, General Alternate	farnesyl diphosphate farnesyl transferase 1, farnesyl-diphosphate farnesyltransferase 1		
3378	16450	NM_019238	C, I, J, FF, OOO, General Alternate	farnesyl diphosphate farnesyl transferase 1, farnesyl-diphosphate farnesyltransferase 1		
3707	15069	NM_031840	I, J, N, T, General Alternate	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase), farnesyl diphosphate synthetase	ESTs, Moderately similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], ESTs, Weakly similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	

TABLE 3							Attorney Docket 44921-5038-01W/O Document No. 1935828.1	
Seq. ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3707	15070	NM_031840	I, T	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) e), farnesyl diphosphate synthetase	ESTs, Moderately similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], ESTs, Weakly similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)			
3707	25460	NM_031840	I, J, T	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) e), farnesyl diphosphate synthetase	ESTs, Moderately similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], ESTs, Weakly similar to A34713 farnesyl-pyrophosphate synthetase, testis - rat [R.norvegicus], farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)			
3157	20819	NM_012847	W, General Alternate	farnesyltransferase, CAAX box, alpha	farnesyltransferase, CAAX box, alpha			
4162	851	U72497	A, B, III, JJ, KKK, OOO, PPP, QQQ, General Core Tox Markers	fatty acid amide hydrolase, fatty acid hydroxylase	RIKEN cDNA 2700038P16 gene, fatty acid amide hydrolase			
3078	17676	NM_012556	N, HH	fatty acid binding protein 1, liver	fatty acid binding protein 1, liver			

TABLE 3 **Attorney Docket 44921-5038-01WO**
Document No. 1935328.1

Seq ID	CLGG ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
4087	40	U02096	II, MM, XX, YY, FFF, TTT	fatty acid binding protein 7, brain	Homo sapiens mRNA; cDNA DKFZp547J2313 (from clone DKFZp547J2313), fatty acid binding protein 7, brain
628	20985	AA893242	H, BBB, CCC, RRR, General Alternate	fatty acid Coenzyme A ligase, long chain 2, fatty acid-Coenzyme A ligase, long-chain 6, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long-chain 2, fatty acid Coenzyme A ligase, long-chain 5, fatty acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipodosis-related protein lipodisin	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long-chain 2, fatty acid Coenzyme A ligase, long-chain 5, fatty acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipodosis-related protein lipodisin
628	20986	AA893242	A, B, BBB, CCC, FFF, General Alternate	fatty acid Coenzyme A ligase, long chain 2, fatty acid-Coenzyme A ligase, long-chain 2, fatty acid-Coenzyme A ligase, long-chain 2	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long-chain 2, fatty acid Coenzyme A ligase, long-chain 5, fatty acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipodosis-related protein lipodisin
1566	20983	A1044900	A, FF, JJ, KK, LL, FFF, HHH, SSS, General Core Tox Markers, General Alternate	fatty acid Coenzyme A ligase, long chain 2, fatty acid-Coenzyme A ligase, long-chain 2, fatty acid-Coenzyme A ligase, long-chain 2	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long-chain 2, fatty acid Coenzyme A ligase, long-chain 5, fatty acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipodosis-related protein lipodisin

TABLE 3						
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 449241-5038-01WO Document No. 1935328.1
2881	20984	D90109	U, FF, FFF, HHH, General Alternate	fatty acid Coenzyme A ligase, long chain 2, fatty acid-Coenzyme A ligase, long-chain 2	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty acid-Coenzyme A ligase, long-chain 1, gonadotropin-regulated long chain acyl-CoA synthetase, lipodosis-related protein lipidosin	
2858	3743	D30666	BBB	fatty acid Coenzyme A ligase, long chain 3, fatty acid-Coenzyme A ligase, long-chain 3	fatty acid Coenzyme A ligase, long chain 3, fatty acid-Coenzyme A ligase, long-chain 3	
3803	15925	NM_053607	B	fatty acid Coenzyme A ligase, long chain 5, fatty acid-Coenzyme A ligase, long-chain 5	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty acid-Coenzyme A ligase, long-chain 5, hypothetical protein PRTD-NY3	

TABLE 3							Attorney Docket 44921-5038-01W0 Document No. 1935828.1	
Seq ID	CLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3803	15926	NM_053607	I, J, General Alternate	fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 5	ESTs, Weakly similar to fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase; acetate-CoA ligase; acetyl-Coenzyme A synthetase 1 (ADP forming); acetyl-CoA synthetase [Mus musculus] [M.musculus], Mus musculus, Similar to fatty-acid-Coenzyme A ligase, long-chain 6, clone MGC:28744 IMAGE:4481949, mRNA, complete cds, Mus musculus, Similar to hypothetical protein FLJ20920, clone MGC:25878 IMAGE:4210220, mRNA, complete cds, fatty acid Coenzyme A ligase, long chain 2, fatty acid Coenzyme A ligase, long chain 5, fatty-acid-Coenzyme A ligase, long-chain 5, hypothetical protein PRTD-NY3			
3806	13005	NM_053623	LL, BBB, CCC, RRR	fatty acid-Coenzyme A ligase, long chain 4, fatty-acid-Coenzyme A ligase, long-chain 4				
3838	20868	NM_053843	O, P, NN, OO, VV	Fc fragment of IgG, low affinity IIIa, receptor for (CD16), Fc receptor, IgG, low affinity III				
3838	20869	NM_053843	O, P, V, NN, OO, VV	Fc fragment of IgG, low affinity IIIa, receptor for (CD16), Fc receptor, IgG, low affinity III				
3736	12363	NM_033351	N	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter				

TABLE 3							Attorney Docket 44921-6038-01WO Document No. 1935323.1	
Seq ID	CLGG ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3736	12365	NM_033351	F	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter	Fc fragment of IgG, receptor, transporter, alpha, Fc receptor, IgG, alpha chain transporter			
3282	21663	NM_017126	E, BBB, CCC	ferredoxin 1	ferredoxin 1, similar to RIKEN cDNA B230118G17 gene			
2104	8215	AI171692	CC, GG, HH, EEE, III, JJJ, MMM, General Core Tox Markers, General Alternate	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 2010009K05 gene, RIKEN cDNA 4933416E14 gene, cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kynurenine aminotransferase), ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide			
2033	8213	AI169883	F, PP, QQ, XX, YY, LLL, UUU	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide			
3473	8211	NM_022500	N, MM, DDD, TTT	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide			
3473	8212	NM_022500	F, N, T, HH, QQ, TT, YY, DDD, LLL, UUU	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide			
4063	8210	S61960	BB, CC, MM, UU, TTT, General Alternate	ferritin light chain 1, ferritin, light polypeptide	ESTs, Moderately similar to ferritin light chain 1 [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to FRL2 MOUSE FERRITIN LIGHT CHAIN 2 [M.musculus], RIKEN cDNA 4933416E14 gene, ferritin light chain 1, ferritin light chain 2, ferritin, light polypeptide			

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935823.1	
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3753	14042	NM_053348	N, YY	fetuin B, fetuin beta	expressed sequence AW413091, fetuin B, fetuin beta, histidine-rich glycoprotein			
3019	20699	M35601	E, KKK	fibrinogen, A alpha polypeptide, fibrinogen, alpha polypeptide				
3019	20700	M35601	E, L, S, X, Y, NNN	fibrinogen, A alpha polypeptide, fibrinogen, alpha polypeptide				
2027	6479	A1169690	BB, CC, DD, EE, LL, SS, DDD, III, JJJ, LLL, NNN, UUU	fibrinogen, gamma polypeptide				
3080	6477	NM_012559	E, N, LL, MM, KKK, NNN, TTT	fibrinogen, gamma polypeptide				
3080	6478	NM_012559	E, J, S, X, Y, DD, EE, KKK, NNN	fibrinogen, gamma polypeptide				
4199	644	X14232	X, Y	fibroblast growth factor 1, fibroblast growth factor 1 (acidic)				
3049	13488	M91599	V	fibroblast growth factor receptor 4				
3049	13489	M91599	UUU	fibroblast growth factor receptor 4				

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	CLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence	Cluster Title		
2941	5616	L00191	C, E, LL, RRR, SSS	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1			
3357	5617	NM_019143	RR, SS, UU	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1			
3357	5619	NM_019143	N, PP, QQ, RR, WW, SSS, UUU	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1			
3357	5621	NM_019143	T, PPP, QQQ	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1			
3357	5622	NM_019143	E, S, U, V, X, Y, BB, CC, LL, III, JJJ, LLL, RRR, SSS, UUU	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1			
4056	5624	R47122	Z, AA	fibronectin 1	EST, Highly similar to FIBRONECTIN PRECURSOR [R.norvegicus], ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR [M.musculus], fibronectin 1			

TABLE 3						
Attorney Docket 44921-6038-01WO Document No. 1995828.1						
Seq ID	GLCC ID No.	Genbank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
4243	20821	X62671	F, T	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived), Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	EST, Moderately similar to I48346 ribosomal protein fau - mouse [M.musculus], EST, Weakly similar to UBIM_HUMAN UBIQUITIN-LIKE PROTEIN FUBI (SUB 1-74 [H.sapiens], EST, Weakly similar to UBIM_RAT UBIQUITIN-LIKE PROTEIN FUBI [R.norvegicus], Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	
2193	6782	A1176170	FFF	FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa)	FK506 binding protein 10 (65 kDa), FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506 binding protein 8 (38 kDa)	
3220	15295	NM_013102	P, HH, JJ	FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa), FK506 binding protein 2 (13 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506 binding protein 8 (38 kDa)	FK506 binding protein 10 (65 kDa), FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506 binding protein 8 (38 kDa)	

TABLE 3

Attorney Docket 44921-5038-01WO Document No. 193538.1						
Seq ID	CLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3220	15296	NM_013102	O, P, HH	FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa), FK506 binding protein 2 (13 kDa), FK506 binding protein 2 (13kD)	FK506 binding protein 10 (65 kDa), FK506 binding protein 1A (12kD), FK506 binding protein 1a (12 kDa), FK506 binding protein 5, FK506 binding protein 7 (23 kDa), FK506 binding protein 8 (38 kDa)	
3141	23445	NM_012792	A, GG, II, TT, III, JJ, LLL, SSS, UUU, General Core		EST, Weakly similar to FMO1 MOUSE DIMETHYLANILINE MONOOXYGENASE [M.musculus], ESTs, Weakly similar to S33758 flavin-containing monooxygenase 1 - rat [R.norvegicus], Mus musculus flavin-containing monooxygenase 4 mRNA, complete cds, expressed sequence AW107733, flavin containing monooxygenase 1, hypothetical protein PRO1257	
3512	24345	NM_022701	Tox Markers	flavin containing monooxygenase 1		
3699	10167	NM_031830	N, PP, QQ	flotillin 1	flotillin 1	
			PP, QQ	flotillin 2	flotillin 2	
3271	1262	NM_017077	R, MM, NN, OO, TTT	forkhead box A3, hepatocyte nuclear factor 3, gamma	ESTs, Weakly similar to HN3G_RAT HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G) [R.norvegicus], RIKEN cDNA 1200010K03 gene, expressed sequence AI450827, forkhead box A3, forkhead box B1, hepatocyte nuclear factor 3, gamma	
4174	906	U83112	X	forkhead box M1		
3791	9267	NM_053567	OO, PP, TT	formiminotransferase cyclodeaminase	ESTs, Moderately similar to formiminotransferase cyclodeaminase; human formiminotransferase cyclodeaminase [Homo sapiens] [H.sapiens], formiminotransferase cyclodeaminase	
509	3844	AA891857	U, FF, RRR, SSS, UUU	fracture callus 1 homolog (rat), fractured callus expressed transcript 1	EST, Moderately similar to IM9B_HUMAN MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 B (FRACTURE CALLUS PROTEIN 1) (FXC1) [H.sapiens], fracture callus 1 homolog (rat), fractured callus expressed transcript 1	

TABLE 3						
Seq ID	GLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	EST, Moderately similar to IM9B_HUMAN MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 B (FRACTURE CALLUS PROTEIN 1) (FXC1) [H.sapiens], fracture callus 1 homolog (rat), fractured callus expressed transcript 1
3756	3842	NM_053371	BBB, CCC	fracture callus 1 homolog (rat), fractured callus expressed transcript 1		
3422	21336	NM_021266	UUU	frizzled homolog 1 (Drosophila), frizzled homolog 1, (Drosophila)		frizzled homolog 1 (Drosophila), frizzled homolog 1, (Drosophila), frizzled homolog 7 (Drosophila)
1790	19373	A1102044	LL, NNN	frizzled homolog 1 (Drosophila), frizzled homolog 1, (Drosophila)		
3248	15621	NM_017005	MM, XX, YY, TTT	fumarate hydratase, fumarate hydratase 1		fumarate hydratase, fumarate hydratase 1
3302	23961	NM_017181	PPP, QQQ	fumarylacetoacetate hydrolase, fumarylacetoacetate hydrolase (fumarylacetoacetase)		ESTs, Weakly similar to FAAA_RAT Fumarylacetoacetase (Fumarylacetoacetate hydrolase) (Beta-diketone) (FAA) [R.norvegicus], fumarylacetoacetate hydrolase, fumarylacetoacetate hydrolase (fumarylacetoacetase)
3663	18368	NM_031648	F, General Alternate	FXD domain containing ion transport regulator 1 (phospholemman), FXD domain-containing ion transport regulator 1		EST, Weakly similar to PLM_HUMAN PHOSPHOLEMMAN PRECURSOR [H.sapiens], FXD domain containing ion transport regulator 1 (phospholemman), FXD domain-containing ion transport regulator 1, FXD domain-containing ion transport regulator 6

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TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1995328.1						
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3663	18369	NM_031648	S, General Alternate	FXYD domain containing ion transport regulator 1 (phospholemman), FXYP domain-containing ion transport regulator 1	EST, Weakly similar to PLM_HUMAN PHOSPHOLEMMAN PRECURSOR [H.sapiens], FXYP domain containing ion transport regulator 1 (phospholemman), FXYP domain-containing ion transport regulator 1, FXYP domain-containing ion transport regulator 6	
2956	1228	L14684	BBB, CCC	G elongation factor, mitochondrial elongation factor G		
857	867	AA943963	P	G protein-coupled receptor kinase 6	ESTs, Weakly similar to GRK6 MOUSE G PROTEIN-COUPLED RECEPTOR KINASE GRK6 [M.musculus], G protein-coupled receptor kinase 6, adrenergic receptor kinase, beta 1	
3694	17194	NM_031814	ZZ, AAA	G protein-coupled receptor kinase-interactor 1	DKFZP434B203 protein, G protein-coupled receptor kinase-interactor 1, G protein-coupled receptor kinase-interactor 2	
3018	1241	M35162	D, Z, AA	gamma-aminobutyric acid (GABA) A receptor, delta, gamma-aminobutyric acid (GABA-A) receptor, subunit delta	ESTs, Moderately similar to GAD_HUMAN GAMMA-AMINO-BUTYRIC-ACID RECEPTOR DELTA SUBUNIT PRECURSOR [H.sapiens], Mus musculus, clone MGC:28005 IMAGE:3602400, mRNA, complete cds, gamma-aminobutyric acid (GABA) A receptor, delta, gamma-aminobutyric acid (GABA-A) receptor, subunit delta	
2400	2052	A1227854	RR	gamma-aminobutyric acid (GABA) B receptor, 1, gamma-aminobutyric acid (GABA-B) receptor, 1		

TABLE 3						
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Seq ID	CLGG ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3332	16839	NM_017291	AA	gamma-aminobutyric acid (GABA) receptor, rho 1, gamma-aminobutyric acid (GABA-A) receptor, subunit rho 1	gamma-aminobutyric acid (GABA) receptor, rho 1, gamma-aminobutyric acid (GABA-A) receptor, subunit rho 1	
3684	11611	NM_031756	C, FF	gamma-glutamyl carboxylase	gamma-glutamyl carboxylase	
4125	368	U38379	XX, YY	gamma-glutamyl hydrolase, gamma-glutamyl hydrolase (conjugase, folypolygammaglutamyl hydrolase)	gamma-glutamyl hydrolase, gamma-glutamyl hydrolase (conjugase, folypolygammaglutamyl hydrolase)	
3385	1143	NM_019280	Z, AA	gap junction membrane channel protein alpha 5, gap junction protein, alpha 5, 40kD (connexin 40)	gap junction membrane channel protein alpha 5, gap junction protein, alpha 5, 40kD (connexin 40)	
4188	614	X04070	General Alternate	gap junction membrane channel protein beta 1, gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)	RIKEN cDNA D230044M03 gene, gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)	

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Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3365	23481	NM_019185	Y	GATA binding protein 6	GATA binding protein 5, GATA binding protein 6
1842	18679	A1103496	AA	GDP dissociation inhibitor 1, guanosine diphosphate (GDP) dissociation inhibitor 1	GDP dissociation inhibitor 1, guanosine diphosphate (GDP) dissociation inhibitor 2
3055	1678	M96674	EEE, MMM, General Alternate	glucagon receptor	ESTs, Weakly similar to GLUCAGON RECEPTOR PRECURSOR [M.musculus], glucagon receptor
3339	20789	NM_017319	M, U, LL	glucose regulated protein, 58 kDa, glucose regulated protein, 58kD	
1083	1322	AA964628	W	glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)	ESTs, Weakly similar to G6PT_RAT Glucose-6-phosphatase (G6Pase) (G-6-Pase) [R.norvegicus], RIKEN cDNA 0710001K01 gene, glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease), glucose-6-phosphatase, catalytic, related sequence, hypothetical protein BC002494, islet-specific glucose-6-phosphatase catalytic subunit-related protein

TABLE 3						
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Seq ID	CLGG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3218	1321	NM_013098	L	glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)	ESTs, Weakly similar to G6PT_RAT Glucose-6-phosphatase (G6Pase) (G-6-Pase) [R.norvegicus], RIKEN cDNA 0710001K01 gene, glucose-6-phosphatase, catalytic, glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease), glucose-6-phosphatase, catalytic, related sequence, hypothetical protein BC002494, islet-specific glucose-6-phosphatase catalytic subunit-related protein	
3653	5496	NM_031589	U, W, TT, WW, EEE, LLL, MMM, RRR, SSS, UUU, General Alternate	glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1	Mus musculus, Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1, clone MGC:28167 IMAGE:3985469, mRNA, complete cds, glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1, solute carrier family 37 (glycerol-3-phosphate transporter), member 1	
3653	5497	NM_031589	L, U, OO, TT, WW, CCC, LLL, SSS, UUU	glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1	Mus musculus, Similar to solute carrier family 37 (glycerol-3-phosphate transporter), member 1, clone MGC:28167 IMAGE:3985469, mRNA, complete cds, glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1, glucose-6-phosphatase, transport protein 1, solute carrier family 37 (glycerol-3-phosphate transporter), member 1	
3249	1399	NM_017006	G, FF	glucose-6-phosphate dehydrogenase, glucose-6-phosphate dehydrogenase X-linked	glucose-6-phosphate dehydrogenase, glucose-6-phosphate dehydrogenase 2, glucose-6-phosphate dehydrogenase X-linked, hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	

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Seq ID	GLCG ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3082	4573	NM_012570	XX, YY	glutamate dehydrogenase, glutamate dehydrogenase 1	glutamate dehydrogenase, glutamate dehydrogenase 1
3082	4574	NM_012570	GG, OO, DDD	glutamate dehydrogenase, glutamate dehydrogenase 1	glutamate dehydrogenase, glutamate dehydrogenase 1
3083	20744	NM_012571	C, I, J, X, EE, MM, UU, WW, KKK, TTT, General Alternate	glutamate oxaloacetate transaminase 1, soluble, glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	
3230	17628	NM_013177	General Alternate	glutamate oxaloacetate transaminase 2, mitochondrial, glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	ESTs, Highly similar to AATM_RAT ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) (GLUTAMATE OXALOACETATE TRANSAMINASE-2) [R.norvegicus], Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930442D24:glutamate oxaloacetate transaminase 2, mitochondrial, full insert sequence, glutamate oxaloacetate transaminase 2, mitochondrial, glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
3268	11150	NM_017073	II, RR, TT, DDD	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	CLGG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3268	11151	NM_017073	N, TT	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase				
3268	11152	NM_017073	II, LL, TT, UU, DDD, LLL, UUU	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase				
3268	11153	NM_017073	G, K, II, TT, DDD, GGG, LLL	glutamate-ammonia ligase (glutamine synthase), glutamine synthetase				
3334	14003	NM_017305	Q, R, S, X, Y, NN, OO, General Alternate	glutamate-cysteine ligase , modifier subunit, glutamate-cysteine ligase, modifier subunit	glutamate-cysteine ligase , modifier subunit, glutamate-cysteine ligase, modifier subunit			
3334	14004	NM_017305	Q, R, T, KKK	glutamate-cysteine ligase , modifier subunit, glutamate-cysteine ligase, modifier subunit	glutamate-cysteine ligase , modifier subunit, glutamate-cysteine ligase, modifier subunit			
2931	1247	J05181	Q, R, S	glutamate-cysteine ligase, catalytic subunit	Homo sapiens, Similar to glutamate-cysteine ligase, catalytic subunit, clone MGC:26341 IMAGE:4814728, mRNA, complete cds, glutamate-cysteine ligase, catalytic subunit			
3459	4561	NM_022278	GG, HH	glutaredoxin (thioltransferase), glutaredoxin 1 (thioltransferase)	glutaredoxin (thioltransferase), glutaredoxin 1 (thioltransferase), glutaredoxin 2 (thioltransferase)			

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLCG ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
1897	23596	AI105435	VV	glutaryl-Coenzyme A dehydrogenase	expressed sequence A1266902, expressed sequence D17825, glutaryl-Coenzyme A dehydrogenase			
3564	1853	NM_030826	MM, TT, TTT	glutathione peroxidase 1	ESTs, Weakly similar to GSHC_RAT Glutathione peroxidase (GSHPX-1) (Cellular glutathione peroxidase) [R.norvegicus], glutathione peroxidase 1, glutathione peroxidase 2, glutathione peroxidase 2 (gastrointestinal)			
3296	17686	NM_017165	I, J, LL	glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)	ESTs, Weakly similar to GSHH_RAT Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (PHGPx) (GPX-4) [R.norvegicus], RIKEN cDNA 2310016C16 gene, RIKEN cDNA 3110050F08 gene, glutathione peroxidase 4, glutathione peroxidase 4 (phospholipid hydroperoxidase)			
3250	18988	NM_017013	V, NN, OO	glutathione S-transferase A2, glutathione S-transferase, alpha 1 (Ya), glutathione S-transferase, alpha 2 (Yc2)	ESTs, Weakly similar to GTA1_RAT GLUTATHIONE S-TRANSFERASE YA (LIGANDIN) (CHAIN 1) (GST CLASS-ALPHA) (CLONES PGST94 & PGTR261) [R.norvegicus], glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)			
3250	18989	NM_017013	F, K, M, N, GG, HH, TT, DDD, EEE, LLL, MMM, UUU	glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)	ESTs, Weakly similar to GTA1_RAT GLUTATHIONE S-TRANSFERASE YA (LIGANDIN) (CHAIN 1) (GST CLASS-ALPHA) (CLONES PGST94 & PGTR261) [R.norvegicus], glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)			
3634	18990	NM_031509	G, K, TT, SSS	glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)	ESTs, Weakly similar to GTA1_RAT GLUTATHIONE S-TRANSFERASE YA (LIGANDIN) (CHAIN 1) (GST CLASS-ALPHA) (CLONES PGST94 & PGTR261) [R.norvegicus], glutathione S-transferase A2, glutathione S-transferase, alpha 2 (Yc2)			

TABLE 3							Attorney Docket 44924-5038-01WO Document No. 1935828.1	
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
2905	21011	H32189	F, PP, QQ, TT, DDD	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2				
2922	21012	J02592	GG, NN, OO, EEE, LLL, MMM	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2				
2926	21014	J03914	N, BB, CC, NN	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2				
3251	21013	NM_017014	F, N, DD, EE, TT, DDD	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2				
3251	21015	NM_017014	F, K, N, TT, DDD	glutathione S-transferase M2 (muscle), glutathione S-transferase, mu 2				
3744	1524	NM_053293	V, General Alternate	glutathione S-transferase theta 1, glutathione S-transferase, theta 1	expressed sequence A118089, glutathione S-transferase theta 1, glutathione S-transferase, theta 1			
1968	961	A1138143	II	glutathione S-transferase theta 2, glutathione S-transferase, theta 2	glutathione S-transferase theta 2, glutathione S-transferase, theta 2			

TABLE 3							Attorney Pcket 44921-5038-01WO Document No. 1935323.1	
Seq ID	GLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster title			
3143	960	NM_012796	V, DD, EE, UU, III, JJ, General	glutathione S-transferase theta 2, glutathione S-transferase, theta 2	glutathione S-transferase theta 2, glutathione S-transferase, theta 2			
2974	6405	L38615	G, H, JJ, KK, GGG	glutathione synthetase	EST, Highly similar to GSHB MOUSE GLUTATHIONE SYNTHETASE [M.musculus], glutathione synthetase			
2974	6406	L38615	GGG	glutathione synthetase	EST, Highly similar to GSHB MOUSE GLUTATHIONE SYNTHETASE [M.musculus], glutathione synthetase			
3554	20380	NM_024381	HHH, General Core Tox Markers, General Alternate	glycerol kinase	ESTs, Weakly similar to GLPK MOUSE GLYCEROL KINASE [M.musculus], RIKEN cDNA 2310009E04 gene, glucokinase activity, related sequence 1, glucokinase activity, related sequence 2, glycerol kinase, glycerol kinase pseudogene 2			
624	1552	AA893219	O, P, X, Y, WW	glycine N-methyltransferase	glycine N-methyltransferase			
3273	1550	NM_017084	F, N, O, P, X, Y, EEE, GGG, MMM	glycine N-methyltransferase	glycine N-methyltransferase			
3273	1551	NM_017084	F, O, P, X, GGG, LLL, UUU	glycine N-methyltransferase	glycine N-methyltransferase			
3833	16311	NM_053818	G, H	glycine transporter 1, solute carrier family 6 (neurotransmitter transporter, glycine), member 9				
323	4048	AA851814	O, VV	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb			

TABLE 3						
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Document No. 1995828.1
1908	4049	AI112012	O, VV	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb	
3934	19456	NM_133298	O, P, VV	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb	
153	16756	AA818089	G, H	glycyl-tRNA synthetase	glycyl-tRNA synthetase	
3353	15977	NM_019132	S	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus, GNAS complex locus	ESTs, Moderately similar to S34421 GTP-binding regulatory protein Gs alpha chain [H.sapiens], GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus, GNAS complex locus, RIKEN cDNA 5530400H20 gene, Sang, XLas protein	
2659	21156	AI234248	N, PP, QQ, XX, YY	golgi SNAP receptor complex member 1	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 IMAGE:4250494, mRNA, complete cds, golgi SNAP receptor complex member 1	
3794	21153	NM_053584	T	golgi SNAP receptor complex member 1	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 IMAGE:4250494, mRNA, complete cds, golgi SNAP receptor complex member 1	
4201	21152	X14848	F, S, FF, HH, SS, WW	golgi SNAP receptor complex member 1	Homo sapiens, Similar to golgi SNAP receptor complex member 1, clone MGC:13657 IMAGE:4250494, mRNA, complete cds, golgi SNAP receptor complex member 1	
3280	20745	NM_017113	C, O, P	granulin	granulin	
3280	20746	NM_017113	O, P	granulin	granulin	
894	17471	AA944965	LL	group specific component, group-specific component (vitamin D binding protein)		

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
2984	4254	M12450	M, S, NNN	group specific component, group-specific component (vitamin D binding protein)				
3535	351	NM_024127	C	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha			
3535	353	NM_024127	C, HH, PP, QQ	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha			
3535	354	NM_024127	C, FF, II, PP, NNN	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible, alpha	growth arrest and DNA-damage-inducible 45 alpha, growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha			
1665	17506	A1070068	I, J, L, M, Z	growth arrest and DNA-damage-inducible, beta	growth arrest and DNA-damage-inducible 45 beta, growth arrest and DNA-damage-inducible, alpha, growth arrest and DNA-damage-inducible, beta			
3876	25290	NM_057100	E, BB, JJ	growth arrest specific 6, growth arrest-specific 6	ESTs, Highly similar to growth arrest specific 6 [Rattus norvegicus] [R.norvegicus], growth arrest specific 6, growth arrest-specific 6			

TABLE 3						
Seq ID	CLCG ID No.	Genbank Accession RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2859	1396	D30735	RR	growth factor, augmentor of liver regeneration (ERV1 homolog, S. cerevisiae), growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	growth factor, augmentor of liver regeneration (ERV1 homolog, S. cerevisiae), growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	
1362	17524	AI010568	General Core Tox Markers	growth hormone receptor	growth hormone receptor	
3274	10886	NM_017094	B, H, S, LLL, PPP, QQQ, General Core Tox Markers, General Alternate	growth hormone receptor	growth hormone receptor	
3274	10887	NM_017094	A, B, T, FF, NN, OO, General Alternate	growth hormone receptor	growth hormone receptor	
3549	15350	NM_024356	L	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-responsive dystonia)	GTP cyclohydrolase 1, GTP cyclohydrolase 1 (dopa-responsive dystonia)	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935828.1						
Seq ID	CLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3142	16947	NM_012793	N, T, HHH, PPP, QQQ, General Alternate	guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	expressed sequence AA571402, guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	
3142	16948	NM_012793	PPP, QQQ	guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	expressed sequence AA571402, guanidinoacetate N-methyltransferase, guanidinoacetate methyltransferase	
1196	3082	AA999172	C, UU, General Alternate	guanine monophosphate synthetase	guanine monophosphate synthetase	
3585	690	NM_031034	RR	guanine nucleotide binding protein (G protein) alpha 12, guanine nucleotide binding protein, alpha 12	ESTs, Moderately similar to guanine nucleotide binding protein (G protein) alpha 12 [Rattus norvegicus] [R.norvegicus], guanine nucleotide binding protein (G protein), alpha 13, guanine nucleotide binding protein, alpha 12, guanine nucleotide binding protein, alpha 13	
3222	19949	NM_013106	L, HHH	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3, guanine nucleotide binding protein, alpha inhibiting 3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3, guanine nucleotide binding protein, alpha inhibiting 3	

TABLE 3						
Attorney Docket 44924-5038-01WO Document No. 1935828.1						
Seq. ID	GLCG ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3924	14959	NM_130734	A, B, JJ, KK, FFF, GGG, HHH, General Alternate	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	EST, Weakly similar to B33928 GTP-binding protein beta chain homolog [H.sapiens], EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo sapiens cDNA: FLJ21913 fis, clone HEP03888, Mus musculus, Similar to hypothetical protein FLJ10385, clone MGC:28622 IMAGE:4220923, mRNA, complete cds, expressed sequence AL033335, guanine nucleotide binding protein (G protein), beta polypeptide 1-like, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	
2088	14960	AI171319	G	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	EST, Weakly similar to B33928 GTP-binding protein beta chain homolog [H.sapiens], EST, Weakly similar to GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 [H.sapiens], Homo sapiens cDNA: FLJ21913 fis, clone HEP03888, Mus musculus, Similar to hypothetical protein FLJ10385, clone MGC:28622 IMAGE:4220923, mRNA, complete cds, SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, expressed sequence AL033335, guanine nucleotide binding protein (G protein), beta polypeptide 1-like, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, guanine nucleotide binding protein, beta 2, related sequence 1	
3084	16024	NM_012578	WW, ZZ, AAA	H1 histone family, member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)	
3084	16025	NM_012578	WW, ZZ, AAA	H1 histone family, member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)	
3084	16026	NM_012578	ZZ, AAA	H1 histone family, member 0	H1 histone family, member 0, H1 histone family, member O (oocyte-specific)	
2763	1488	AI237016	DDD	H2A histone family, member Y	H2A histone family, member Y, RIKEN cDNA 4933432H23 gene	
2937	1264	K01933	S, SS, WW, NNN	haptoglobin		

TABLE 3						
Seq ID	GLGC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence	Cluster Title
3184	5033	NM_012966	L, PPP, QQQ	heat shock 10 kDa protein 1 (chaperonin 10)	ESTs, Weakly similar to S47532 chaperonin groES [H.sapiens], expressed sequence AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1 (chaperonin 10)	
3184	5034	NM_012966	RR	heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1 (chaperonin 10)	ESTs, Weakly similar to S47532 chaperonin groES [H.sapiens], expressed sequence AW108200, heat shock 10 kDa protein 1 (chaperonin 10), heat shock 10kD protein 1 (chaperonin 10)	
2990	1466	M14050	LL	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	EST, Weakly similar to GR78_RAT 78 KD GLUCOSE-REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN) (BIP) (STEROIDOGENESIS-ACTIVATOR POLYPEPTIDE) [R.norvegicus], expressed sequence AL022860, heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	
3548	17764	NM_024351	Z, AA, FF	heat shock 70kD protein 8	EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEI [H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone [H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular chaperone hsc70 - mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], ESTs, Weakly similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], heat shock 70kD protein 8	
3548	17765	NM_024351	GG	heat shock 70kD protein 8	EST, Moderately similar to HS7C_HUMAN HEAT SHOCK COGNATE 71 KDA PROTEI [H.sapiens], EST, Weakly similar to A27077 dnaK-type molecular chaperone [H.sapiens], EST, Weakly similar to A45935 dnaK-type molecular chaperone hsc70 - mouse [M.musculus], ESTs, Moderately similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], ESTs, Weakly similar to HS7C MOUSE HEAT SHOCK COGNATE 71 KDA PROTEIN [M.musculus], heat shock 70kD protein 8	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1995923.1
Seq ID	CLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence	Cluster Title	
3675	21693	NM_031714	A, B, RRR, SSS, UUU, General Alternate	heat-responsive protein 12, translational inhibitor protein p14.5	Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300015121:heat-responsive protein 12, full insert sequence, heat-responsive protein 12, translational inhibitor protein p14.5		
2353	16081	A1179610	B, E, Q, PP, EEE, MMM	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1		
3085	16080	NM_012580	E, OO, PP, EEE, MMM	heme oxygenase (decycling) 1	heme oxygenase (decycling) 1		
2836	19703	AJ001517	E, BB, CC, II	hemochromatosis	EST, Highly similar to HFE_HUMAN HEREDITARY HAEMOCHROMATOSIS PROTEIN PRECURSOR [H.sapiens], hemochromatosis		
					EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1		
2323	18907	A1178971	T	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1		
2370	1687	A1179971	T	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1		
2512	1688	A1230970	T	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1		

TABLE 3						Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
2731	1689	AI236360	T, XX, YY	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1		
3217	1684	NM_013096	T	hemoglobin alpha, adult chain 2, hemoglobin, alpha 1	EST, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], EST, Weakly similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], ESTs, Moderately similar to HBA_RAT HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS [R.norvegicus], RIKEN cDNA 2510042H12 gene, hemoglobin alpha chain complex, hemoglobin alpha, adult chain 1, hemoglobin, alpha 1, hemoglobin, alpha 2, hemoglobin, theta 1		
445	18897	AA875207	C, T, Z, AA	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta		
3734	17829	NM_033234	T, HH, NNN	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta		
3734	17832	NM_033234	T	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta		
3734	25468	NM_033234	K, T, HH, XX, YY	hemoglobin beta chain complex, hemoglobin, beta	EST, Moderately similar to HBB1_RAT Hemoglobin beta chain, major-form [R.norvegicus], expressed sequence A1036344, hemoglobin, beta, hemoglobin, beta adult major chain, hemoglobin, beta adult minor chain, hemoglobin, delta		
3746	13164	NM_053318	E, S, PP, QQ, WW	hemopexin			
3770	22586	NM_053469	L, M	hepcidin antimicrobial peptide	hepcidin antimicrobial peptide		

TABLE 3:						
Attorney Docket 44921-5038-01WO Document No. 1935828.1						
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
4256	1548	X70900	V, General Alternate	hepsin, hepsin (transmembrane protease, serine 1)	ESTs, Weakly similar to HEP5_RAT SERINE PROTEASE HEP5IN [R.norvegicus], ESTs, Weakly similar to TMS2_MOUSE TRANSMEMBRANE PROTEASE, SERINE 2 (EPITHELIALIN) (PLASMIC TRANSMEMBRANE PROTEIN X) [M.musculus], Mus musculus airway trypsin-like protease mRNA, complete cds, Mus musculus, Similar to transmembrane protease, serine 4, clone MGC:29209 IMAGE:5030266, mRNA, complete cds, hepsin, hepsin (transmembrane protease, serine 1)	
1875	4235	A1104524	HHH, General Alternate	heterogeneous nuclear ribonucleoprotein A/B	DAZ associated protein 1, Musashi homolog 1 (Drosophila), Musashi homolog 2 (Drosophila), RIKEN cDNA 4933434H11 gene, expressed sequence AA959857, heterogeneous nuclear ribonucleoprotein A/B, musashi homolog 1 (Drosophila)	
3626	4234	NM_031330	A, B, I, L, Y, MM, HHH, KKK, OOO, TTT, General Alternate	heterogeneous nuclear ribonucleoprotein A/B	DAZ associated protein 1, Musashi homolog 1 (Drosophila), Musashi homolog 2 (Drosophila), RIKEN cDNA 4933434H11 gene, expressed sequence AA959857, heterogeneous nuclear ribonucleoprotein A/B, musashi homolog 1 (Drosophila)	
3317	17502	NM_017248	O, P, JJ, KK, VV, HHH	heterogeneous nuclear ribonucleoprotein A1	ESTs, Highly similar to I52962 FBRNP [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) [R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1	

TABLE 3						
Seq ID	CLC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster title	Attorney Docket 44921-6038-01WO Document No. 1935328.1
3317	15012	NM_017248	VV	heterogeneous nuclear ribonucleoprotein A1	ESTs, Highly similar to I52962 FBRNP [H.sapiens], ESTs, Highly similar to S12520 core protein A1 [H.sapiens], ESTs, Highly similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Moderately similar to heterogeneous ribonuclear particle protein A1 [H.sapiens], ESTs, Weakly similar to ROA1_RAT Heterogeneous nuclear ribonucleoprotein A1 (HDP) [R.norvegicus], Homo sapiens cDNA: FLJ22720 fis, clone HSI14320, Mus musculus, Similar to TAR DNA binding protein, clone MGC:19284 IMAGE:4016437, mRNA, complete cds, RIKEN cDNA 2610510D13 gene, RIKEN cDNA 4930547K05 gene, heterogeneous nuclear ribonucleoprotein A1, heterogeneous nuclear ribonucleoprotein A3	
3	2417	AA684857	VV	heterogeneous nuclear ribonucleoprotein K	ESTs, Highly similar to heterogeneous nuclear ribonucleoprotein K, isoform b; dC-stretch binding protein; transformation upregulated nuclear protein [Homo sapiens] [H.sapiens], ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein K [Rattus norvegicus] [R.norvegicus], heterogeneous nuclear ribonucleoprotein K, poly(rC) binding protein 3, poly(rC) binding protein 4	
2766	2416	A1237051	LL	heterogeneous nuclear ribonucleoprotein K	ESTs, Highly similar to heterogeneous nuclear ribonucleoprotein K, isoform b; dC-stretch binding protein; transformation upregulated nuclear protein [Homo sapiens] [H.sapiens], ESTs, Weakly similar to heterogeneous nuclear ribonucleoprotein K [Rattus norvegicus] [R.norvegicus], heterogeneous nuclear ribonucleoprotein K, poly(rC) binding protein 3, poly(rC) binding protein 4	
789	16944	AA925541	SSS	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L	
789	16945	AA925541	C, BBB, HHH	heterogeneous nuclear ribonucleoprotein L	heterogeneous nuclear ribonucleoprotein L	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935323.1	
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
				heterogeneous nuclear ribonucleoprotein U, heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	E1B-55kDa-associated protein 5, EST, Weakly similar to heterogeneous nuclear ribonucleoprotein U; scaffold attachment factor A; nuclear matrix protein sp120 [Mus musculus] [M.musculus], expressed sequence A1465155, heterogeneous nuclear ribonucleoprotein U			
3886	19833	NM_057139	GG		ESTs, Weakly similar to A35244 hexokinase [M.musculus], Mus musculus, Similar to hexokinase 1, clone MGC:28816 IMAGE:4504302, mRNA, complete cds, hexokinase 1			
3130	1371	NM_012734	D, V, GG	hexokinase 1	EST, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], ESTs, Weakly similar to HXK2 MOUSE HEXOKINASE TYPE II [M.musculus], hexokinase 2			
3131	11839	NM_012735	Z, AA, NNN	hexokinase 2	ESTs, Weakly similar to HGF-regulated tyrosine kinase substrate [Mus musculus] [M.musculus], HGF-regulated tyrosine kinase substrate, RIKEN cDNA 1700013B03 gene, WD40- and FYVE-domain containing protein 2, hepatocyte growth factor-regulated tyrosine kinase substrate, myotubularin related protein 3, phosphoinositide-binding protein SR1, target of myb1 homolog (chicken), zinc finger protein, subfamily 2A (FYVE domain containing), 1			
1258	10108	A1007857	Q, R		ESTs, Highly similar to HIPP_HUMAN Neuron specific calcium-binding protein hippocalcin (P23K) (Calcium-binding protein BDR-2) [R.norvegicus], ESTs, Weakly similar to HIPP RAT NEURON SPECIFIC CALCIUM-BINDING PROTEIN HIPPOCALCIN [M.musculus], hippocalcin			
2845	1375	D12573	Z, AA	hippocalcin				
3027	70	M58308	K, GG, OO, General Alternate	histidine ammonia lyase, histidine ammonia-lyase	histidine ammonia lyase, histidine ammonia-lyase			
3036	17344	M75168	C	HLA-B associated transcript 1A	ESTs, Highly similar to S33681 translation initiation factor eIF-4A.I [H.sapiens], ESTs, Weakly similar to A42811 nuclear RNA helicase (DEAD family) homolog - rat [R.norvegicus], RIKEN cDNA 2610307C23 gene, hypothetical protein MGC6664			

TABLE 3						
Seq ID	CLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935828.1
1347	11460	A1010293	K	HLA-B associated transcript 3, HLA-B-associated transcript 3	HLA-B associated transcript 3, HLA-B-associated transcript 3, Mus musculus, clone IMAGE:4010394, mRNA, partial cds, Mus musculus, clone IMAGE:5321785, mRNA, cystin 1, enabled homolog (Drosophila), expressed sequence AA408914, hypothetical protein MGC10820, zinc finger protein, multiplicity 1	
3550	20772	NM_024363	A	HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae), heterogenous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae)	EST, Moderately similar to ANM1_HUMAN PROTEIN ARGININE N-METHYLTRANSFERASE 1 [H.sapiens], EST, Weakly similar to ANM1_HUMAN PROTEIN ARGININE N-METHYLTRANSFERASE 1 [H.sapiens], ESTs, Moderately similar to ANM1_MOUSE PROTEIN ARGININE N-METHYLTRANSFERASE 1 [M.musculus], ESTs, Weakly similar to ANM1_MOUSE PROTEIN ARGININE N-METHYLTRANSFERASE 1 [M.musculus], HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae), RIKEN cDNA 2410018A17 gene, coactivator-associated arginine methyltransferase 1, coactivator-associated arginine methyltransferase-1, heterogenous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae), heterogenous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae), related sequence	
4261	1955	X76453	M	HRAS like suppressor 3, HRAS-like suppressor 3	ESTs, Weakly similar to R107_RAT H-rev 107 protein [R.norvegicus], H-rev107-like protein 5, HRAS-like suppressor, HRAS-like suppressor 2, HRAS-like suppressor 3, Ha-Ras suppressor A-C1, Harvey rat sarcoma virus oncogene related suppressor, Mus musculus, Similar to HRAS-like suppressor 3, clone MGC:37701 IMAGE:5065247, mRNA, complete cds, RIKEN cDNA 4921526K24 gene, expressed sequence C78643, retinoic acid receptor responder (tazarotene induced) 3	
2362	23120	A1179857	S	huntingtin interacting protein 2	EST, Weakly similar to UBC1_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-25 KD [H.sapiens], ESTs, Weakly similar to ubiquitin-conjugating enzyme E2D 2 [Rattus norvegicus] [R.norvegicus], RIKEN cDNA 0910001J09 gene, RIKEN cDNA 1700013N18 gene, RIKEN cDNA 6720465F12 gene, huntingtin interacting protein 2, ubiquitin-conjugating enzyme E2D 2, ubiquitin-conjugating enzyme E2L 3, ubiquitin-conjugating enzyme E2N	

TABLE 3						
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	ESTs, Highly similar to GLO2_HUMAN HYDROXYACYLGLUTATHIONE HYDROLASE [H.sapiens], Mus musculus, Similar to hydroxyacyl glutathione hydrolase, clone MGC:6697 IMAGE:3583919, mRNA, complete cds, RIKEN cDNA 0610025L15 gene, RIKEN cDNA 1500017E18 gene, brain protein 17, hydroxyacyl glutathione hydrolase
2558	573	A1232087	A, B, M, OOO, UUU, General Core Tox Markers	hydroxyacid oxidase (glycolate oxidase) 3, hydroxyacid oxidase 3 (medium-chain)		
1430	1409	A1012802	A, B, M, HH, SS, UU, III, JJ, KKK, OOO, General Core Tox Markers	hydroxyacyl glutathione hydrolase		
3667	15175	NM_031682	A, B, P, U, BBB, CCC, RRR, SSS, General Alternate	hydroxyacyl-Coenzyme A dehydrogenase, type II, hydroxysteroid (17-beta) dehydrogenase 10		
3272	23660	NM_017080	T, U, RRR, SSS	hydroxysteroid (11-beta) dehydrogenase 1, hydroxysteroid 11-beta dehydrogenase 1		

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TABLE 3						
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935828.1
3033	13547	M63983	EE	hypoxanthine guanine phosphoribosyl transferase, hypoxanthine phosphoribosyl transferase 1 (Lesch-Nyhan syndrome)	EST, Moderately similar to The Crystal Structure Of Icam-2 {SUB 25-216 [H.sapiens], ESTs, Weakly similar to S18140 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - rat [R.norvegicus], hypoxanthine guanine phosphoribosyl transferase, hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	
4284	1146	Y09507	WW	hypoxia inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	Mus musculus inhibitory PAS domain protein (Ipas) mRNA, complete cds, hypoxia inducible factor 1, alpha subunit, hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor), neuronal PAS domain protein 1, single-minded 1, single-minded 2, single-minded homolog 1 (Drosophila)	
3543	22079	NM_024157	BBB, CCC	I factor (complement), complement component factor i	I factor (complement), complement component factor i	
2975	1427	L38644	O, P, X, Y, VW	importin beta, karyopherin (importin) beta 1	importin beta, karyopherin (importin) beta 1, karyopherin (importin) beta 3	
3144	10247	NM_012797	V	inhibitor of DNA binding 1, inhibitor of DNA binding 1, dominant negative helix-loop-helix protein		

TABLE 3						
Seq ID	CLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1995823.1
3144	10248	NM_012797	DD, EE, JJ, General Core Tox Markers	Inhibitor of DNA binding 1, inhibitor of DNA binding 1, dominant negative helix-loop-helix protein		
1958	16510	A1137583	L, T	Inhibitor of DNA binding 2, inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ESTs, Weakly similar to JC2112 helix-loop-helix protein, Id2 - rat [R.norvegicus], inhibitor of DNA binding 2, inhibitor of DNA binding 2, dominant negative helix-loop-helix protein, inhibitor of DNA binding 4, inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	
3723	18640	NM_032057	C, I, J, TT, OOO	inositol (myo)-1(or 4)-monophosphate 1, inositol (myo)-1(or 4)-monophosphate 1, inositol (myo)-1(or 4)-monophosphate 1, inositol (myo)-1(or 4)-monophosphate 1	inositol (myo)-1(or 4)-monophosphate 1, inositol (myo)-1(or 4)-monophosphate 2, inositol (myo)-1(or 4)-monophosphate 1	
3523	19669	NM_022944	ZZ	inositol polyphosphate phosphatase-like 1	EWS/FLI1 activated transcript 2, SH2 domain protein 1A, inositol polyphosphate phosphatase-like 1	
409	23336	AA859981	U, GG, HH, BBB, CCC, RRR	inositol (myo)-1(or 4)-monophosphate 2	ESTs, Moderately similar to A Chain A, Inositol Monophosphatase [H.sapiens], RIKEN cDNA 2900059K10 gene, inositol (myo)-1(or 4)-monophosphate 1, inositol (myo)-1(or 4)-monophosphate 2	
3266	24719	NM_017071	RR	insulin receptor	apoptosis-associated tyrosine kinase, insulin receptor	
3739	25431	NM_052807	D, SS	insulin-like growth factor 1 receptor, insulin-like growth factor 1 receptor	EST, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR PRECURSOR [M.musculus], EST, Moderately similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR PRECURSOR [M.musculus], ESTs, Highly similar to IG1R_MOUSE INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR PRECURSOR [M.musculus], insulin receptor-related receptor, insulin-like growth factor 1 receptor, insulin-like growth factor 1 receptor	

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Seq ID	GLGC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
2839	21051	D00698	D, G, H, GG, DDD	insulin-like growth factor 1 (somatomedin C)	
2993	21052	M15481	H, S, GGG, PPP, QQQ, General Alternate	insulin-like growth factor 1 (somatomedin C)	
2993	21053	M15481	G, H, PPP, QQQ	insulin-like growth factor 1 (somatomedin C)	
4190	21054	X06107	G, H, M, S, GGG	insulin-like growth factor 1 (somatomedin C)	
3088	15097	NM_012588	Z	insulin-like growth factor binding protein 3	
3088	15098	NM_012588	GG, II	insulin-like growth factor binding protein 3	

TABLE 3						
Seq ID	CLIC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3749	21977	NM_053329	G, BB, CC, GGG, III, JJJ, KKK, LLL, NNN, OOO, PPP, QQQ, SSS, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit	ESTs, Weakly similar to A41915 insulin-like growth factor-binding complex acid-labile chain precursor [H.sapiens], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR [M.musculus], RIKEN cDNA 1200009O22 gene, glycoprotein A repetitions predominant, glycoprotein Ib (platelet), alpha polypeptide, insulin-like growth factor binding protein, acid labile subunit, toll-like receptor 3, toll-like receptor 4, toll-like receptor 5	
3749	21978	NM_053329	BB, PPP, QQQ, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit	ESTs, Weakly similar to A41915 insulin-like growth factor-binding complex acid-labile chain precursor [H.sapiens], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR [M.musculus], RIKEN cDNA 1200009O22 gene, glycoprotein A repetitions predominant, glycoprotein Ib (platelet), alpha polypeptide, insulin-like growth factor binding protein, acid labile subunit, toll-like receptor 3, toll-like receptor 4, toll-like receptor 5	
3749	25480	NM_053329	G, S, CC, GGG, III, JJJ, KKK, OOO, PPP, QQQ, General Core Tox Markers	insulin-like growth factor binding protein, acid labile subunit	ESTs, Weakly similar to A41915 insulin-like growth factor-binding complex acid-labile chain precursor [H.sapiens], ESTs, Weakly similar to ALS MOUSE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR [M.musculus], RIKEN cDNA 1200009O22 gene, glycoprotein A repetitions predominant, glycoprotein Ib (platelet), alpha polypeptide, insulin-like growth factor binding protein, acid labile subunit, toll-like receptor 3, toll-like receptor 4, toll-like receptor 5	

TABLE 3						
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Seq ID	GLCG ID No.	Genbank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2266	14989	AI177366	HHH	integrin beta 1 (fibronectin receptor beta), integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	integrin beta 1 (fibronectin receptor beta), integrin beta 2, integrin beta 7, integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit), integrin, beta 7	
4285	1818	Y11283	D, E, S, CC, MM, TTT	inter alpha-trypsin inhibitor, heavy chain 4, inter-alpha (globulin) inhibitor H4 (plasma kallikrein- sensitive glycoprotein)	EST, Weakly similar to JC5953 inter-alpha-inhibitor H4P heavy chain - rat [R.norvegicus], ESTs, Weakly similar to INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR [M.musculus], inter alpha-trypsin inhibitor, heavy chain 4, inter- alpha (globulin) inhibitor H4 (plasma kallikrein-sensitive glycoprotein)	
3185	2554	NM_012967	W	intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ESTs, Weakly similar to ICA1_HUMAN INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR [H.sapiens], intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion molecule 3, intercellular adhesion molecule 5, telencephalin	
3185	2555	NM_012967	W, BB, CC, NN, OO, PP	intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ESTs, Weakly similar to ICA1_HUMAN INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR [H.sapiens], intercellular adhesion molecule, intercellular adhesion molecule 1 (CD54), human rhinovirus receptor, intercellular adhesion molecule 3, intercellular adhesion molecule 5, telencephalin	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935823.1
Seq ID	CLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
					ESTs, Moderately similar to sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae) [Rattus norvegicus], Mus musculus, Similar to sirtuin silent mating type information regulation 2 homolog 7 (S. cerevisiae), clone MGC:37560 IMAGE:4987746, mRNA, complete cds, expressed sequence A1646973, interferon regulatory factor 1, interferon regulatory factor 2, interferon regulatory factor 4, interferon regulatory factor 5, sirtuin 1 (silent mating type information regulation 2, homolog) 1 (S. cerevisiae), sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae), sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae)		
3089	20126	NM_012591	T, W	interferon regulatory factor 1	expressed sequence A1646973, interferon regulatory factor 1, interferon regulatory factor 2, interferon regulatory factor 4, interferon regulatory factor 5		
3089	21162	NM_012591	W	interferon regulatory factor 1	ESTs, Weakly similar to IFR1_RAT INTERFERON-RELATED DEVELOPMENTAL REGULATOR 1 (NERVE GROWTH FACTOR-INDUCIBLE PROTEIN PC4) (IRPR) [R. norvegicus], interferon-related developmental regulator 1, interferon-related developmental regulator 2		
3379	17908	NM_019242	Q, W, MM, QQ, TTT	interferon-related developmental regulator 1			
3636	24710	NM_031512	W	interleukin 1 beta, interleukin 1, beta			
				interleukin 18, interleukin 18 (interferon-gamma-inducing factor)	interleukin 18, interleukin 18 (interferon-gamma-inducing factor)		
4171	1520	U77777	V	interleukin 4 receptor, interleukin 4 receptor, alpha	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage), interleukin 4 receptor, interleukin 4 receptor, alpha		
3937	656	NM_133380	Y	interleukin 6 receptor, interleukin 6 receptor, alpha	interleukin 6 receptor		
3253	6598	NM_017020	DD, EE, SS, WW, UUU				

TABLE 3						
Seq ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935328.1
4106	202	U20181	N	Iron responsive element binding protein 2, iron-responsive element binding protein 2		
3635	17427	NM_031510	Q, R, GG, PPP, QQQ, General Alternate	isocitrate dehydrogenase 1 (NADP+), soluble	ESTs, Highly similar to IDHC_RAT ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP) [R.norvegicus], expressed sequence A1788952, isocitrate dehydrogenase 1 (NADP+), soluble, isocitrate dehydrogenase 2 (NADP+), mitochondrial	
3809	15090	NM_053638	B, HHH	isocitrate dehydrogenase 3 (NAD+) alpha	isocitrate dehydrogenase 3 (NAD+) alpha	
3809	23305	NM_053638	KK, WW, HHH	isocitrate dehydrogenase 3 (NAD+) alpha	isocitrate dehydrogenase 3 (NAD+) alpha	
3090	4449	NM_012592	F, V, Z, AA, XX, YY, General Alternate	isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	
3090	4450	NM_012592	A, B, V, BB, CC, II, OOO, General Alternate	isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	
3090	4451	NM_012592	VV, General Alternate	isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	

TABLE 3						
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Human Homologous Sequence Cluster Title
3090	4452	NM_012592	VV, General Alternate	isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase	ESTs, Moderately similar to IVD_HUMAN ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL PRECURSOR [H.sapiens], isovaleryl Coenzyme A dehydrogenase, isovaleryl coenzyme A dehydrogenase
2834	25233	AJ000556	T	Janus kinase 1, Janus kinase 1 (a protein tyrosine kinase)		
3372	2632	NM_019213	S	jumping translocation breakpoint	ESTs, Highly similar to jumping translocation breakpoint [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to jumping translocation breakpoint [Rattus norvegicus] [R.norvegicus], jumping translocation breakpoint	ESTs, Highly similar to jumping translocation breakpoint [Rattus norvegicus] [R.norvegicus], ESTs, Moderately similar to jumping translocation breakpoint [Rattus norvegicus] [R.norvegicus], jumping translocation breakpoint
3438	22352	NM_021835	I, J, II	Jun oncogene, v-jun sarcoma virus 17 oncogene homolog (avian)	Jun oncogene, v-jun sarcoma virus 17 oncogene homolog (avian)	Jun oncogene, v-jun sarcoma virus 17 oncogene homolog (avian)
3127	24722	NM_012725	F, G, U, WW	kalikrein B, plasma 1	ESTs, Weakly similar to dJ1170K4.2 [H.sapiens], Mus musculus mRNA for serine protease-like 1, complete cds, Mus musculus, Similar to mosaic serine protease, clone IMAGE:3490022, mRNA, partial cds, RIKEN cDNA 160027G01 gene, RIKEN cDNA 1700049K14 gene, RIKEN cDNA 2010015P21 gene, RIKEN cDNA 4931440B09 gene, coagulation factor XI (plasma thromboplasmin antecedent), distal intestinal serine protease, kallikrein B, plasma 1, kallikrein B, Fletcher factor) 1, kallikrein B, plasma 1	ESTs, Weakly similar to dJ1170K4.2 [H.sapiens], Mus musculus mRNA for serine protease-like 1, complete cds, Mus musculus, Similar to mosaic serine protease, clone IMAGE:3490022, mRNA, partial cds, RIKEN cDNA 160027G01 gene, RIKEN cDNA 1700049K14 gene, RIKEN cDNA 2010015P21 gene, RIKEN cDNA 4931440B09 gene, coagulation factor XI (plasma thromboplasmin antecedent), distal intestinal serine protease, kallikrein B, plasma 1, kallikrein B, Fletcher factor) 1, kallikrein B, plasma 1

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935823.1						
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3691	15864	NM_031797	WW, OOO A, B, BB, CC, HH, OO, EEE, GG, II, JJ, MMM, General Core Tox Markers	kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))	kangai 1 (suppression of tumorigenicity 6, prostate), kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)), tetraspan 1	
3710	16726	NM_031855		ketoheokinase, ketoheokinase (fructokinase)	ketoheokinase, ketoheokinase (fructokinase)	
2291	659	AI178208	W	KIAA0618 gene product, nuclear pore membrane protein 121	EST, Moderately similar to N121_HUMAN NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KDA) (P145) [H.sapiens], EST, Weakly similar to N121_HUMAN NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KDA) (P145) [H.sapiens], ESTs, Weakly similar to nuclear pore membrane glycoprotein 121 kD [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to DDX9 MOUSE ATP-DEPENDENT RNA HELICASE A [M.musculus], KIAA0410 gene product, KIAA0618 gene product, Mus musculus, clone IMAGE:4949762, mRNA, partial cds, Mus musculus, clone IMAGE:5148310, mRNA, Mus musculus, clone IMAGE:5321620, mRNA, partial cds, POM (POM121 rat homolog) and ZP3 fusion, Snf2-related CBP activator protein, melanoma antigen, family D, 3	

TABLE 3						
Attorney Docket 44924-5038-01WO Document No. 1935828.1						
Seq ID	GLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3209	16472	NM_013062	JJJ	kinase insert domain protein receptor, kinase insert domain receptor (a type III receptor tyrosine kinase)		
3120	1850	NM_012696	D, E, M, BB, CC, III, JJJ	kininogen	kininogen	
3120	1854	NM_012696	D, E, M, BB	kininogen	kininogen	
1586	6697	A1045340	MM, TTT	Kirsten rat sarcoma oncogene 2, expressed, v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	ESTs, Weakly similar to RASL MOUSE TRANSFORMING PROTEIN P21/K-RAS 2B [M.musculus], Mus musculus, Similar to v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog, clone MGC:6244 IMAGE:3158212, mRNA, complete cds, RAS-like protein expressed in many tissues, Ric-like, expressed in many tissues (Drosophila), v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	
3782	14380	NM_053536	W	Kruppel-like factor 15		
3895	8640	NM_057211	KKK	Kruppel-like factor 9, basic transcription element binding protein 1	ESTs, Moderately similar to Kruppel-like factor 9 [Rattus norvegicus] [R.norvegicus], Kruppel-like factor 9, basic transcription element binding protein 1, expressed sequence AL022736	
3895	8641	NM_057211	C, DD, EE, SS	Kruppel-like factor 9, basic transcription element binding protein 1	ESTs, Moderately similar to Kruppel-like factor 9 [Rattus norvegicus] [R.norvegicus], Kruppel-like factor 9, basic transcription element binding protein 1, expressed sequence AL022736	

TABLE 3						
Seq ID	GLGC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster	Human Homologous Sequence Cluster
4158	794	U68168	B, G, M, GG, HH, NN, OO, FFF, GGG, III, JJ, General Core Tox Markers	kynureninase (L-kynurenine hydrolase)	Mus musculus, Similar to kynureninase (L-kynurenine hydrolase), clone MGC:30315 IMAGE:5136970, mRNA, complete cds, kynureninase (L-kynurenine hydrolase)	
3889	6613	NM_057186	A, U	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	ESTs, Highly similar to JC4879 3-hydroxyacyl-CoA dehydrogenase [H.sapiens], L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	
3255	17807	NM_017025	C, U, FF, HH, YY	lactate dehydrogenase 1, A chain, lactate dehydrogenase A	lactate dehydrogenase 1, A chain, lactate dehydrogenase A, lactate dehydrogenase A - like, lactate dehydrogenase C	
3285	24885	NM_017138	F, G, H, General Alternate	laminin receptor 1 (67kD, ribosomal protein SA)	EST, Weakly similar to 1405340A protein 40kD [M.musculus], EST, Weakly similar to RSP4 MOUSE 40S RIBOSOMAL PROTEIN SA [M.musculus], ESTs, Highly similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTs, Moderately similar to laminin-binding protein [H.sapiens], expressed sequence AL022858, laminin receptor 1 (67kD, ribosomal protein SA)	
3285	24886	NM_017138	F, G, H, VW	laminin receptor 1 (67kD, ribosomal protein SA)	EST, Weakly similar to 1405340A protein 40kD [M.musculus], EST, Weakly similar to RSP4 MOUSE 40S RIBOSOMAL PROTEIN SA [M.musculus], ESTs, Highly similar to A31233 ribosomal protein RS.40K, cytosolic [H.sapiens], ESTs, Moderately similar to laminin-binding protein [H.sapiens], expressed sequence AL022858, laminin receptor 1 (67kD, ribosomal protein SA)	

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TABLE 3					
Seq. ID	CLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
4219	670	X54096	XX, YY, CCC, PPP, QQQ	lecithin cholesterol acyltransferase, lecithin-cholesterol acyltransferase	EST, Weakly similar to LCAT MOUSE PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR [M.musculus], EST, Weakly similar to LCAT_HUMAN PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR [H.sapiens], ESTs, Moderately similar to LCAT_HUMAN PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR [H.sapiens], expressed sequence C87498, lecithin cholesterol acyltransferase, lecithin-cholesterol acyltransferase, lysophospholipase 3, lysophospholipase 3 (lysosomal phospholipase A2)
3460	10562	NM_022280	General Alternate	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase), lecithin-retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase), lecithin-retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)
3700	22321	NM_031832	O, BB, PP, VV, EEE, MMM, General Alternate	lectin, galactose binding, soluble 3, lectin, galactoside-binding, soluble, 3 (galectin 3)	EST, Weakly similar to A35820 galectin 3 [H.sapiens], galectin-related inter-fiber protein, lectin, galactoside-binding, soluble, 3 (galectin 3)
905	22283	AA945172	LL	leucine aminopeptidase 3	aminopeptidase-like 1, leucine aminopeptidase 3
2861	1351	D31874	RRR	LIM domain kinase 2, LIM motif-containing protein kinase 2	EST, Moderately similar to LIK2_RAT LIM domain kinase 2 (LIMK-2) [R.norvegicus], LIM domain kinase 2, LIM motif-containing protein kinase 2

TABLE 3						
Seq ID	CLCG ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44321-5038-01WO Document No. 1935323.1
845	1682	AA943555	SS	linker of T-cell receptor pathways, lymphocyte adaptor protein	ESTs, Weakly similar to linker of T-cell receptor pathways [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to ShcC [M.musculus], linker of T-cell receptor pathways, lymphocyte adaptor protein, src homology 2 domain-containing transforming protein C1, src homology 2 domain-containing transforming protein D	
3129	10260	NM_012732	T, GG, HH, LL	lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12, D3Wox13, D3Wox26 and D3Mgh25 [Rattus norvegicus] [R.norvegicus], lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	
3129	25563	NM_012732	DD, EE	lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	ESTs, Weakly similar to cholesterol esterase (pancreatic), see D3Wox12, D3Wox13, D3Wox26 and D3Mgh25 [Rattus norvegicus] [R.norvegicus], lipase A, lysosomal acid, cholesterol esterase (Wolman disease), lysosomal acid lipase 1	
2995	2505	M16235	B, F, G, NN, OO, GGG, LLL, General Core Tox Markers	lipase, hepatic	ESTs, Weakly similar to S15893 triacylglycerol lipase [M.musculus], lipase, hepatic	
3309	20529	NM_017208	A, D, E, V, W, BB, NN, EEE, III, JJJ, MMM	lipopolysaccharide binding protein	ESTs, Weakly similar to I56246 lipopolysaccharide binding protein - rat [R.norvegicus], ESTs, Weakly similar to LBP MOUSE LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR [M.musculus], bactericidal/permeability-increasing protein, cholesterol ester transfer protein, plasma, lipopolysaccharide binding protein, phospholipid transfer protein	
3091	18385	NM_012598	O, P, EEE, MMM	lipoprotein lipase	ESTs, Highly similar to JH0790 lipoprotein lipase (EC 3.1.1.34) precursor - rat [R.norvegicus], lipase, endothelial, lipoprotein lipase	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935828.1						
Seq. ID	CLIC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3457	10509	NM_022268	B, I, J, V, GGG, OOO, General Core Tox Markers	liver glycogen phosphorylase, phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	
3457	25814	NM_022268	I, FF, General Alternate	liver glycogen phosphorylase, phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	
4291	1541	Z50144	F	L-kynurenine/alpha-amino acid aminotransferase, kynurenine aminotransferase II		
4291	1542	Z50144	F, XX, YY	L-kynurenine/alpha-amino acid aminotransferase, kynurenine aminotransferase II		
317	21713	AA851637	D	Lutheran blood group (Auberg b antigen included)	Lutheran blood group (Auberg b antigen included)	

TABLE 3							Attorney Docket 44921-5033-01WO Document No. 1935828.1	
Seq ID	GLGC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3160	18770	NM_012857	EE	lysosomal membrane glycoprotein 1, lysosomal-associated membrane protein 1	CD68 antigen, ESTs, Weakly similar to LMP1_RAT LYOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 1 PRECURSOR (LAMP-1) (120 KD LYOSOMAL MEMBRANE GLYCOPROTEIN) (LGP-120) (CD107A) [R.norvegicus], chromosome 20 open reading frame 103, lysosomal membrane glycoprotein 1, lysosomal-associated membrane protein 1, lysosomal-associated membrane protein 3			
3265	6653	NM_017068	LL, XX, YY, LLL	lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	CD68 antigen, ESTs, Weakly similar to JC4317 lysosome-associated membrane protein 2 precursor, splice form B [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2			
3265	6654	NM_017068	LL	lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2	CD68 antigen, ESTs, Weakly similar to JC4317 lysosome-associated membrane protein 2 precursor, splice form B [H.sapiens], lysosomal membrane glycoprotein 2, lysosomal-associated membrane protein 2			
588	12118	AA892775	OO, VV, XX, YY	lysozyme, lysozyme (renal amyloidosis)	EST, Weakly similar to LYC1_RAT Lysozyme C, type 1 precursor (1,4-beta-N-acetylmuramidase C) [R.norvegicus], RIKEN cDNA 9530003J23 gene, lysozyme, lysozyme (renal amyloidosis), similar to lysozyme C-1 (1,4-beta-N-acylmuramidase C, EC 3.2.1.17)			
3367	15242	NM_019191	O, P, EE	MAD homolog 2 (Drosophila), MAD, mothers against decapentaplegic homolog 2 (Drosophila)	MAD homolog 2 (Drosophila), MAD, mothers against decapentaplegic homolog 2 (Drosophila)			
4155	871	U66479	BB, CC	MAD homolog 3 (Drosophila), MAD, mothers against decapentaplegic homolog 3 (Drosophila)	Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo sapiens mad protein homolog (hMAD-3) mRNA, MAD homolog 3 (Drosophila), MAD, mothers against decapentaplegic homolog 3 (Drosophila)			

TABLE 3							Attorney Docket 44921-5038-01W/O Document No. 1935323.1	
Seq ID	GLCC ID No.	GenBank Accession RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
1265	17353	A1008020	BBB, CCC	malic enzyme 1, NADP(+)-dependent, cytosolic, malic enzyme, supernatant				
3093	18746	NM_012600	BBB	malic enzyme 1, NADP(+)-dependent, cytosolic, malic enzyme, supernatant				
3093	18747	NM_012600	T, X, Y, BBB, LLL, RRR, SSS, UUU	malic enzyme 1, NADP(+)-dependent, cytosolic, malic enzyme, supernatant				
3093	18749	NM_012600	X, Y, BBB, LLL, RRR, SSS, UUU	malic enzyme 1, NADP(+)-dependent, cytosolic, malic enzyme, supernatant				
3304	24437	NM_017190	D	malignancy- associated protein, myelin-associated glycoprotein	CD33 antigen (gp67), ESTs, Weakly similar to MAG_RAT Myelin-associated glycoprotein precursor (L-MAG/S-MAG) (Brain neuron cytoplasmic protein 3) [R.norvegicus], Mus musculus sialic acid-binding lectin Siglec-F mRNA, complete cds, myelin-associated glycoprotein, sialic acid binding Ig-like lectin 5			
3513	24434	NM_022704	H, S, HH, FFF, GGG, General Core Tox Markers	mannose binding lectin, serum (C), mannose-binding lectin (protein C) 2, soluble (opsonic defect)	mannose binding lectin, serum (C), mannose-binding lectin (protein C) 2, soluble (opsonic defect)			

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	CLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
2965	395	L24374	SS	matrix metalloproteinase 7, matrix metalloproteinase 7 (matrilysin, uterine)				
3762	19322	NM_053409	GG	melanoma antigen, family D, 1	RIKEN cDNA 170056A17 gene, RIKEN cDNA 170080O16 gene, RIKEN cDNA 2410003J06 gene, RIKEN cDNA 3830417A13 gene, melanoma antigen, family D, 1, melanoma antigen, family L, 2			
3731	17933	NM_032615	U, BBB, CCC, RRR, SSS	membrane interacting protein of RGS16				
3731	17934	NM_032615	U, V, BBB, CCC	membrane interacting protein of RGS16				
3731	17935	NM_032615	RRR, SSS	membrane interacting protein of RGS16				
3982	15189	NM_138826	C, E, L, T, W, BB, DD, KKK, NNN	metallothionein 1, metallothionein 1A (functional)	EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to MT1_RAT METALLOTHIONEIN-1 (MT-1) [R.norvegicus], metallothionein 1, metallothionein 4, metallothionein IV			
3982	15190	NM_138826	C, E, L, T, DD, SS, WW, KKK, NNN	metallothionein 1, metallothionein 1A (functional)	EST, Moderately similar to Cd-7 Metallothionein-2 [H.sapiens], EST, Moderately similar to SMHU1E metallothionein 1E [H.sapiens], ESTs, Moderately similar to MT1_RAT METALLOTHIONEIN-1 (MT-1) [R.norvegicus], metallothionein 1, metallothionein 4, metallothionein IV			
3493	20762	NM_022588	YY	metastasis associated 1	ESTs, Highly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to metastasis associated 1 [Rattus norvegicus] [R.norvegicus], KIAA1266 protein, KIAA1610 protein, metastasis associated 1, metastasis associated 1-like 1, metastasis associated 3, metastasis-associated 1-like 1			
203	576	AA819118	C, YY	methionine adenosyltransferase I, alpha	Mus musculus, clone MGC:6545 IMAGE:2655444, mRNA, complete cds, expressed sequence A1046368, methionine adenosyltransferase I, alpha			

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	GLGG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
4205	575	X15734	F, L, T, RR, SS, WW, SSS, UUU	methionine adenosyltransferase I, alpha	Mus musculus, clone MGC:6545 IMAGE:2655444, mRNA, complete cds, expressed sequence A1046368, methionine adenosyltransferase I, alpha			
3483	8983	NM_022539	D	methionine aminopeptidase 2, methionyl aminopeptidase 2	ESTs, Moderately similar to AMP2 MOUSE METHIONINE AMINOPEPTIDASE 2 [M.musculus], methionine aminopeptidase 2, methionyl aminopeptidase 2			
3483	8984	NM_022539	B, K, GGG, HHH, PPP, QQQ, General Alternate	methionine aminopeptidase 2, methionyl aminopeptidase 2	ESTs, Moderately similar to AMP2 MOUSE METHIONINE AMINOPEPTIDASE 2 [M.musculus], methionine aminopeptidase 2, methionyl aminopeptidase 2			
3962	15017	NM_134349	M, S, DD, EE, NNN	microsomal glutathione S-transferase 1				
3146	17992	NM_012811	XX, YY	milk fat globule-EGF factor 8 protein	EGF-like repeats and discordin I-like domains 3, ESTs, Weakly similar to JC4915 ags protein precursor - rat [R.norvegicus], milk fat globule-EGF factor 8 protein, retinoschisis 1 homolog (human)			
3944	15542	NM_133539	G, H	mitochondrial ribosomal protein L17				
3944	15543	NM_133539	G, H	mitochondrial ribosomal protein L17				
3479	5666	NM_022529	D, JJ, KK	mitochondrial ribosomal protein L23				
3932	17564	NM_133283	I, J, DD, EE	mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase 2				

TABLE 3						Attorney Docket 44921-5038-01WO Document No. 1935828.1	
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
3932	21848	NM_133283	I, J, RRR, UUU	mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase 2			
3932	21849	NM_133283	U, RRR	mitogen activated protein kinase kinase 2, mitogen-activated protein kinase kinase 2			
3207	12371	NM_013055	C	mitogen activated protein kinase kinase 12, mitogen-activated protein kinase kinase 12	ESTs, Highly similar to A55318 serine/threonine protein kinase [M.musculus], Mus musculus, Similar to mitogen-activated protein kinase kinase 9, clone MGC:27778 IMAGE:3156324, mRNA, complete cds, RIKEN cDNA 913001915 gene, expressed sequence C81508, mitogen activated protein kinase kinase 11, mitogen activated protein kinase kinase 12, mitogen-activated protein kinase kinase 10, mitogen-activated protein kinase kinase 11, mitogen-activated protein kinase kinase 12, mitogen-activated protein kinase kinase 13, mitogen-activated protein kinase kinase 7		
3659	14956	NM_031622	C	mitogen-activated protein kinase 6	ESTs, Weakly similar to B40033 protein kinase (EC 2.7.1.37) ERK3 - rat [R.norvegicus], mitogen-activated protein kinase 4, mitogen-activated protein kinase 6		
3659	14957	NM_031622	C, TT	mitogen-activated protein kinase 6	ESTs, Weakly similar to B40033 protein kinase (EC 2.7.1.37) ERK3 - rat [R.norvegicus], mitogen-activated protein kinase 4, mitogen-activated protein kinase 6		
4095	58	U09870	W, General Alternate	Mitral valve prolapse, familial, major vault protein			
3972	12215	NM_138502	K, BBB	monoglyceride lipase	Homo sapiens cDNA: FLJ22330 fis, clone HRC05729, highly similar to AF131821 Homo sapiens clone 24877 mRNA sequence, monoglyceride lipase		

TABLE 3						
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 49241-5038-01WO Document No. 1935323.1
3751	14934	NM_053337	T, OO	Msx-interacting-zinc finger, Protein inhibitor of activated STAT X	DNA segment, Chr 11, Brigham & Women's Genetics 0280e expressed, Msx-interacting-zinc finger, Protein inhibitor of activated STAT X	
1220	15292	AF012714	Q, MM, TTT, General Alternate	multiple inositol polyphosphate histidine phosphatase 1, multiple inositol polyphosphate histidine phosphatase, 1		
1898	15291	A1111401	Q, SS, General Alternate	multiple inositol polyphosphate histidine phosphatase 1, multiple inositol polyphosphate histidine phosphatase, 1		
3666	17448	NM_031668	C, PPP, QQQ, General Alternate	MYB binding protein (P160) 1a		
2017	7253	A1169378	RR	myelin basic protein	ESTs, Highly similar to MBP_HUMAN Myelin basic protein (MBP) (Myelin A1 protein) (Myelin membrane encephalitogenic protein) [H.sapiens], myelin basic protein	
3126	22294	NM_012720	AA, SS	myelin-associated oligodendrocyte basic protein, myelin-associated oligodendrocytic basic protein	myelin-associated oligodendrocyte basic protein, myelin-associated oligodendrocytic basic protein	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1995828.1						
Seq ID	GLCG ID No.	Genbank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3094	2629	NM_012603	W	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)	myelocytomatosis oncogene, v-myc myelocytomatosis viral oncogene homolog (avian)	EST, Highly similar to MY1A_RAT Myosin IA (Myosin I alpha) (MML1a) (Myosin heavy chain myr 1) [R.norvegicus], EST, Weakly similar to MYOSIN I ALPHA [M.musculus], Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010010B23:myosin, heavy polypeptide-like (110kD), full insert sequence, myosin IB
3864	17653	NM_053986	C, SS, WW, SSS, UUU	myosin IB		
2929	1421	J04733	N, BBB, CCC, RRR	N-acylaminoacyl-peptide hydrolase, acylpeptide hydrolase	Mus musculus, clone IMAGE:4974221, mRNA, partial cds, N-acylaminoacyl-peptide hydrolase	
3247	1698	NM_017000	K, S, GG, HH, GGG	NAD(P)H dehydrogenase, quinone 1	ESTs, Weakly similar to A34162 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) - rat [R.norvegicus], NAD(P)H dehydrogenase, quinone 1, NAD(P)H dehydrogenase, quinone 2, NAD(P)H menadione oxidoreductase 2, dioxin inducible	
2090	4428	A1171362	CCC	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	
2471	3099	A1229680	RRR	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1955828.1						
Seq ID	GLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3375	20938	NM_019223	V, EE	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase), NADH dehydrogenase Fe-S protein 6	ESTs, Highly similar to NUMM MOUSE NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT [M.musculus], NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase)	
20	16901	AA799479	FF	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase)	
3644	18389	NM_031545	PP, UU, III	natriuretic peptide precursor B, natriuretic peptide precursor type B	EST, Moderately similar to ANFB MOUSE BRAIN NATRIURETIC PEPTIDE PRECURSOR [M.musculus], natriuretic peptide precursor B, natriuretic peptide precursor type B	
3095	1299	NM_012610	V	nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16)	Mus musculus, clone IMAGE:5097359, mRNA, partial cds, nerve growth factor receptor, nerve growth factor receptor (TNFR superfamily, member 16), p75-like apoptosis-inducing death domain protein PLAIDD	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1995828.1	
Seq. ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3902	16108	NM_080585	Z, AA	N-ethylmaleimide sensitive fusion protein attachment protein alpha, N-ethylmaleimide-sensitive fusion attachment protein, alpha	N-ethylmaleimide sensitive fusion protein attachment protein alpha, N-ethylmaleimide sensitive fusion protein attachment protein gamma, N-ethylmaleimide-sensitive factor attachment protein, alpha, N-ethylmaleimide-sensitive factor attachment protein, gamma			
3902	16109	NM_080585	RR, SS	N-ethylmaleimide sensitive fusion protein attachment protein alpha, N-ethylmaleimide-sensitive factor attachment protein, alpha	N-ethylmaleimide sensitive fusion protein attachment protein beta, N-ethylmaleimide sensitive fusion protein attachment protein gamma, N-ethylmaleimide-sensitive factor attachment protein, alpha, N-ethylmaleimide-sensitive factor attachment protein, gamma			
3452	20450	NM_022239	Z, AA, SS	neuromedin, neuromedin U	neuromedin, neuromedin U			
4269	570	X82445	BBB, CCC	nuclear distribution gene C homolog (A. nidulans), nuclear distribution gene C homolog (Aspergillus)	ESTs, Moderately similar to A55897 prolactin-induced T cell protein c15 - rat [R.norvegicus], KIAA1068 protein, Mus musculus, Similar to KIAA1068 protein, clone IMAGE:4236345, mRNA, partial cds, expressed sequence AL022907, nuclear distribution gene C homolog (A. nidulans), nuclear distribution gene C homolog (Aspergillus)			
3188	763	NM_012988	KK	nuclear factor I/A	nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)			
4273	764	X84210	F, HH, JJ, KK	nuclear factor I/A	nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)			
1209	17962	AB012230	General Alternate	nuclear factor I/B	Nuclear Factor I/A, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)			

TABLE 3						
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5038-01WO Document No. 1935823.1
1210	17963	AB012231	FFF, General Core Tox Markers, General Alternate	nuclear factor I/B	Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)	
2209	24763	AI176488	Y, LLL, General Core Tox Markers, General Alternate	nuclear factor I/B	Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)	
1211	24414	AB012234	D, SS	nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)	Nuclear Factor IA, nuclear factor I/A, nuclear factor I/B, nuclear factor I/C, nuclear factor I/X, nuclear factor I/X (CCAAT-binding transcription factor)	
4244	25089	X63594	I, J	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha		

TABLE 3						
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44924-5038-01WO Document No. 1935828.1
4244	25090	X63594	J	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha		
1221	1597	AF014503	W, MM, TTT	nuclear protein 1, p8 protein (candidate of metastasis 1)	EST; Weakly similar to P8_HUMAN P8 PROTEIN [H.sapiens], nuclear protein 1, p8 protein (candidate of metastasis 1)	
4099	1639	U11685	W, DD, EE, KKK, NNN, General Alternate	nuclear receptor subfamily 1, group H, member 3	EST; Moderately similar to NRH3_RAT Oxysterols receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan receptor LXR-alpha) (RLD-1) [R.norvegicus], EST, Weakly similar to I38975 nuclear orphan receptor LXR-alpha [H.sapiens], expressed sequence AU018371, nuclear receptor subfamily 1, group H, member 3	
3433	19712	NM_021745	A, B, General Core Tox Markers, General Alternate	nuclear receptor subfamily 1, group H, member 4	EST; Weakly similar to I38975 nuclear orphan receptor LXR-alpha [H.sapiens], ESTs, Moderately similar to JC4014 steroid hormone-nuclear receptor NER [H.sapiens], expressed sequence AI957360, nuclear receptor subfamily 1, group H, member 4	
1247	18731	AF093139	R	nuclear RNA export factor 1, nuclear RNA export factor 1 homolog (S. cerevisiae)		

TABLE 3						
Seq ID	CLGG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44924-5038-01WO Document No. 1935828.1
438	4339	AA875121	UU	nuclear transcription factor Y, gamma, nuclear transcription factor-Y gamma		
3648	16163	NM_031563	MM, TTT	nuclease sensitive element binding protein 1	ESTs, Highly similar to l39382 Y box-binding protein 1 - human [H.sapiens], ESTs, Moderately similar to PS0015 DNA-binding protein B [H.sapiens], RIKEN cDNA 1700102N10 gene, Y box protein 2, nuclease sensitive element binding protein 1	
3648	16164	NM_031563	RR, VV	nuclease sensitive element binding protein 1	ESTs, Highly similar to l39382 Y box-binding protein 1 - human [H.sapiens], ESTs, Moderately similar to PS0015 DNA-binding protein B [H.sapiens], RIKEN cDNA 1700102N10 gene, Y box protein 2, nuclease sensitive element binding protein 1	
3648	16165	NM_031563	D	nuclease sensitive element binding protein 1	ESTs, Highly similar to l39382 Y box-binding protein 1 - human [H.sapiens], ESTs, Moderately similar to PS0015 DNA-binding protein B [H.sapiens], RIKEN cDNA 1700102N10 gene, Y box protein 2, nuclease sensitive element binding protein 1	
3189	17393	NM_012992	D, JJ, HHH	nucleophosmin (nucleolar phosphoprotein B23, numatrin), nucleophosmin 1	ESTs, Highly similar to A32915 nucleophosmin [H.sapiens], nucleophosmin 1	
3189	17394	NM_012992	FFF, General Alternate	nucleophosmin (nucleolar phosphoprotein B23, numatrin), nucleophosmin 1	ESTs, Highly similar to A32915 nucleophosmin [H.sapiens], nucleophosmin 1	
4178	1401	U93692	ZZ, AAA	nucleoporin 88kD, preimplantation protein 2	nucleoporin 88kD, preimplantation protein 2	

TABLE 3						Attorney Docket 44921-5033-01WO Document No. 1935828.1	
Seq ID	CLCC ID No.	Genbank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
			General Core Tox Markers, General Alternate		ESTs, Highly similar to 2008109A set gene [Rattus norvegicus] [R.norvegicus], ESTs, Highly similar to SET_HUMAN SET PROTEIN [H.sapiens], SET translocation, SET translocation (myeloid leukemia-associated), nucleosome assembly protein 1-like 1		
1515	7665	AI030668		nucleosome assembly protein 1-like 1			
3579	1792	NM_030996	K, KKK	opioid receptor, sigma 1	opioid receptor, sigma 1, sigma receptor (SR31747 binding protein 1)		
3214	13282	NM_013078	WW, FFF, General Alternate	ornithine carbamoyltransferase, ornithine transcarbamylase	ornithine carbamoyltransferase, ornithine transcarbamylase		
3214	13283	NM_013078	A, B, NN, OO	ornithine carbamoyltransferase, ornithine transcarbamylase	ornithine carbamoyltransferase, ornithine transcarbamylase		
3096	23522	NM_012615	A	ornithine decarboxylase 1, ornithine decarboxylase, structural	ESTs, Highly similar to DCOR_MOUSE ORNITHINE DECARBOXYLASE [M.musculus], ESTs, Weakly similar to DCOR_MOUSE ORNITHINE DECARBOXYLASE [M.musculus], ESTs, Weakly similar to DCOR_HUMAN ORNITHINE DECARBOXYLASE [H.sapiens], ornithine decarboxylase 1, ornithine decarboxylase, structural, ornithine decarboxylase-like protein		
3096	23523	NM_012615	B, H, I, J	ornithine decarboxylase 1, ornithine decarboxylase, structural	ESTs, Highly similar to DCOR_MOUSE ORNITHINE DECARBOXYLASE [M.musculus], ESTs, Weakly similar to DCOR_MOUSE ORNITHINE DECARBOXYLASE [M.musculus], ESTs, Weakly similar to DCOR_HUMAN ORNITHINE DECARBOXYLASE [H.sapiens], ornithine decarboxylase 1, ornithine decarboxylase, structural, ornithine decarboxylase-like protein		
3492	21062	NM_022585	DD, EE, MM, UU, TTT	ornithine decarboxylase antizyme inhibitor	ESTs, Weakly similar to ODCI_MOUSE Ornithine decarboxylase antizyme inhibitor [M.musculus], ornithine decarboxylase antizyme inhibitor		

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935828.1						
Seq ID	GLC ID No	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3492	21063	NM_022585	C, MM, UU, TTT	ornithine decarboxylase antizyme inhibitor	ESTs, Weakly similar to ODCI_MOUSE Ornithine decarboxylase antizyme inhibitor [M.musculus], ornithine decarboxylase antizyme inhibitor	
3998	15134	NM_139081	E, K	ornithine decarboxylase antizyme, ornithine decarboxylase antizyme 1		
3998	25250	NM_139081	LL	ornithine decarboxylase antizyme, ornithine decarboxylase antizyme 1		
4181	412	V01216	D, E, BB, CC, III, JJJ	orosomucoid 1	orosomucoid 1, orosomucoid 2, orosomucoid 3	
3697	15840	NM_031817	WW	osteomodulin	osteoglycin, osteomodulin	
2883	1921	E01524	I, L, WW, OOO, General Alternate	P450 (cytochrome) oxidoreductase		
3651	1919	NM_031576	I, L, WW	P450 (cytochrome) oxidoreductase		
3651	1920	NM_031576	C, I, L, MM, WW, OOO, TTT, General Alternate	P450 (cytochrome) oxidoreductase		

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1935323.1	
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title			
3192	24263	NM_012999	BB, CC	paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	EST, Highly similar to I53282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6			
3192	24264	NM_012999	MM, TTT	paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6	EST, Highly similar to I53282 gene PACE4 protein - rat [R.norvegicus], RIKEN cDNA A930029K19 gene, paired basic amino acid cleaving system 4, proprotein convertase subtilisin/kexin type 6			
3403	18820	NM_019367	D, V	palmitoyl-protein thioesterase 2	palmitoyl-protein thioesterase 2			
1600	24374	A1045973	E	partner of RAC1 (arfaptin 2)	partner of RAC1 (arfaptin 2)			
37	1647	AA799575	G, H, II	peptidylglycine alpha-amidating monooxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monooxygenase			
133	1650	AA817825	II	peptidylglycine alpha-amidating monooxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monooxygenase			
465	1644	AA891068	G, II	peptidylglycine alpha-amidating monooxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monooxygenase			
1853	1649	A1103782	H	peptidylglycine alpha-amidating monooxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monooxygenase			
2411	1651	A1228068	F	peptidylglycine alpha-amidating monooxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monooxygenase			

TABLE 3						
Seq ID	GLCC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-6038-01WO Document No. 1995828.1
2642	1653	AI233806	F, G, II, UUU	peptidylglycine alpha-amidating monoxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monoxygenase	
2660	1654	AI234258	X, Y, II	peptidylglycine alpha-amidating monoxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monoxygenase	
2884	1641	E03428	BB, CC, PP, QQ, EEE, MMM, UUU	peptidylglycine alpha-amidating monoxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monoxygenase	
3193	1640	NM_013000	II, LLL, UUU	peptidylglycine alpha-amidating monoxygenase	ESTs, Weakly similar to AMD MOUSE PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR [M.musculus], peptidylglycine alpha-amidating monoxygenase	
3278	4391	NM_017101	II	peptidylprolyl isomerase A, peptidylprolyl isomerase A (cyclophilin A)	EST, Moderately similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Highly similar to CYPH MOUSE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [M.musculus], ESTs, Moderately similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Weakly similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to CYPH_RAT Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) (P31) [R.norvegicus], RIKEN cDNA 2510026K04 gene, expressed sequence AI256741, expressed sequence AW457192, peptidylprolyl isomerase A	

TABLE 3						Attorney Docket 44921-5038-01WO
						Document No. 1935323.1
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3278	4392	NM_017101	XX, YY	peptidylprolyl isomerase A, peptidylprolyl isomerase A (cyclophilin A)	EST, Moderately similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Highly similar to CYPH MOUSE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [M.musculus], ESTs, Moderately similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to A Chain A, Cyclophilin A [H.sapiens], ESTs, Weakly similar to A Chain A, Human Cyclophilin A Complexed With 2-Thr Cyclosporin [H.sapiens], ESTs, Weakly similar to CYPH_RAT Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) (P31) [R.norvegicus], RIKEN cDNA 2510026K04 gene, expressed sequence A1256741, expressed sequence AW457192, peptidylprolyl isomerase A	
3298	14498	NM_017169	EE	peroxiredoxin 2	Homo sapiens cDNA FLJ12333 fis, clone MAMMA1002198, highly similar to THIOREDOXIN PEROXIDASE 1, expressed sequence AL022839, peroxiredoxin 2	
3927	9268	NM_130756	U, LL, BBB, CCC, LLL, RRR, SSS, UUU	peroxisomal acyl-CoA thioesterase, peroxisomal acyl-CoA thioesterase 1	EST, Moderately similar to PTE1_MOUSE Peroxisomal acyl-coenzyme A thioester hydrolase 1 (Peroxisomal long-chain acyl-coA thioesterase 1) [M.musculus], peroxisomal acyl-CoA thioesterase, peroxisomal acyl-CoA thioesterase 1	
1212	22567	AB017544	W, DD, EE	peroxisomal biogenesis factor 14	peroxisomal biogenesis factor 14	
4253	405	X70223	O, P, FFF, General Alternate	peroxisomal membrane protein 2 (22kD), peroxisomal membrane protein 2, 22 kDa	ESTs, Weakly similar to MPV1 MOUSE MPV17 PROTEIN [M.musculus], MpV17 transgene, murine homolog, glomerulosclerosis, MpV17 transgene, kidney disease mutant, peroxisomal membrane protein 2, 22 kDa	
3098	6055	NM_012619	WW, LLL, RRR, SSS, UUU	phenylalanine hydroxylase	ESTs, Highly similar to WHHUF phenylalanine 4-monooxygenase [H.sapiens], phenylalanine hydroxylase	

TABLE 3					
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Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3336	23130	NM_017307	V, FF	phosphate cytidyltransferase 1, choline, alpha isoform	ESTs, Weakly similar to PM34_MOUSE PEROXISOMAL MEMBRANE PROTEIN PMP34 (34 KDA PEROXISOMAL MEMBRANE PROTEIN) (SOLUTE CARRIER FAMILY 25, MEMBER 17) [M.musculus], ESTs, Weakly similar to TXTP_HUMAN TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR [H.sapiens], ESTs, Weakly similar to TXTP_RAT Tricarboxylate transport protein, mitochondrial precursor (Citrate transport protein) (CTP) (Tricarboxylate carrier protein) [R.norvegicus], Mus musculus, Similar to hypothetical protein FLJ20551, clone MGC:18873 IMAGE:4235245, mRNA, complete cds, RIKEN cDNA 1300019P08 gene, expressed sequence AI194714, expressed sequence AW108044, ornithine transporter 2, solute carrier family 25 (mitochondrial carrier), member 18, solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21, uncoupling protein 2, mitochondrial
3315	15598	NM_017236	V	phosphatidylethanolamine binding protein, prostatic binding protein	Homo sapiens, clone MGC:22776 IMAGE:4700840, mRNA, complete cds, RIKEN cDNA 1700023A18 gene, RIKEN cDNA 1700081D17 gene, phosphatidylethanolamine binding protein, prostatic binding protein
3315	15599	NM_017236	I, J, GG	phosphatidylethanolamine binding protein, prostatic binding protein	Homo sapiens, clone MGC:22776 IMAGE:4700840, mRNA, complete cds, RIKEN cDNA 1700023A18 gene, RIKEN cDNA 1700081D17 gene, phosphatidylethanolamine binding protein, prostatic binding protein
3313	24598	NM_017231	T	phosphatidylinositol transfer protein, phosphatidylinositol transfer protein	EST, Weakly similar to PPI1_RAT PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA) [R.norvegicus], phosphatidylinositol transfer protein, phosphatidylinositol transfer protein, retinal degeneration B2 homolog (Drosophila)
4288	442	Z22867	Z, AA	phosphodiesterase 3B, cGMP-inhibited	ESTs, Highly similar to CN3B_MOUSE CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B [M.musculus], ESTs, Highly similar to CN3B RAT CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B [R.norvegicus], ESTs, Highly similar to CN3B_HUMAN CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE B [H.sapiens], expressed sequence AI847709, phosphodiesterase 3B, cGMP-inhibited

TABLE 3						Attorney Docket 44921-5038-01WO Document No. 1935328.1	
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
3219	24	NM_013101	Z, AA, RRR, SSS	phosphodiesterase 4A, cAMP specific, phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 duncce homolog, Drosophila)			
57	14250	AA799729	W	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 duncce homolog, Drosophila)	phosphodiesterase 4B, cAMP specific, phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 duncce homolog, Drosophila), phosphodiesterase 9A		
4113	1340	U25651	SS	phosphofructokinase, muscle	ESTs, Highly similar to phosphofructokinase, muscle; expressed sequence AI131669, isozyme [Mus musculus] [M.musculus], expressed sequence AI131669, phosphofructokinase, muscle		
3256	24861	NM_017033	T	phosphoglucosyltransferase 1, phosphoglucosyltransferase 2	ESTs, Highly similar to PMRT phosphoglucosyltransferase (EC 5.4.2.2) 1 - rat [R.norvegicus], ESTs, Highly similar to S62628 phosphoglucosyltransferase-related protein - mouse [M.musculus], ESTs, Moderately similar to S62628 phosphoglucosyltransferase-related protein - mouse [M.musculus], RIKEN cDNA 2610020G18 gene, phosphoglucosyltransferase 1		
3256	24862	NM_017033	HH, UU	phosphoglucosyltransferase 1, phosphoglucosyltransferase 2	ESTs, Highly similar to PMRT phosphoglucosyltransferase (EC 5.4.2.2) 1 - rat [R.norvegicus], ESTs, Highly similar to S62628 phosphoglucosyltransferase-related protein - mouse [M.musculus], ESTs, Moderately similar to S62628 phosphoglucosyltransferase-related protein - mouse [M.musculus], RIKEN cDNA 2610020G18 gene, phosphoglucosyltransferase 1		
3012	1312	M31788	I, J, LLL	phosphoglycerate kinase 1	ESTs, Highly similar to A33792 phosphoglycerate kinase (EC 2.7.2.3) - rat [R.norvegicus], phosphoglycerate kinase 1, phosphoglycerate kinase 2		

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1995828.1						
Seq ID	GLCG ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
			X, Y, FFF, GGG, General Core Tox Markers, General Alternate	phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	
2018	4091	AI169417		phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	
2437	4092	AI228723	K, DDD	phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	
2552	4093	AI232001	S, GGG, LLL	phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	
3743	4090	NM_053290	JJ, KK, GGG, HHH	phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	
3743	25499	NM_053290	G, H, X, Y	phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	ESTs, Highly similar to PMGB_HUMAN PHOSPHOGLYCERATE MUTASE, BRAIN FORM [H.sapiens], phosphoglycerate mutase 1, phosphoglycerate mutase 1 (brain)	
3844	11405	NM_053866	Q, R, PPP, QQQ	phospholipase A2, activating protein, phospholipase A2-activating protein	phospholipase A2, activating protein, phospholipase A2-activating protein	
4207	1893	X51529	NN, EEE, MMM	phospholipase A2, group IIA (platelets, synovial fluid)	phospholipase A2, group IIA (platelets, synovial fluid), phospholipase A2, group IIF	

TABLE 3: Human Homologous Sequence Cluster						
Seq ID	GLCG ID No.	GenBank Accession RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3370	20435	NM_019202	UUU	phospholipase A2, group IIC, phospholipase A2, group IIC (possible pseudogene)	Mus musculus, Similar to hypothetical gene LOC127733, clone MGC:32424 IMAGE:5041000, mRNA, complete cds, phospholipase A2, group IIC, phospholipase A2, group IIF, phospholipase A2, group V	
87	4832	AA800190	ZZ, AAA	phosphorylase, glycogen; brain	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; brain	
1304	4833	A1009178	E	phosphorylase, glycogen; brain	liver glycogen phosphorylase, muscle glycogen phosphorylase, phosphorylase, glycogen; brain	
3817	13368	NM_053742	T, PP, QQ	phosphatidylinositol transfer protein, beta	ESTs, Highly similar to PPI2_HUMAN PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM [H.sapiens], phosphatidylinositol transfer protein, beta	
3817	13369	NM_053742	C, UU, HHH, General Alternate	phosphatidylinositol transfer protein, beta	ESTs, Highly similar to PPI2_HUMAN PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM [H.sapiens], phosphatidylinositol transfer protein, beta	
3661	6554	NM_031640	V, II, RRR, General Core Tox Markers	plasma glutamate carboxypeptidase	plasma glutamate carboxypeptidase	
2578	19287	A1232379	LLL, UUU	platelet derived growth factor receptor, alpha polypeptide, platelet-derived growth factor receptor, alpha polypeptide	platelet derived growth factor receptor, alpha polypeptide, platelet-derived growth factor receptor, alpha polypeptide, platelet-derived growth factor receptor, beta polypeptide	

TABLE 3						
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-5088-01WO Document No. 1935828.1
				pleiotropic regulator 1 (PRL1 homolog, Arabidopsis).		
3435	20090	NM_021757	E, TT, ZZ, JJJ	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	WD repeat domain 12, f-box and WD-40 domain protein 4, katanin p80 (WD40-containing) subunit B 1, pleiotropic regulator 1 (PRL1 homolog, Arabidopsis), pleiotropic regulator 1, PRL1 homolog (Arabidopsis), transducin (beta)-like 2	
4096	1392	U10188	V	polo-like kinase (Drosophila), polo-like kinase homolog, (Drosophila)	Rattus norvegicus polo-like kinase isoform mRNA, partial cds, endoplasmic reticulum (ER) to nucleus signalling 1, polo-like kinase (Drosophila), polo-like kinase homolog, (Drosophila)	
2616	5778	A1233246	G, H	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	EST, Weakly similar to T42723 probable DNA-directed RNA polymerase (EC 2.7.7.6) I second largest chain - mouse [M.musculus], ESTs, Weakly similar to RNA polymerase I (127 kDa subunit) [Rattus norvegicus] [R.norvegicus], ESTs, Weakly similar to T42723 probable DNA-directed RNA polymerase (EC 2.7.7.6) I second largest chain - mouse [M.musculus], RIKEN cDNA 2700078H01 gene, RNA polymerase 1-2 (128 kDa subunit), RNA polymerase I (127 kDa subunit), polymerase (RNA) II (DNA directed) polypeptide B (140kD)	
3854	15857	NM_053948	ZZ, AAA	polymerase (RNA) II (DNA directed) polypeptide G	polymerase (RNA) II (DNA directed) polypeptide G	
3413	15911	NM_019907	ZZ, AAA	postsynaptic protein CR1PT, postsynaptic protein Crip1		
3277	15517	NM_017099	NN, OO	potassium inwardly-rectifying channel, subfamily J, member 8	potassium inwardly-rectifying channel, subfamily J, member 8	

TABLE 3							Attorney Docket 44921-5038-01WO Document No. 1995828.1
Seq ID	CLCG ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title		
3279	15776	NM_017108	SS	potassium voltage-gated channel, subfamily H (eag-related), member 3	RIKEN cDNA C030044P22 gene, expressed sequence AU019351, potassium voltage-gated channel, subfamily H (eag-related), member 3		
2677	2789	A1234949	MM, TTT	preimplantation protein 3	preimplantation protein 3		
4281	1620	X97374	D, Z, AA	prepronociceptin			
3363	20256	NM_019163	JJ, KK	presenilin 1, presenilin 1 (Alzheimer disease 3)	presenilin 1, presenilin 1 (Alzheimer disease 3)		
					ESTs, Weakly similar to Ser/Arg-related nuclear matrix protein; plenty-of-prolines-101; serine/arginine repetitive matrix protein 1 [Mus musculus] [M.musculus], Mus musculus, Similar to hypothetical protein MGC13125, clone MGC:38070 IMAGE:5252666, mRNA, complete cds, PRKC, apoptosis, WT1, regulator, expressed sequence A1480556, glucocorticoid-induced gene 1, serine/arginine repetitive matrix 1		
3737	23895	NM_033485	A, B, HHH	PRKC, apoptosis, WT1, regulator	EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PCO1_RAT Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type 1 procollagen C-proteinase enhancer protein) [R.norvegicus], expressed sequence A1043106, membrane frizzled-related protein, procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhancer 2, procollagen C-proteinase enhancer protein		
3377	15503	NM_019237	NN, EEE, MMM	procollagen C-endopeptidase enhancer, procollagen C-proteinase enhancer protein			

TABLE 3						
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-6038-01WO Document No. 1935828.1
3377	15504	NM_019237	NN	procollagen C-endopeptidase enhancer, procollagen C-proteinase enhancer protein	EST, Weakly similar to PCO1_HUMAN PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR [H.sapiens], ESTs, Weakly similar to PCO1_RAT Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type 1 procollagen C-proteinase enhancer protein) [R.norvegicus], expressed sequence A1043106, membrane frizzled-related protein, procollagen C-endopeptidase enhancer, procollagen C-endopeptidase enhancer 2, procollagen C-proteinase enhancer protein	
3191	19391	NM_012998	U, FF, RRR	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55), prolyl 4-hydroxylase, beta polypeptide		
3191	19392	NM_012998	D, BB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55), prolyl 4-hydroxylase, beta polypeptide		

TABLE 3					
Attorney Docket 44921-5068-01WO Document No. 1935823.1					
Seq ID	GLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
				collagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55), prol 4-hydroxylase, beta polypeptide	
3191	19393	NM_012998	FF		
3406	20298	NM_019374	O, P, BB, CC	prodynorphin	
3437	17936	NM_021766	Y	progesterone receptor membrane component 1	Homo sapiens, clone MGC:32124 IMAGE:4877960, mRNA, complete cds, RIKEN cDNA 4631434O19 gene, progesterone receptor membrane component 1
3040	21670	M80601	R	programmed cell death 2	ESTs, Weakly similar to A41257 apoptosis protein RP-8 - rat (fragment) [R.norvegicus], RIKEN cDNA 6030457N17 gene, programmed cell death 2
2296	5459	A1178246	RR	programmed cell death 6 interacting protein	EST, Moderately similar to T14756 hypothetical protein DKFZp564F0923.1 [H.sapiens], EST, Weakly similar to proline rich protein 2 [Mus musculus] [M.musculus], EST, Weakly similar to PRP4_HUMAN SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR [H.sapiens], ESTs, Weakly similar to proline rich protein 2 [Mus musculus] [M.musculus], ESTs, Weakly similar to T14355 protein-tyrosine-phosphatase [R.norvegicus], expressed sequence A4408880, expressed sequence A1462446, proline rich protein 2, proline-rich protein BstNI subfamily 3, proline-rich protein BstNI subfamily 4, protein tyrosine phosphatase TD14, protein tyrosine phosphatase, non-receptor type 23

TABLE 3						
Attorney Docket 44921-5033-01WO Document No. 1935823.1						
Seq ID	CLIC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3708	15601	NM_031851	U, LL, RR, SS, BBB, CCC, LLL, RRR, SSS	prohibitin	B-cell receptor-associated protein 37, EST, Moderately similar to PHB MOUSE PROHIBITIN (B-CELL RECEPTOR ASSOCIATED PROTEIN 32) (BAP_32) [R.norvegicus], ESTs, Moderately similar to PHB MOUSE PROHIBITIN [M.musculus], Homo sapiens, clone MGC:20874 IMAGE:4547239, mRNA, complete cds, hypothetical protein MGC13071, prohibitin, repressor of estrogen receptor activity	
2638	22866	A1233754	E, HH	prolactin regulatory element binding	ESTs, Highly similar to PREB_RAT Prolactin regulatory element-binding protein [R.norvegicus], Homo sapiens cDNA FLJ11114 fis, clone PLACE1005951, Homo sapiens cDNA FLJ13343 fis, clone OVARC1001987, highly similar to Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, prolactin regulatory element binding	
3463	11454	NM_022381	VW	proliferating cell nuclear antigen	proliferating cell nuclear antigen	
3463	11455	NM_022381	VW, General Alternate	proliferating cell nuclear antigen	proliferating cell nuclear antigen	
3196	23543	NM_013013	V, UU	prosaposin, prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)		
3196	23544	NM_013013	MM, TTT	prosaposin, prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)		

TABLE 3						Attorney Docket 44921-5038-01WO Document No. 1935823.1
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
2872	1125	D82071	OOO	prostaglandin D2 synthase 2, hematopoietic, prostaglandin D2 synthase, hematopoietic	prostaglandin D2 synthase 2, hematopoietic, prostaglandin D2 synthase, hematopoietic	
3380	21109	NM_019243	PP, QQ, BBB, CCC	prostaglandin F2 receptor negative regulator	RIKEN cDNA 4833439O17 gene, immunoglobulin superfamily, member 2, immunoglobulin superfamily, member 3, immunoglobulin superfamily, member 8, prostaglandin F2 receptor negative regulator	
3717	15469	NM_031978	Q, R	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1, proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	
3320	15224	NM_017264	N, LL	proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	proteasome (prosome, macropain) 28 subunit, 3, proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha), proteasome (prosome, macropain) activator subunit 3 (PA28 gamma: Ki)	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1995828.1						
Seq. ID	GLGC ID No.	GenBank Accor. RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3320	15225	NM_017264	N	proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	proteasome (prosome, macropain) 28 subunit, 3, proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha), proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	
3320	15227	NM_017264	HH	proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	proteasome (prosome, macropain) 28 subunit, 3, proteasome (prosome, macropain) 28 subunit, alpha, proteasome (prosome, macropain) activator subunit 1 (PA28 alpha), proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	
3318	18750	NM_017257	II, EEE, MMM	proteasome (prosome, macropain) 28 subunit, beta, proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	expressed sequence AA589371, expressed sequence A1788882, proteasome (prosome, macropain) 28 subunit, beta, proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	

TABLE 3						
Attorney Docket 44921-5038-01WO Document No. 1935828.1						
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3323	15141	NM_017278	A, D, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1	proteasome (prosome, macropain) subunit, alpha type 1, proteasome (prosome, macropain) subunit, alpha type, 1	
3324	5747	NM_017279	D, General Alternate	proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	RIKEN cDNA 5430437J10 gene, proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	
3324	5748	NM_017279	X, Y	proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	RIKEN cDNA 5430437J10 gene, proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	

TABLE 3						
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-50338-01WO Document No. 1935323.1
3324	5749	NM_017279	D, LL, YY, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	RIKEN cDNA 5430437J10 gene, proteasome (prosome, macropain) subunit, alpha type 2, proteasome (prosome, macropain) subunit, alpha type, 2	
260	18673	AA849028	DDD	proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3	EST, Weakly similar to SNHUC8 multicatalytic endopeptidase complex [H.sapiens], ESTs, Highly similar to PRC8 MOUSE PROTEASOME COMPONENT C8 [M.musculus], ESTs, Weakly similar to PRC8 MOUSE PROTEASOME COMPONENT C8 [M.musculus], proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3	
3325	3987	NM_017280	GGG, HHH	proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3	EST, Weakly similar to SNHUC8 multicatalytic endopeptidase complex [H.sapiens], ESTs, Highly similar to PRC8 MOUSE PROTEASOME COMPONENT C8 [M.musculus], ESTs, Weakly similar to PRC8 MOUSE PROTEASOME COMPONENT C8 [M.musculus], proteasome (prosome, macropain) subunit, alpha type 3, proteasome (prosome, macropain) subunit, alpha type, 3	

TABLE 3					
Attorney Docket 44921-5038-01WO Document No. 1935823.1					
Seq ID	GLGC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3326	1447	NM_017281	A, BBB, CCC, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 4, proteasome (prosome, macropain) subunit, alpha type, 4	EST, Moderately similar to PRC9_HUMAN PROTEASOME COMPONENT C9 [H.sapiens], proteasome (prosome, macropain) subunit, alpha type 4, proteasome (prosome, macropain) subunit, alpha type, 4
2021	3256	A169479	H, K, LLL, SSS, UUU	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type, 5	
3327	3253	NM_017282	ZZ, AAA	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type, 5	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type, 5

TABLE 3						
Attorney Docket 44924-5038-01WO Document No. 1935828.1						
Seq ID	CLCC ID No.	GenBank Accor RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3327	3254	NM_017282	TT, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type 5	proteasome (prosome, macropain) subunit, alpha type 5, proteasome (prosome, macropain) subunit, alpha type 5	
3328	15535	NM_017283	S, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type 6	ESTs, Highly similar to S30274 multicatalytic endopeptidase complex [H.sapiens], ESTs, Weakly similar to JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46) [R.norvegicus], proteasome (prosome, macropain) subunit, alpha type 6	
3328	15538	NM_017283	NNN	proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type 6, proteasome (prosome, macropain) subunit, alpha type 6	ESTs, Highly similar to S30274 multicatalytic endopeptidase complex [H.sapiens], ESTs, Weakly similar to JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46) [R.norvegicus], proteasome (prosome, macropain) subunit, alpha type 6	

TABLE 3						
Seq ID	CLC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	Attorney Docket 44921-6038-01WO Document No. 1935828.1
2860	9029	D30804	A, B, RR, WW, SSS	proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7	EST, Highly similar to PSA7_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 7 (PROTEASOME SUBUNIT RC6-1) (PROTEASOME SUBUNIT XAPC7) [H.sapiens], EST, Highly similar to S60038 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha chain RC6-1 - rat [R.norvegicus], Homo sapiens, similar to Proteasome subunit alpha type 7 (Proteasome subunit RC6-1), clone MGC:26605 IMAGE:4829939, mRNA, complete cds, RIKEN cDNA 2410072D24 gene, proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7	
2860	25281	D30804	G, H, K, X, Y, LLL, SSS, UUU	proteasome (prosome, macropain) subunit, alpha type 7, proteasome (prosome, macropain) subunit, alpha type, 7		
3329	8956	NM_017284	PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 2, proteasome (prosome, macropain) subunit, beta type, 2		

TABLE 3					
Seq ID	CLCC ID No.	GenBank Acc or RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title
3329	8957	NM_017284	PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 2, proteasome	proteasome (prosome, macropain) subunit, beta type 2, proteasome (prosome, macropain) subunit, beta type, 2
3330	12523	NM_017285	G, H, PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 3, proteasome	EST, Moderately similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus], ESTs, Weakly similar to proteasome (prosome, macropain) subunit, beta type, 3 [Mus musculus] [M.musculus], ESTs, Weakly similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus], proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain) subunit, beta type, 3
3330	12524	NM_017285	G, H, S, X, Y, GGG, PPP, QQQ	proteasome (prosome, macropain) subunit, beta type 3, proteasome	EST, Moderately similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus], ESTs, Weakly similar to proteasome (prosome, macropain) subunit, beta type, 3 [Mus musculus] [M.musculus], ESTs, Weakly similar to S40468 proteasome subunit RC10-li - rat [R.norvegicus], proteasome (prosome, macropain) subunit, beta type 3, proteasome (prosome, macropain) subunit, beta type, 3

TABLE 3						
Attorney Docket 44924-5038-01WO Document No. 1995328.1						
Seq ID	GLCC ID No.	Genbank Accession RefSeq ID	Model Code	Human Homologous Known Gene Name	Human Homologous Sequence Cluster Title	
3660	20940	NM_031629	G, H, X, Y, SSS	proteasome (prosome, macropain) subunit, beta type 4, proteasome (prosome, macropain) subunit, beta type 4	proteasome (prosome, macropain) subunit, beta type 4, proteasome (prosome, macropain) subunit, beta type 4	
3660	20942	NM_031629	UUU	proteasome (prosome, macropain) subunit, beta type 4, proteasome (prosome, macropain) subunit, beta type 4	proteasome (prosome, macropain) subunit, beta type 4, proteasome (prosome, macropain) subunit, beta type 4	
2867	9135	D45247	N, RRR	proteasome (prosome, macropain) subunit, beta type 5, proteasome (prosome, macropain) subunit, beta type 5	EST, Moderately similar to PSB5_RAT Proteasome subunit beta type 5 precursor (Proteasome epsilon chain) (Macropain epsilon chain) (Multicatalytic endopeptidase complex epsilon chain) (Proteasome subunit X) (Proteasome chain 6) [R. norvegicus], RIKEN cDNA 5830406J20 gene, proteasome (prosome, macropain) subunit, beta type 5, proteasome (prosome, macropain) subunit, beta type 5	

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